Mitochondrial dysfunction in Neurodegenerative diseases

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List of Abbreviations

AD—Alzheimer’s disease
Aβ—β-amyloid peptide
ALS—Amyotrophic lateral sclerosis
APP—Amyloid precursor protein
ATP—Adenosine triphosphate
COX2—Cytochrome c oxidase 2
Cyt c—Cytochrome c
DA—Dopaminergic
Drp1—Dynamin related-protein 1
ERRα—Estrogen related receptor α
Fis1—Fission 1
FUS/TLS—FUered/Translocated in LipoSarcoma
HD—Huntington’s disease
htt—huntingtin
MBP—Myelin basic protein
Mfn1—Mitofusin 1
Mfn2—Mitofusin 2
MSNs—Medium spiny neurons
mtDNA—Mitochondrial DNA
MPTP—1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine
nDNA—Nuclear DNA
NFTs—Neurofibrillary tangles
OXPHOS—Oxidative phosphorylation
NRF-1, NRF-2—Nuclear respiratory factor 1, 2
3-NP—3-nitropropionic acid
OPA1—Optic atrophy 1
PARIS—Parkin-interacting substrate
PD—Parkinson’s disease
PGC-1α—Peroxisome proliferator-activated receptor-γ coactivator-1α
PPAR—Peroxisome proliferator-activated receptor
PINK1—PTEN-induced putative kinase 1
ROS—Reactive oxygen species
SN—Substantia nigra
SOD2—Superoxide dismutase 2
TCA—Tricarboxylic acid cycle
TDP-43—TAR DNA-binding protein 43
Tfam—Mitochondrial transcription factor A
VCP—Valosin-containing protein
VTA—Ventral tegmental area
Abstract

Neurodegenerative diseases are a large group of disabling disorders of the nervous system, characterized by the relative selective death of neuronal subtypes. In most cases, there is overwhelming evidence of impaired mitochondrial function as a causative factor in these diseases. More recently, evidence has emerged for impaired mitochondrial dynamics (shape, size, fission-fusion, distribution, movement etc.) in neurodegenerative diseases such as Parkinson’s disease (PD), Huntington’s disease (HD), Amyotrophic lateral sclerosis (ALS) and Alzheimer’s disease (AD). Here we provide a concise overview of the major findings in recent years highlighting the importance of healthy mitochondria for a healthy neuron.
1. Functions of mitochondria

Mitochondria, aptly termed “powerhouses of the cell”, are responsible for production of most of the cell’s “energy currency”, in the form of adenosine triphosphate (ATP). ATP is the end product of a series of pathways involving oxidation of substrates, mainly carbohydrates and fat; in cytosol (glycolysis) and in mitochondria (pyruvate decarboxylation, tricarboxylic acid cycle (TCA or Krebs cycle) and oxidative phosphorylation (OXPHOS/respiratory chain complex)). The respiratory chain complex consists of 4 distinct multi-subunit complexes (I-IV) and 2 electron carriers, that generate a proton gradient across the mitochondrial inner membrane, which in turn drives ATP synthase (complex V), to generate ATP. Mitochondria are also the seat of many of the cell’s housekeeping functions, including the biosynthesis of amino acids and steroids, beta-oxidation of fatty acids, maintaining cytosolic calcium homeostasis, buffering calcium fluctuations, and production and modulation of reactive oxygen species (ROS). Mitochondria also play a central role in apoptosis (Davis and Williams, 2012). Considering the intense energy demands and limited regenerative capacity of neurons, improper functioning of mitochondria can have devastating effects on neuronal survival. There is ample evidence of impaired mitochondrial function as a cause rather than consequence of neurodegeneration.

2. Mitochondrial dynamics

Mitochondria are dynamic organelles that are transported on cytoskeletal proteins (mitochondrial trafficking), they fuse and divide (fusion- mediated by OPA1, Mfn1, and Mfn2, and fission- mediated by the proteins Fis1 and Drp1), fragment, swell, extend and are recycled (mitophagy or vesicle formation) constantly and in a regulated fashion. Unbalanced fusion leads
to mitochondrial elongation, and unbalanced fission leads to excessive mitochondrial fragmentation and small mitochondria; both of which impair the function of mitochondria. It has been shown that exchange of mitochondrial contents is important for mitochondrial function as well as organelle distribution in neurons. Mitochondrial fusion, in particular that mediated by Mfn2, is required for proper development and maintenance of the cerebellum (Chen et al., 2007). Mutations in the Mfn2 gene cause the neurodegenerative disease Charcot-Marie-Tooth type 2A and mutations in OPA1 cause dominantly inherited optic atrophy. There is now increasing evidence of altered mitochondrial trafficking and fusion-fission dynamics in Alzheimer’s disease (AD), Parkinson’s disease (PD), Huntington’s disease (HD) and Amyotrophic lateral sclerosis (ALS).

3. Mitochondrial dysfunction, altered mitochondrial dynamics and neurodegeneration

Alzheimer’s disease (AD) is defined by progressive impairments in memory and cognition and by the presence of extracellular neuritic plaques and intracellular neurofibrillary tangles (NFTs). β-amyloid peptide (Aβ) is the major component of the plaque, while the tangles are composed of hyperphosphorylated tau proteins. The molecular events leading to the development of sporadic late-onset AD have not been defined. Advanced age is the greatest risk factor for AD, and glucose/energy metabolism is diminished in AD. It has been proposed that in sporadic AD, mitochondrial dysfunction is the primary event that causes Aβ deposition, synaptic degeneration, and formation of NFTs (Swerdlow et al., 2010). Energy deficiency is a fundamental characteristic feature of both AD brains, as well as peripheral cells derived from AD patients (Gibson et al., 1998; Manczak et al., 2004; Reviewed in Beal, 2005). Activities of the
three key TCA enzyme complexes, pyruvate dehydrogenase, isocitrate dehydrogenase, and α-ketoglutarate dehydrogenase, are impaired in postmortem AD brain and fibroblasts from AD patients (Bubber et al., 2005). Reduced OXPHOS complex I, III and IV activities were reported in platelets and lymphocytes from AD patients and in postmortem brain tissue (Kish et al., 1992; Bosetti et al., 2002; Summarized in Table 1). Several studies have reported impaired mitochondrial dynamics that involve the abnormal expression of Drp1 in postmortem brains from AD patients, AD mouse models, and APP cell lines (Reviewed in Reddy et al., 2011, Cho et al., 2009). There is also impaired mitochondrial biogenesis (Sheng et al., 2012).

*Parkinson’s disease (PD)*, is the second most common neurodegenerative disorder, after AD. Clinically, PD is characterized by the triad of resting tremor, bradykinesia and rigidity. These symptoms are considered to be a direct consequence of neurodegeneration and loss of dopaminergic neurons. Pathologically, the hallmark feature of PD is loss of pigmented dopaminergic neurons in the substantia nigra and the presence of abnormal protein aggregates called Lewy bodies, which are cytoplasmic eosinophilic inclusions composed of the presynaptic protein α-synuclein. Over the last several decades, evidence has accumulated that mitochondrial dysfunction is strongly associated with PD. A mild deficiency in mitochondrial electron transport chain NADH dehydrogenase (Complex I) activity was first found in the substantia nigra of patients with PD, followed by studies identifying a similar Complex I deficit in platelets, lymphocytes, and, less consistently, in muscle tissue from PD patients (Reviewed in Beal, 2007). Consistent with this, inhibitors of OXPHOS complex I, such as rotenone and 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP), in animal models, produce
neuropathologic and behavioral symptoms similar to human PD. A number of proteins that are genetically linked to familial PD, PTEN-induced putative kinase 1 (PINK1), DJ-1, α-synuclein, leucine-rich repeat kinase 2, and parkin, are either mitochondrial proteins or are associated with mitochondria (Table 2). There is evidence to suggest that parkin and PINK1 have a direct role in the cell’s mitochondrial quality control pathways—identifying impaired mitochondria with reduced membrane potential—and selectively eliminating them from the mitochondrial network by mitophagy. This implicates a failure of mitophagy as playing a role in the pathogenesis of PD (Narendra and Youle, 2011). Moreover, there is evidence for a direct involvement of PINK1 and parkin in abnormal mitochondrial dynamics in fly, rat and mouse models of PD (Reviewed in Reddy et al., 2011; Wang et al., 2011).

The “MitoPark” mice are an excellent example of the “mitochondrial hypothesis” of PD. In MitoPark mice, mitochondrial function is selectively disrupted in dopaminergic (DA) neurons by elimination of the mitochondrial transcription factor A (Tfam) gene (Ekstrand et al., 2007). The Tfam gene is encoded in the nuclear genome, and the Tfam protein is subsequently imported into mitochondria, where it acts as a DNA binding protein, essential for both transcription and maintenance of mitochondrial DNA (mtDNA) in mammals: It stabilizes mtDNA, regulates mtDNA copy number in vivo and is essential for mitochondrial biogenesis (Larsson et al., 1998). The MitoPark mice survive to adulthood and then slowly develop a Parkinsonian phenotype (Ekstrand et al., 2007; Galter et al., 2010). Furthermore, cellular changes similar to those seen in idiopathic PD are observed, such as intracellular inclusions in DA neurons, degeneration of DA
pathways, and loss of striatal dopamine. Also similar to PD, the SN pars compacta DA neurons of MitoPark mice, degenerate before those in the ventral tegmental area (VTA).

_Huntington’s disease (HD),_ is a dominantly inherited progressive neurodegenerative disease, caused by an abnormal CAG repeat expansion in the huntingtin (htt) gene. The disease is characterized by progressive motor impairment, personality changes, psychiatric illness and gradual intellectual decline. Pathologically, there is a preferential and progressive loss of the medium spiny neurons (MSNs) in the striatum, as well as cortical atrophy, and degeneration of other brain regions later in the disease. There is extensive evidence for bioenergetic deficits and mitochondrial dysfunction in HD: such as a pronounced weight loss despite sustained caloric intake; nuclear magnetic resonance spectroscopy showing increased lactate in the cerebral cortex and basal ganglia; decreased activities of OXPHOS complexes II and III, and reduced aconitase activity in the basal ganglia; abnormal mitochondrial membrane depolarization in patient lymphoblasts; abnormal ultrastructure of mitochondria in cortical biopsies obtained from patients with both juvenile and adult-onset HD; and pathologic grade dependent reductions in numbers of mitochondria in HD postmortem brain tissue; and in striatal cells from mutant htt-knock-in mice: both mitochondrial respiration and ATP production are significantly impaired (Reviewed in Browne and Beal, 2004; Table 1). We showed that the phenotypic and neuropathologic features of HD can be modeled in rodents and primates, with the mitochondrial toxin 3-nitropropionic acid (3-NP) (Beal et al., 1993). We and others have shown impaired brain creatine kinase activity and significant alterations in levels of high-energy phosphate intermediates in transgenic mouse models of HD (Zhang et al., 2011; Mochel et al.,
We also found a reduction in numbers and size of mitochondria, identified by a reduction in immunohistochemical markers for COX2, SOD2 and cytochrome c (Cyt c), that worsened with increasing disease severity (Kim et al., 2010). In addition, both the Tfam—a regulator of mtDNA transcription and replication, and peroxisome proliferator-activated receptor (PPAR)-γ coactivator-1α (PGC-1α)—a key transcriptional regulator of energy metabolism and mitochondrial biogenesis, are significantly reduced as disease severity increases. Abnormalities in mitochondrial dynamics were observed: Drp1 was found to be significantly increased and Mfn1 was significantly decreased (Kim et al., 2010). In addition, a direct interaction of mutant htt with mitochondria or with various protein complexes has been proposed to play an important role in disease pathogenesis, by regulating mitochondrial fission-fusion events, and mitochondrial trafficking along axons and dendrites (Reviewed in Bossy-Wetzel et al., 2008; Reddy et al., 2009; Johri et al., 2011a; Table 2).

Amyotrophic lateral sclerosis (ALS) is a progressive neurodegenerative disease that targets motor neurons in the brain and spinal cord, resulting in muscle weakness, atrophy, and eventual death. Although there have been extensive research efforts investigating the pathogenesis of ALS, its etiology is still largely unknown. In about 20% of the familial ALS cases, the disease is associated with one or more mutations in the gene that encodes copper–zinc superoxide dismutase (SOD1). Dominant mutations in two DNA/RNA binding proteins, TDP-43 and FUS/TLS, are also reported and account for ~5% and 4% of ALS cases respectively (Da Cruz and Cleveland, 2011). Mutations in the valosin-containing protein (VCP, also known as transitional endoplasmic reticulum ATPase) gene were recently reported to be the cause of 1%–
2% of familial ALS cases and they have effects on regulation of mitochondrial calcium. The ultimate cause of neuronal death and the debilitating phenotypes in ALS is currently unknown; however, several studies have reported mitochondrial damage and dysfunction in human ALS patients and in SOD1 mutant transgenic mice (Reviewed in Beal, 2005). Furthermore, degenerating mitochondria in the perinuclear region have been reported in ALS transgenic mice with TDP43 or FUS mutations. Mitochondrial abnormalities (e.g., swelling, deformed cristae, defects in respiratory chain activity, and a decrease in mtDNA copy number) are amongst the earliest signs of disease onset in the transgenic mouse models with SOD1 mutations. Disruption of axonal transport was shown in both ALS patients, and in mutant SOD1 transgenic mice (Reviewed in Magrane and Manfredi, 2009). A proportion of SOD1 mutant protein is misfolded onto the cytoplasmic surface of mitochondria, and the axonal mitochondria of motor neurons are the primary in vivo targets for misfolded SOD1 (Vande Velde et al., 2011). Mutant SOD1 alters axonal mitochondrial morphology and distribution, with dismutase active SOD1 causing mitochondrial clustering at the proximal side of Schmidt-Lanterman incisures within motor axons, and dismutase inactive SOD1 producing aberrantly elongated axonal mitochondria beginning pre-symptomatically and increasing in severity as the disease progresses. Somal mitochondria are altered by mutant SOD1, with loss of the characteristic cylindrical, networked morphology and its replacement by a less elongated, more spherical shape (Vande Velde et al., 2011). Recently, Magrane et al. (2012) showed that mutant SOD1 motor neurons have impaired mitochondrial fusion in both axons and in cell bodies. There is selective impairment of retrograde axonal transport, smaller mitochondrial size, decreased mitochondrial density, and defective mitochondrial membrane potential. Furthermore, mis-localization of mitochondria at
synapses among motor neurons, in vitro, correlates with abnormal synaptic number, structure, and function (Magrane et al., 2012). Expressing mutant SOD1 confined to mitochondria is sufficient to produce loss of motor neurons and an ALS phenotype (Igoudjil et al., 2011).

4. Mitochondrial DNA mutations and neurodegeneration

Mitochondria have their own DNA (mtDNA) that encodes 13 of the 92 polypeptides of the OXPHOS system, the remaining structural polypeptides and assembly factors are encoded by nuclear DNA (nDNA). Mutations in either mtDNA or nDNA, resulting in OXPHOS dysfunction, are particularly known to affect tissues with high energy demands such as the central nervous system, skeletal muscle or heart. Mitochondria are thought to contribute to aging through the accumulation of mtDNA mutations and net production of reactive oxygen species (ROS). Mitochondrial DNA mutations, mitochondrial abnormalities and mitochondrial respiratory chain deficient cells, are also present in age-related neurodegenerative diseases such as PD and AD (De Coo et al., 1999; Coskun et al., 2004; Smigrodzki et al., 2004; Parker and Parks, 2005; Bender et al., 2006, 2008; Reeve et al., 2008). The types of mtDNA deletions in the substantia nigra neurons from patients with PD and age-matched controls were found to be similar to those which occur in patients with Kearns-Sayre or Twinkle or multiple-deletion disorder (Reeve et al., 2008).

5. PGC-1α in mitochondrial dysfunction and neurodegeneration

Peroxisome proliferator-activated receptor (PPAR)-γ coactivator (PGC)-1α is a transcriptional coactivator that interacts with a broad range of transcription factors involved in a wide variety
of biological processes and/or responses including mitochondrial biogenesis, OXPHOS, antioxidant defense, adaptive thermogenesis, glucose/fatty acid metabolism, fiber type switching in skeletal muscle, and heart development (Puigserver and Spiegelman, 2003; Liang and Ward, 2006; St-Pierre et al., 2006). PGC-1α does not bind to DNA directly, but forms heteromeric complexes with transcription factors, including nuclear respiratory factors, NRF-1 and NRF-2, and the nuclear receptors, PPARα, PPARδ, PPARγ, estrogen related receptor α (ERRα) (Lin et al., 2005). These transcription factors, in turn, regulate the expression of many nuclear-encoded mitochondrial genes, such as Cyt c, complexes I–V and Tfam (Kelly and Scarpulla, 2004; Handschin and Spiegelman, 2006). In recent years, impaired PGC-1α expression and/or function has emerged as a common underlying cause of mitochondrial dysfunction in neurodegenerative diseases such as HD, PD and AD.

There is substantial evidence for impairment of PGC-1α levels and activity in HD (Cui et al., 2006; Weydt et al., 2006; Chaturvedi et al., 2009, 2010; Johri et al., 2011b). Involvement of PGC-1α in HD was first indicated by the findings that PGC-1α knockout mice exhibit mitochondrial dysfunction, defective bioenergetics, a hyperkinetic movement disorder and striatal degeneration, which are features also observed in HD (Lin et al., 2004; Leone et al., 2005). Selective ablation of PGC-1α leads to increased striatal neuron degeneration, and increased susceptibility to the mitochondrial toxin 3-NP in HD transgenic mice (Cui et al., 2006). Furthermore, impaired PGC-1α function and levels occur in striatal cell lines, transgenic mouse models of HD and in postmortem brain tissue from HD patients (Cui et al., 2006; Weydt et al., 2006). We showed a pathologic grade-dependent significant reduction in numbers of
mitochondria in striatal spiny neurons, which correlated with reductions in PGC-1α and Tfam (Kim et al., 2010). Sequence variation in the PGC-1α gene modifies the age of onset of HD (Weydt et al., 2009; Taherzadeh-Fard et al., 2009). Recent studies showed that expression of mutant htt in primary oligodendrocytes results in decreased expression of PGC-1α, and decreased expression of myelin basic protein (MBP) and deficient myelination were found in the R6/2 mouse model of HD (Xiang et al., 2011). A decrease in MBP and deficient postnatal myelination also occurs in the striatum of PGC-1α knockout mice (Xiang et al., 2011).

A meta-analysis of 17 independent genome-wide gene expression microarray studies revealed the strongest association between PD and nuclear genes encoding for OXPHOS subunits in mitochondria and for enzymes involved in glucose metabolism, all of which are regulated by PGC-1α (Zheng et al., 2010). These genes showed decreased expression in (laser microdissected) substantia nigra dopaminergic neurons even in the earliest stages of PD. Activation of PGC-1α results in increased expression of OXPHOS subunits and blocks the dopaminergic neuron loss induced by mutant α-synuclein, or the pesticide rotenone, in cultured dopaminergic neurons from embryonic rat midbrain and in human catecholaminergic SH-SY5Y cells (Zheng et al., 2010). Transgenic mice overexpressing PGC-1α in dopaminergic neurons are resistant against cell degeneration induced by the neurotoxin MPTP (Mudo et al., 2011). Earlier, it was noted that genetic ablation of the PGC-1α gene markedly enhances MPTP-induced loss of TH-positive neurons in the substantia nigra (St-Pierre et al., 2006). Recently, a parkin-interacting substrate (PARIS) was identified, that accumulates in models of parkin inactivation and in human PD brain and it was shown to repress the expression of PGC-1α and
its target gene, NRF-1 by binding to insulin response sequences in the PGC-1α promoter (Shin et al., 2011). Clark et al. (2011) provided limited evidence of an association of certain PGC-1α single nucleotide polymorphisms (SNPs) with the risk or age of onset of PD.

Using genome-wide complementary DNA microarray analysis, Qin et al. (2009) showed that PGC-1α expression is decreased in the brain of AD patients as a function of dementia severity. PGC-1α protein content was negatively associated with both, AD-type neuritic plaque pathology and β-amyloid contents. The authors also showed that adenoviral-mediated exogenous PGC-1α expression in Tg2576 neurons attenuated the hyperglycemic-mediated β-amyloidogenesis (Qin et al., 2009).

Recently, Liang et al. (2011) showed an age-dependent decrease in PGC-1α in SOD1-G93A mice. Moreover, they showed that overexpression of PGC-1α slowed the progression of ALS, moderately extended the lifespan, and improved motor (rotarod) performance. These improvements were associated with a significant decrease in motor neuron cell death and less neuromuscular junction damage in the G93A mice that overexpressed PGC-1α (Liang et al., 2011). In the same year, the Pasinetti lab also showed that PGC-1α overexpression significantly improves motor function and survival of SOD1-G93A mice (Zhao et al., 2011). The behavioral improvements were accompanied by reduced blood glucose levels and by protection against motor neuron loss, restoration of mitochondrial electron transport chain activities and inhibition of stress signaling in the spinal cord (Zhao et al., 2011).

6. **Transcriptional approaches to improve mitochondrial function**
PGC-1α and PPARs: PGC-1α is now increasingly being recognized as an important therapeutic target for neurodegenerative disorders. As discussed above, PGC-1α expression and/or function is impaired in all major neurodegenerative diseases, therefore pharmacologic/transcriptional activation of the PGC-1α pathway is expected to have neuroprotective effects. Indeed, overexpression of PGC-1α was shown to reduce Aβ plaque in an in vitro model of AD; produced neuroprotective effects in transgenic mouse model of ALS; and enhanced the mitochondrial membrane potential and reduced mitochondrial toxicity in in vitro models of HD (Qin et al., 2009; Liang et al., 2011; Zhao et al., 2011; Weydt et al., 2006). Lentiviral delivery of PGC-1α to the striatum of R6/2 HD mice prevented striatal atrophy at the site of PGC-1α injections (Cui et al., 2006). Recently, Da Cruz et al. showed that increasing PGC-1α activity in muscle in a transgenic mouse model of ALS caused by a mutation in SOD1, is able to sustain muscle function throughout the disease course, although survival was not extended (Da Cruz et al., 2012). Another potential approach to activate the PGC-1α pathway, and thereby improve mitochondrial function, is via activation of peroxisome proliferator-activated receptors (PPARs). The PPARs are a subfamily of nuclear receptors, which are ligand-modulated transcription factors that regulate gene-expression programs of metabolic pathways. PPAR agonists increase oxidative phosphorylation capacity in mouse and human cells, and enhance mitochondrial biogenesis. Administration of a PPARγ agonist, thiazolidinedione, was shown to produce beneficial effects on weight loss, mhtt aggregates and global ubiquitination profiles in R6/2 mice (Chiang et al., 2010). Earlier, it was shown in STHdhQ111 cells, that PPARγ activation by rosiglitazone prevents mitochondrial dysfunction and oxidative stress that occurs when
mutant striatal cells are challenged with pathological increases in calcium (Quintanilla et al., 2008). We recently showed that bezafibrate, which is a pan-PPAR agonist, improved expression of PGC-1α and downstream target genes, improved behavioral deficits, survival, and striatal atrophy and reduced oxidative damage, in the R6/2 transgenic mouse model of HD (Johri et al., 2011c). Both, pioglitazone and rosiglitazone, which are PPAR-γ agonists, were shown to exert beneficial effects in in vitro and in vivo models of PD and AD (Reviewed in Chaturvedi and Beal, 2008; Mandrekar-Colucci and Landreth, 2011).

PGC-1α, SIRT1 and AMPK: Sirtuins (silent information regulators) are members of the NAD⁺-dependent histone deacetylase family of proteins in yeast; and its homologs in mice and humans participate in a variety of cellular processes, including mitochondrial functions, cellular metabolism, energy metabolism, gluconeogenesis, cell survival, and aging. Although the role of sirtuins in promoting lifespan extension in lower organisms has been contested recently, there is strong evidence to suggest that sirtuins are an integrative link between metabolic control and transcriptional regulation, and the role of SIRT1 in activating the master regulator PGC-1α remains uncontested. Increased intracellular NAD⁺ concentrations activate SIRT1 in brain following caloric restriction, resulting in a reduction in amyloid pathology in a mouse model of AD; increased SIRT1 protects against hippocampal degeneration in a mouse model of AD; and direct injection of SIRT1 lentivirus in the hippocampus of AD transgenic mice produces significant neuroprotection (Reviewed in Chaturvedi and Beal, 2008). A SIRT1 activator, resveratrol, increases the activity of PGC-1α and improves mitochondrial activity as a consequence of SIRT1 mediated deacetylation of PGC-1α, which increases its effects on liver,
fat and muscle metabolism. SIRT1 activation by resveratrol increases the survival of motor neurons in transgenic ALS mice, and reduces learning impairments and neurodegeneration in AD mouse models, by decreasing the acetylation of the SIRT1 substrates PGC-1α and p53 (Kim et al., 2007). Resveratrol also protects against 3-NP induced motor and behavioral deficits. We showed that resveratrol treatment of the N171-82Q HD transgenic mice, produced increased PGC-1α and reduced the apparent vacuolization in brown adipose tissue and reduced glucose levels, but there were no beneficial effects in the striatum, probably due to poor brain penetration (Ho et al., 2010). Overexpression of SIRT1 improves motor function, reduces brain atrophy and attenuates mutant htt mediated metabolic abnormalities in three different transgenic mouse models of HD (Jiang et al., 2012; Jeong et al., 2012). Recently, it was shown that SIRT1 protects against α-synuclein aggregation by activating molecular chaperones, heat shock factor1 (HSF1) and heat shock protein70 (HSP70), in brains of mice with the A53T alpha-synuclein mutation (Donmez et al., 2012). Another sirtuin, which is of particular interest as a target for therapeutic intervention, is SIRT3. It is one of the three sirtuins that are located in mitochondria, where it interacts with Complex I of the respiratory chain and deacetylates several proteins in Complex I. It also increases fatty acid oxidation, SOD2 activity, levels of glutathione, and inhibits activation of the mitochondrial permeability transition.

AMP-activated protein kinase (AMPK) is a Ser/Thr kinase that is activated as a consequence of increased AMP levels, reflecting low ATP availability and low energy reserve. AMPK activation results in a cascade of phosphorylation-dependent adaptive modifications of several factors, including PGC-1α, in order to switch on the catabolic pathways (such as fatty acid oxidation and
mitochondrial respiratory chain activity) to produce ATP, while simultaneously shutting down energy-consuming anabolic processes. 5-aminoimidazole-4-carboxamide ribonucleoside (AICAR) is a compound that has been used to activate PGC-1α through AMPK. It does so by generating inosine monophosphate, which acts as an AMPK agonist by mimicking AMP. AICAR was shown to inhibit tau phosphorylation in an in vitro model of AD, however AMPK activation by AICAR was shown to produce adverse effects in R6/2 HD mice in that it enhanced brain atrophy, neuronal loss, and aggregate formation in the striatum. Recently, it was shown that AMPK activity is increased in spinal cord cultures expressing mutant SOD1, as well as in spinal cord lysates from mutant SOD1 mice (Lim et al., 2012). Reducing AMPK activity either pharmacologically or genetically prevented mSOD1-induced motor neuron death in vitro (Lim et al., 2012). Metformin is another AMPK activator which was shown to be effective in male HD transgenic mice in that it prolonged survival and decreased hind limb clasping (Ma et al., 2007).

Though the effects of resveratrol and SIRT1 on PGC-1α are well established; lately there has been a great deal of controversy about the mechanism by which this regulation is achieved. The ability of resveratrol to elicit cellular changes in a SIRT1-independent manner, combined with the observations that AMPK-deficient mice exhibit a blunted response to resveratrol treatment, pointed towards AMPK as a critical mediator of resveratrol action (Um et al., 2010). Studies by Park et al. (2012) suggested that resveratrol does not target SIRT1 directly but instead stimulates the AMPK pathway by inhibiting cAMP-degrading phosphodiesterases (mainly PDE4), resulting in increased cAMP levels, which in turn increases cellular calcium levels, thereby stimulating phosphorylation of AMPK (Park et al., 2012). It was proposed that AMPK then
activates SIRT1 indirectly by elevating intracellular levels of its cosubstrate, NAD⁺ (Canto et al., 2009; Fulco et al., 2008). Recently, this issue was addressed in an elegant manner in a study by Sinclair’s group, who used a conditional SIRT1 knockout mouse to show that with moderate doses of resveratrol in vitro or in vivo, the increases in phosphorylated AMPK, NAD⁺, LKB1 acetylation, and mitochondrial function were entirely dependent on SIRT1 (Price et al., 2012).

Using this adult-inducible SIRT1 knockout (KO) mouse strain, the authors showed that the beneficial effects of resveratrol treatment on muscle mitochondrial function are dependent upon SIRT1 in vivo. They also showed that overexpression of SIRT1 in a transgenic mouse strain mimicked the effects of resveratrol treatment in skeletal muscle. These studies support a model in which lower doses of resveratrol stimulate SIRT1 upstream of AMPK via deacetylation of LKB1, one of the activating protein kinases of AMPK (Price et al., 2012). At present, the entire resveratrol, sirtuin field seems to be changing at daunting speed and much remains to be proven/disproven about the elusive mechanisms of action of resveratrol and sirtuins, and their potential role in neurodegeneration and life extension. However, the beneficial effects of resveratrol and SIRT1 that were observed in several mouse models of neurodegenerative diseases cannot be overlooked, and the quest for small molecule activators of sirtuins with potential neuroprotective effects should continue.

Nrf2/ARE pathway: ROS damage to mitochondria is well known in all the major neurodegenerative disorders, therefore therapies targeting Nrf2/antioxidant response element (ARE) pathway are of particular interest. Synthetic triterpenoids (TP) are analogues of oleonolic acid, and are powerful inhibitors of oxidative stress and cellular inflammatory processes.
Synthetic TP compounds are potent inducers of the ARE/Nrf2/Keap1 signaling pathway. Following activation by TP, Nrf2 dissociates from Keap1, translocates to the nucleus and binds to the ARE promoter sequences, leading to coordinated induction of a battery of cytoprotective genes including antioxidants and anti-inflammatory genes. Neuronal cultures derived from Nrf2 knock-out mice show increased susceptibility to oxidative damage, as well as damage produced by mitochondrial electron transport gene complex inhibitors such as MPP⁺ and rotenone. Nrf2 deficient mice show increased susceptibility to the mitochondrial toxins MPTP and 3-NP. Recently, we tested neuroprotective effects of the synthetic triterpenoid CDDO methylamide (CDDO-MA), which is a potent activator of the Nrf2/ARE signaling pathway (Yang et al., 2009). CDDO-MA produced marked protection in the 3-NP rat model, and both the acute and chronic MPTP mouse models. CDDO-MA exerted significant protection against tertbutylhydroperoxide induced ROS in vitro. It increased the expression of genes involved in mitochondrial biogenesis, as well as those involved in glutathione synthesis and in expression of antioxidant enzymes (Yang et al., 2009). Triterpenoids also protect in transgenic mouse models of ALS, HD and AD.

Several bioenergetic agents have efficacy in improving mitochondrial function including creatine, coenzyme Q10, nicotinamide, riboflavin and lipoic acid (Reviewed in Beal, 2009). Coenzyme Q (CoQ) is an essential biologic factor of electron transport chain where it accepts electrons from complexes I and II. It also serves as an important antioxidant in mitochondrial lipid membranes. We showed that oral administration of CoQ10 protects against lesions produced by aminoxyacetic acid, and the mitochondrial toxins malonate and 3-NP. We also found modest neuroprotective effects of COQ10 in a transgenic mouse model of ALS and more
marked neuroprotective effects in transgenic mouse models of HD. We recently found that CoQ10 treatment decreases brain oxidative stress, Aβ42 levels and β-amyloid plaque area and number, and improves cognition in a transgenic mouse model of AD. High dose CoQ10 significantly extends survival, improves motor performance, grip strength and brain atrophy in R6/2 HD mice in a dose-dependent manner. Furthermore, we found that the combination of creatine and CoQ10 exerts additive neuroprotective effects in the MPTP model of PD, the 3-NP model of HD, and in a transgenic mouse model of HD (Yang et al., 2009). These compounds, therefore, show neuroprotective effects, which may be a useful target for treating neurodegenerative diseases.

A new concept emerging in the field of neurodegenerative diseases, and which opens up new avenues for understanding disease progression and developing novel therapeutics, is that of the prion—like spread of misfolded proteins. The prion concept was developed by Prusiner and involves proteinaceous particles, the prions, which are the infectious agents in Jacob-Creutzfeld and other neurological disorders. This concept may also be applicable to neurodegenerative diseases with genetic experiments providing convincing evidence that mutant Aβ, α-synuclein and tau can be transferred between neighboring neurons, and then induce pathological changes in these neurons (de Calignon et al., 2012; Harris et al., 2010; Luk et al., 2012).

7. Conclusion and future perspectives

As discussed above, there is strong evidence implicating the role of mitochondrial dysfunction in the pathogenesis of neurodegenerative diseases. In a number of instances, there is direct involvement of the genetic defect with mitochondria such as in Friedreich’s ataxia. In a number
of neurodegenerative diseases, the genetic evidence is more indirect. This is the case in AD and HD. In AD, the mitochondrial dysfunction may be a consequence of accumulation of Aβ within mitochondria. Similarly, in PD α-synuclein has been demonstrated to associate with mitochondria and recent studies have shown that LRRK2, which is localized on the outer surface of mitochondria, may increase mitochondrial fission (Niu et al., 2012). The autosomal recessive genes involved in PD are all linked with mitochondrial dysfunction. For instance, both parkin and PINK1 play a role in mitophagy, and DJ1 modulates oxidative damage within mitochondria. In HD, the mitochondrial impairment may be due to an impairment of the activity of PGC-1α, although there is other evidence that mutant htt can directly associate with mitochondria, and may increase mitochondrial fission (Costa et al., 2010; Song et al., 2011; Shirendeb et al., 2011; Johri et al., 2011a). There is recent evidence showing an impairment of PGC-1α in PD based on findings in microarray studies as well as in transgenic mouse models in which a parkin deficiency leads to impaired PGC-1α transcription, which is due to an accumulation of the protein PARIS.

The field of mitochondrial dynamics, which is involved in the trafficking and turnover of mitochondria, is another area in which there is increasing evidence for a critical role in neurodegenerative diseases. Mutations in the mitochondrial fusion proteins, mitofusin 2 and OPA1, are responsible for Charcot-Marie Tooth disease and autosomal dominant optic atrophy respectively. Mutant htt binds to DRP1 and increases its GTPase activity, and similar effects have been reported in AD (Manczak et al., 2011). There is evidence that mutant SOD1, a cause of autosomal dominant ALS, forms aggregates which then binds to the outer mitochondrial
membrane impairing the activity of the VDAC channel, Bcl-2, as well as impairing protein uptake (Israelson et al., 2010).

The field of mitochondrial-targeted therapeutics is one that is growing and is of great importance. The development of transgenic mouse models of neurodegenerative diseases has been valuable in providing ways of testing and developing new therapies. Creatine is involved in buffering energy metabolism, and produces neuroprotective effects in transgenic mouse models of HD and ALS, and is protective in the MPTP model of PD (Beal, 2011). It is presently being tested in Phase III clinical trials in both PD and HD. Similarly, coenzyme Q is a component of the electron transport chain which is also an important antioxidant, and it is effective in transgenic mouse models of neurodegenerative diseases as well as MPTP, and 3-NP. A recent Phase III clinical trial in PD was unsuccessful (unpublished), however, trials in HD and Friedreich’s ataxia are continuing. Several compounds have been developed which can specifically target mitochondria. These include compounds such as mitoQ, a form of coenzyme Q linked to triphosphonium ions, which results in selective accumulation within mitochondria. There are also novel peptide antioxidants termed SS31 and SS20 which bind to the inner mitochondrial membrane, and are neuroprotective in transgenic mouse models of ALS as well as in neurotoxin models (Petri et al., 2006). Dexpramipexole, an isomer of the dopamine agonist pramipexole, accumulates in mitochondria, where it exerts antioxidant effects, and inhibits the activation of the mitochondrial permeability transition. Dexpramipexole has shown efficacy in a Phase II clinical trial in ALS, where it produced improvement on the ALS functional rating scale, as well as on mortality (Cudkowicz et al., 2011).
Other approaches are to modulate transcription, such as the Nrf2/ARE pathway, which when activated by triterpenoids exerts neuroprotective effects in transgenic mouse models of AD, HD, and ALS, and against MPTP. Dimethylfumarate, another agent which activates this pathway, is protective in multiple sclerosis (Gold et al., 2012). PGC-1α induces mitochondrial biogenesis and expression of antioxidant enzymes, and we and others showed that pharmacologic agents which activate PGC-1α are protective in transgenic mouse models of neurodegenerative diseases including HD, ALS and Aβ toxicity. PGC-1α activity is modulated by SIRT1, an NAD dependent deacetylase, and activation of SIRT1 is protective in models of HD (Jiang et al., 2012; Jeong et al., 2012). There are therefore a number of promising new compounds and therapeutic targets which modulate mitochondria and produce neuroprotective effects (Figure 1). These compounds show great promise for treating patients who suffer from neurodegenerative diseases, for which there is as yet no effective treatment to slow or halt the underlying disease processes.

Acknowledgments: The authors apologize for the inability to cite several articles due to space limitations.

Authorship contributions: Wrote the manuscript: AJ and MFB; Tables and Figure: AJ.
References:


Manczak M, Calkins MJ and Reddy PH (2011) Impaired mitochondrial dynamics and abnormal interaction of amyloid beta with mitochondrial protein Drp1 in neurons from patients


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Figure Legend:

Figure 1. Structures of the compounds that produce beneficial effects in mice against mitochondrial dysfunction
Table-1: Known OXPHOS Complex (ETC) deficiencies in major neurodegenerative disorders

<table>
<thead>
<tr>
<th>OXPHOS Complex</th>
<th>Huntington’s disease</th>
<th>Alzheimer’s disease</th>
<th>Parkinson’s disease</th>
<th>Amyotrophic lateral sclerosis</th>
</tr>
</thead>
<tbody>
<tr>
<td>Complex I</td>
<td>Unaltered in brain of HD patients, but reduced in skeletal muscle</td>
<td>Reduced in mitochondria, platelets and lymphocytes from AD patients and postmortem brain tissue</td>
<td>Impaired Complex I activity is seen in substantia nigra, platelets and skeletal muscle of PD patients.</td>
<td>Increased in familial ALS</td>
</tr>
<tr>
<td>NADH dehydrogenase</td>
<td>Unaltered in brain of HD patients, but reduced in skeletal muscle</td>
<td>Reduced in mitochondria, platelets and lymphocytes from AD patients and postmortem brain tissue</td>
<td>Impaired Complex I activity is seen in substantia nigra, platelets and skeletal muscle of PD patients.</td>
<td>Increased in familial ALS</td>
</tr>
<tr>
<td>NADH:ubiquinone oxidoreductase</td>
<td>Unaltered in brain of HD patients, but reduced in skeletal muscle</td>
<td>Reduced in mitochondria, platelets and lymphocytes from AD patients and postmortem brain tissue</td>
<td>Impaired Complex I activity is seen in substantia nigra, platelets and skeletal muscle of PD patients.</td>
<td>Increased in familial ALS</td>
</tr>
<tr>
<td>Complex II</td>
<td>Reduced enzyme activity in brain of advanced-stage HD patients and transgenic mice; complex II inhibitors produce a HD</td>
<td>Reduced in mitochondria from AD patients</td>
<td>Reduced activities are reduced in spinal cords of ALS</td>
<td>Complex II+III</td>
</tr>
<tr>
<td>Succinate dehydrogenase</td>
<td>Reduced enzyme activity in brain of advanced-stage HD patients and transgenic mice; complex II inhibitors produce a HD</td>
<td>Reduced in mitochondria from AD patients</td>
<td>Reduced activities are reduced in spinal cords of ALS</td>
<td>Complex II+III</td>
</tr>
</tbody>
</table>
phenotype in mice and primates

<table>
<thead>
<tr>
<th>Complex III</th>
<th>Reduced</th>
<th>Core 1 protein is significantly reduced in</th>
<th>Complex I+III activities reduced in spinal cords of ALS patients</th>
</tr>
</thead>
<tbody>
<tr>
<td>(CoQ-enzyme activity</td>
<td>in advanced-stage HD</td>
<td>temporal cortex of AD patients. Also reduced in mitochondria, platelets and lymphocytes from AD patients and postmortem brain tissue</td>
<td></td>
</tr>
</tbody>
</table>

| Complex IV | Reduced COX activity in myoblasts and brain samples from HD patients | Decreased activity and mRNA levels reported in platelet mitochondria and lymphocytes from AD patients and skeletal muscle from PD patients of patients with |
|------------|-------------------------|---------------------------------|-----------------|-----------------|-----------------|-----------------|
| (Cytochrome c oxidase) | | | Reduced Complex IV activity was activity in individual motor neurons, spinal cords and |

This article has not been copyedited and formatted. The final version may differ from this version.
Sporadic ALS.

Decreased COX subunits in G93A ALS mice

| Complex V (ATP synthase) | ATP production is impaired in striatal cells from mutant htt mice | Reduced in mitochondria from AD patients | Reduced enzyme activity for Complex V in skin fibroblast cultures from PD patients | Levels of different enzyme subunits (D, α and β) are decreased in G93A ALS mice |
Table-2: Proteins implicated in the pathogenesis of major neurodegenerative disorders and their association/interaction with mitochondria

<table>
<thead>
<tr>
<th>Protein</th>
<th>Disease</th>
<th>Mitochondrial association</th>
</tr>
</thead>
<tbody>
<tr>
<td>Huntingtin (htt)</td>
<td>HD</td>
<td>1. Although largely cytosolic, htt is also present on outer mitochondrial membrane (OMM).</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2. Htt expression correlated with elevated lactate levels, decreased mitochondrial membrane potential (MMP), decreased respiratory function through complex II, defects in mitochondrial calcium uptake, reduced mitochondrial mobility and mitochondrial ultrastructural changes.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3. Rat cortical neurons treated with 3-nitropropionic acid have fragmentation and condensation of mitochondria which can be prevented by antioxidant treatment.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4. In HeLa cells over-expressing mutant htt (mhtt) with a 74 glutamine repeat, there is fragmentation of mitochondria, reduced mitochondrial fusion, reduced ATP and increased cell death. Expression of either dominant-negative pro-fission protein Drp1, or pro-fusion protein Mfn2, not only prevents this change in mitochondrial morphology but also restores ATP levels and attenuates cell death.</td>
</tr>
<tr>
<td></td>
<td></td>
<td>5. mhtt binds more tightly to Drp1 on mitochondria and triggers mitochondrial fragmentation.</td>
</tr>
</tbody>
</table>
| Amyloid precursor protein (APP) | AD | 1. APP accumulates in the protein import channels of mitochondria from human AD brains where it was found to be stably associated with translocases of the outer and inner mitochondrial membrane (TOM40 and TIM23).
|                              |    | 2. Exposure of neuronal cells to conditioned medium from cells stably expressing mutant forms of APP leads to increased mitochondrial fission, loss of dendritic spines and eventually cell death. This increase in mitochondrial fission was traced to elevated levels of S-nitrosylated Drp1 (SNO-Drp1). Increased levels of SNO-Drp1 were found in brain samples from AD patients and AD mouse models.
|                              |    | 3. APP over-expression in M17 neuroblastoma cells resulted in predominantly fragmented mitochondria, decreased levels of Drp1 and OPA1, and a defect in neuronal differentiation. Over-expression of Drp1 or OPA1 could partially rescue different aspects of these defects.

| Presenilins (PS1 and PS2) | AD | 1. Presenilins form the γ-secretase complex that together with β-secretase, cleaves APP to produce Aβ.
|                           |    | 2. PS1 and PS2 are enriched in mitochondria-associated membranes (MAM), which is a specialized sub-compartment
of the endoplasmic reticulum (ER) involved in lipid metabolism and calcium homeostasis. PS1 presence was also reported in mitochondria.

3. Knock-out of PS2 in contrast to PS1 results in reduced mitochondrial function in vivo.

4. PS2 increases endoplasmic reticulum (ER)-mitochondria tethering, which could result in a chronic, toxic, mitochondrial Ca$^{2+}$ overload.

### Amyloid-β (Aβ)

1. Mitochondrial accumulation of Aβ has been shown in AD patients, APP transgenic mice and cellular models of AD.

2. Mitochondria localized Aβ was shown to inhibit Aβ binding alcohol dehydrogenase, disrupt mitochondrial permeability transition pore functions and impair the respiratory chain Complex III and IV.

3. Intracellular accumulated Aβ induces age-dependent changes, including depletion of presynaptic mitochondria, slowdown of bi-directional transports of axonal mitochondria, decreased synaptic vesicles, increased large vacuoles, and elevated synaptic fatigue.

4. Cells overproducing Aβ showed impairment of mitochondrial function such as reduced mitochondrial respiration, strongly altered morphology, and reduced intracellular mobility of mitochondria. Antioxidants reduced Aβ production and
rescued mitochondrial function.

5. Aβ increases expression of mitochondrial fission genes and reduces the expression of fusion genes \textit{in vitro}.

<table>
<thead>
<tr>
<th>Tau</th>
<th>AD/PD</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Tau mediates the effects of Aβ on axonal transport and a reduction of tau protects against Aβ-induced axonal transport abnormalities.</td>
<td></td>
</tr>
<tr>
<td>3. N-terminal truncated tau localizes to mitochondrial membranes and was found to be highly enriched in mitochondria from cryopreserved synaptosomes of human AD brains.</td>
<td></td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>α-synuclein</th>
<th>PD</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. α-synuclein is present predominantly on OMM in mouse brain and on IMM in human brain.</td>
<td></td>
</tr>
<tr>
<td>2. Higher accumulation of α-synuclein was reported in mitochondria from striatum and substantia nigra of PD patients compared to normal subjects.</td>
<td></td>
</tr>
<tr>
<td>3. Accumulation of α-synuclein in the mitochondria of human dopaminergic neurons reduced mitochondrial complex I activity and increased production of reactive oxygen species (ROS).</td>
<td></td>
</tr>
<tr>
<td>4. N-terminal 32 amino acids of α-synuclein were shown to function as a targeting sequence for the import of α-</td>
<td></td>
</tr>
</tbody>
</table>
synuclein into mitochondria in an energy- and import channel-dependent manner.

5. Mitochondrial association of α-synuclein in cells was linked to oxidation of mitochondrial proteins and increased levels of calcium and nitric oxide.

6. Mitochondrial abnormalities were observed in transgenic mouse models over-expressing wild-type (wt) or mutant α-synuclein: selective oxidation of mitochondria-associated metabolic proteins; degenerating mitochondria containing α-synuclein; reduced complex IV activity; mitochondrial DNA damage; and increased mitochondrial pathology after treatment with MPTP.

7. Studies in α-synuclein knockout mice suggest that α-synuclein controls synaptic vesicle dynamics and may regulate mitochondrial membrane lipid composition and complex I activity.

<table>
<thead>
<tr>
<th>Parkin</th>
<th>PD</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Parkin is a largely cytosolic E3 ubiquitin ligase, which, along with PINK1, is involved in mitochondrial quality control pathways i.e. mitophagy.</td>
<td></td>
</tr>
<tr>
<td>2. Although primarily cytosolic, Parkin is recruited to mitochondria under conditions of bioenergetic stress/loss of mitochondrial membrane potential such as in presence of chemical uncouplers andOXPHOS inhibitors; by relatively</td>
<td></td>
</tr>
</tbody>
</table>
long exposure to oxidative stress (after treatment with paraquat); chronic loss of mitochondrial fusion, or loss of mtDNA integrity.

3. Loss of Parkin in *Drosophila* not only causes degeneration of flight muscles and dopaminergic neurons, but their mitochondria become dysmorphic and dysfunctional with less efficient OXPHOS and increased ROS production.

4. Parkin ubiquitinates OMM proteins, VDAC1 in mammals and Marf (an ortholog of mammalian mitofusins) in *Drosophila*. Ubiquitination (therefore elimination/inhibition) of Marf by Parkin promotes mitochondrial fission.

<table>
<thead>
<tr>
<th><strong>PTEN-induced putative kinase1 (PINK1)</strong></th>
<th><strong>PD</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>1. PINK1 gene encodes a mitochondrially localized serine/threonine kinase. PINK1 is normally kept at low levels on the OMM of healthy mitochondria. However, it is also imported into mitochondria, and rapidly and selectively accumulates on the outer membrane of mitochondria that have lost membrane potential.</td>
<td></td>
</tr>
<tr>
<td>2. Mutations in the PINK1 and Parkin genes result in enlarged or swollen mitochondria.</td>
<td></td>
</tr>
<tr>
<td>3. <em>Drosophila</em> null for Pink1 have the same unusual phenotype as Parkin knockout flies.</td>
<td></td>
</tr>
<tr>
<td>4. PINK1 was associated genetically with proteins involved in mitochondrial morphogenesis such as HtrA2, Drp1 and...</td>
<td></td>
</tr>
</tbody>
</table>
5. PINK1 acts upstream of Parkin, and expression of PINK1 is necessary for the recruitment of Parkin to depolarized mitochondria. Parkin recruitment tags the impaired mitochondria for degradation (mitophagy).

6. Mice null for Pink1 or Parkin exhibit synaptic dysfunction in neurons projecting to the striatum and this synaptic dysfunction correlates with progressive loss of mitochondrial function and increased oxidative stress in the striatum with age.

7. Loss of function mutations in PINK1 or Parkin have also been associated with mitochondrial dysfunction in cells from patients with familial forms of parkinsonism.

8. PINK1 phosphorylates Miro (which links mitochondria to microtubules via kinesin and Milton, for transport), resulting in Parkin-dependent proteasomal degradation of Miro. This prevents mitochondrial movement and probably quarantines damaged mitochondria prior to clearance by mitophagy.

9. Phosphorylation of Drp1 and the mitochondrial intermembrane proteins, TRAP-1 and HtrA2/Omi, is also dependent on PINK1. HtrA2 phosphorylation increases its proteolytic activity and may serve to proteolytically degrade
misfolded mitochondrial proteins in order to maintain mitochondrial integrity. HtrA2 phosphorylation is decreased in brains of patients with PD carrying mutations in PINK1.

<table>
<thead>
<tr>
<th>DJ-1</th>
<th>PD</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. DJ-1 protein is mostly located in the cytosol and only a fraction is present in the nucleus and mitochondria, where it preferentially partitions to the matrix and inter-membrane space of mitochondria and it impairs degradation.</td>
<td></td>
</tr>
<tr>
<td>2. Upon oxidative stress, DJ-1 protein rapidly translocates to the mitochondria and, to a lesser extent, to the nucleus, acting as a neuroprotective intracellular redox sensor.</td>
<td></td>
</tr>
<tr>
<td>3. DJ-1 and its mutants were found to be strongly associated with Hsp70, the co-chaperone CHIP, and a mitochondria-resident Hsp70 complex in PD patients. In vitro, association of wt-DJ-1 with mitochondrial Hsp70 was further increased under oxidative stress, indicating that the translocation of DJ-1 to mitochondria may occur by binding to mitochondrial chaperones.</td>
<td></td>
</tr>
<tr>
<td>4. DJ-1 protects dopaminergic neurons from oxidative stress by stabilizing Nrf2 and through up-regulation of glutathione synthesis and from the toxic consequences of A53T α-synuclein through increased expression of Hsp70.</td>
<td></td>
</tr>
<tr>
<td>5. DJ-1 knockout in fly and mice produced decreased mtDNA levels, respiratory control ratio, and ATP levels. DJ-1</td>
<td></td>
</tr>
</tbody>
</table>
deficient mice are more sensitive to MPTP-induced loss of dopamine neurons.

6. Loss of DJ-1 in flies and mice was associated with increased sensitivity of mitochondria to complex I inhibitors and oxidative stress.

7. *In vitro*, reduction of DJ-1 was associated with lowered MMP, an increase in mitochondria fragmentation, autophagy and oxidative stress, and reduced mitochondrial fusion. DJ-1 was also found to directly bind to the mitochondrial complex I subunits; and loss of function of DJ-1 led to a decrease of mitochondrial complex I activity, but not complex III; whereas overexpression of DJ-1 conferred protection against the complex I inhibitor MPTP.

8. DJ-1 inhibits the aggregation and toxicity of α-synuclein by increasing Nrf2, a direct interaction is not known; DJ-1 binds to PINK1 and increases PINK1 levels under conditions of PINK1 overexpression; DJ-1 and Parkin interact under conditions of oxidative stress.

9. DJ-1 activates transcription of Mn-SOD gene, which encodes an essential mitochondrial anti-oxidant enzyme.

**LRRK2**

1. LRRK2 immunoreactivity was shown to partially overlap with mitochondrial and lysosomal markers in the mammalian brain, and ultrastructural analysis revealed that LRRK2 is
associated with intracellular membranes, including lysosomes, transport vesicles, and mitochondria.

2. LRRK2 can bind to the OMM in mammalian brain. About 10% of wt and mutant LRRK2 were present in the mitochondrial fraction in cells over-expressing the proteins.

3. Patients with G2019S mutation had a decrease in MMP and ATP.

4. Over-expression of G2019S mutant LRRK2 in differentiated human neuroblastoma cells caused neurite retraction and shortening, which correlated with increased autophagy.

5. LRRK2 mutations increase the kinase activity of LRRK2, which results in increased neurotoxicity.

6. Overexpression of either, wt- or mutant- (R1441C or G2019S) LRRK2 caused mitochondrial fragmentation; reduced mitochondrial fusion; increased Drp1 recruitment to mitochondria by direct interaction with LRRK2 \textit{in vitro}.

\begin{tabular}{|c|c|}
  \hline
  SOD1 & ALS \\
  \hline
  1. Wild-type SOD1 is predominantly cytosolic, however, a small fraction resides in mitochondria. & \\
  2. SOD1 and its copper chaperone, CCS, enter mitochondria through the Erv1/Mia40 oxidative folding mechanism of import, that involves a formation of mixed disulfide bonds between CCS and Mia40, and is sensitive to oxygen concentrations. & \\
  \hline
\end{tabular}
3. Wild-type SOD1 helps in prevention of the oxidation of mitochondrial proteins and thus in the preservation of mitochondrial homeostasis. Mice lacking SOD1 show a distal motor neuropathy accompanied by decreased mitochondrial density and increased oxidative stress in mitochondria, that is rescued by SOD1 targeted to the mitochondrial intermembrane space.

4. A proportion of SOD1 mutant protein is misfolded onto the cytoplasmic surface of mitochondria, and the axonal mitochondria of motor neurons are the primary in vivo targets for misfolded SOD1.

5. A small fraction of the enzyme resides in various mitochondrial sub-compartments, mutant SOD1 to a greater extent than wild-type.

6. Mutant SOD1 alters axonal mitochondrial morphology and distribution.

7. Somal mitochondria are altered by mutant SOD1, with loss of the characteristic cylindrical, networked morphology and its replacement by a less elongated, more spherical shape.

8. Mutant SOD1 motor neurons have impaired mitochondrial fusion in both, the axons and in the cell bodies; there is selective impairment of retrograde axonal transport, smaller mitochondrial size, decreased mitochondrial density, and
defective MMP.

9. Expression of mutant SOD1 elicits a clear deficit in the electron transport chain, mishandling of mitochondrial calcium, increased production of ROS and activation of the apoptotic pathway.

10. Overexpression of mutant SOD1 induces the activation of autophagy, as measured by the activation of LC3 (microtubule-associated protein1 light chain 3) and increases the association of PINK1 with mitochondria.
Figure 1. Structures of the compounds that produce beneficial effects in mice against mitochondrial dysfunction