

Stress-Induced Mitochondrial DJ-1: Role of Parkin, Pink1 and VDAC1

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Abstract

Parkinson's disease (PD) is the second most common neurodegenerative disease and is characterized by motor symptoms such as tremor, rigidity, akinesia and postural instability. Approximately 90% of the cases are due to unknown causes however a familial inheritance has been shown for about 10% of cases. Loss-of-function mutations in DJ-1 cause early-onset PD. Originally identified as an oncogene, DJ-1 has since had many functions attributed to it but its major role in the cell seems to be oxidative stress handling. We have previously demonstrated that DJ-1 deficiency results in hypersensitivity of cells to oxidative stress. Additionally, mitochondria from DJ-1 null mice are fragmented and produce more ROS. To better understand the relationship between DJ-1, cell survival and mitochondria, we investigated the possible interaction between DJ-1 and the mitochondrial protein voltage dependent anion channel 1 (VDAC1). Here we show mitochondrial translocation of DJ-1 following oxidative stress in murine embryonic fibroblasts (MEFs) and primary cortical neurons, a process dependent on Pink1 and Parkin. Additionally, we confirm that DJ-1 and VDAC1 interact and that stress-induced mitochondrial translocation of DJ-1 depends on VDAC1. Deficiency of VDAC1 in primary cortical neurons results in decreased survival, increased ROS production following extended stress, fragmented mitochondria and decreased mitochondrial ATP production. We also demonstrate that there is substantially less matrix-localized DJ-1 in VDAC1 deficient cells. Finally, we demonstrate that decreased mitochondria ATP production can signal for DJ-1 translocation to mitochondria. Taken together, we suggest that mitochondrial translocation of DJ-1 is a two-step process. First, a signal, perhaps decreased mitochondrial ATP production, induces DJ-1 translocation to

mitochondria. Second, DJ-1 localizes to the matrix in a VDAC1-dependent manner. Our work suggests that stress-induced mitochondrial localization of DJ-1, specifically to the matrix, is regulated by VDAC1 to promote survival possibly by promoting ATP production.

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If you can imagine it, you can achieve it

If you dream it, you can become it

– William Arthur Ward

List of Manuscripts

I. ROS-dependent regulation of Parkin and DJ-1 localization during oxidative stress in neurons.

Joselin AP[#], **Hewitt SJ[#]**, Callaghan SM, Kim RH, Chung YH, Mak TW, Shen J, Slack RS, Park DS.

Human Molecular Genetics. 2012 Nov 15;21(22):4888-903. Epub 2012 Aug 7.

#Authors contributed equally

II. VDAC1 is important for sub-mitochondrial localization of DJ-1.

Hewitt SJ, Callaghan SM, Brini M, Craigen WJ, Figeys D, Slack RS, Park DS.

This manuscript is in preparation for submission.

Appended Articles:

I. DJ-1 protects the nigrostriatal axis from the neurotoxin MPTP by modulation of the AKT pathway.

Aleyasin H[#], Rousseaux MW[#], Marcogliese PC, **Hewitt SJ**, Irrcher I, Joselin AP, Parsanejad M, Kim RH, Rizzu P, Callaghan SM, Slack RS, Mak TW, Park DS.

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II. Loss of the Parkinson's disease-linked gene DJ-1 perturbs mitochondrial dynamics.

Irrcher I, Aleyasin H, Seifert EL, **Hewitt SJ**, Chhabra S, Phillips M, Lutz AK, Rousseaux MW, Bevilacqua L, Jahani-Asl A, Callaghan S, MacLaurin JG, Winklhofer KF, Rizzu P, Rippstein P, Kim RH, Chen CX, Fon EA, Slack RS, Harper ME, McBride HM, Mak TW, Park DS.

Human Molecular Genetics. 2010 Oct 1;19(19):3734-46. Epub 2010 Jul 16.

III. Progressive dopaminergic cell loss with unilateral-to-bilateral progression in a genetic model of Parkinson disease.

Rousseaux MW, Marcogliese PC, Qu D, **Hewitt SJ**, Seang S, Kim RH, Slack RS, Schlossmacher MG, Lagace DC, Mak TW, Park DS.

Proceedings of the National Academy of Science USA. 2012 Sep 25;109(39):15918-23. Epub 2012 Sep 10.

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Abbreviations

AAV	Adeno-Associated Virus
AD	Autosomal Dominant
ADP	Adenosine DiPhosphate
AIF	Apoptosis-Inducing Factor
ANOVA	ANalysis Of VAriance
ANT	Adenine-Nucleotide Transferase
Apaf-1	Apoptosis activating factor 1
AR	Autosomal Recessive
ARe	Androgen Receptor
ATP	Adenosine TriPhosphate
ATP β	ATP synthase, β subunit
Bcl-2	B-cell lymphoma-2
Bcl-x _L	B-cell lymphoma-eXtra Large
Ca ²⁺	Calcium
CCCP	Carbonyl Cyanide m-Chloro Phenyl hydrazine
CM-H2DCFDA	5-(and-6)-ChloroMethyl-2', 7'-dichlorodiHydroFluorescin DiAcetate
CNS	Central Nervous System
COXI	Cytochrome c OXidase subunit I
COXV	Cytochrome c OXidase subunit V
DBS	Deep Brain Stimulation
DIABLO	Direct Inhibitor of Apoptosis Binding protein with LOw pI
DIV	Days <i>In Vitro</i>

DNA	DeoxyriboNucleic Acid
Drp1	Dynamamin-related protein 1
ER	Endoplasmic Reticulum
ETC	Electron Transport Chain
FBS	Fetal Bovine Serum
Fis1	Mitochondrial Fission protein 1
GBA	β -GlucocereBrosidAse
GFP	Green Fluorescent Protein
GPe	Globus Pallidus external segment
GPi	Globus Pallidus internal segment
GSH	reduced Glutathione
GSSG	oxidized Glutathione
GST	Glutathione S-Transferase
HDAC1	Histone DeACetylase 1
HEK293	Human Embryonic Kidney 293 cell line
HRP	HorseRadish Peroxidase
IMM	Inner Mitochondrial Membrane
IMS	Inner Mitochondrial membrane Space
Kb	Kilo base pairs
KDa	KiloDalton
Keap1	Kelch-like ECH-associated protein 1
KO	KnockOut
LB	Lewy Body

LC	Locus Coeruleus
LC3	microtubule-associated protein Light Chain 3
L-DOPA	LevoDOPA
LHON	Leber's Hereditary Optic Neuropathy
LN	Lewy Neurite
LRRK2	Leucine Rich Repeat Kinase 2
MEFs	Mouse Embryonic Fibroblasts
Mff	Mitochondrial fission factor
Mfn	Mitofusin
MOI	Multiplicity Of Infection
mnSOD	manganese SuperOxide Dismutase
MPP ⁺	1-Methyl-4-PhenylPyridinium ion
MPPP	1-Methyl-4-Phenyl-4-Propionoxy Piperidine
mPTP	mitochondrial Permeability Transition Pore
MPTP	1-Methyl-4-Phenyl-1,2,5,6-TetrahydroPyridine
MQC	Mitochondrial Quality Control
mRNA	messenger Ribosomal Nucleic Acid
mtDNA	mitochondrial DNA
mtHSP70	mitochondrial Heat Shock Protein 70
NAC	N-Acetyl-Cysteine
NDUFA9	39kDa subunit of Complex I
Nrf2	Nuclear factor erythroid 2-related factor
O ₂ ⁻	superOxide

OH·	HydrOxyl radical
OMM	Outer Mitochondrial Membrane
Opa1	Optic atrophy 1
PBS	Phosphate Buffered Saline
PD	Parkinson's Disease
PERK	Pancreatic ER Kinase
PGC-1 α	Peroxisome proliferator-activated receptor- γ Co-activator 1 α
PIAS	Protein Inhibitor of Activated Signal transducers and activators of transcription
Pink1	PTEN-induced putative kinase 1
PSF	Pyrimidine tract-binding protein-associated Splicing Factor
PTEN	Phosphatase and TENsin homolog
PVDF	PolyVinylidene Fluoride
REM	Rapid Eye Movement
ROS	Reactive Oxygen Species
SDS	Sodium Dodecyl Sulfate
SEM	Standard Error of the Mean
SNc	Substantia Nigra pars compacta
SNr	Substantia Nigra pars reticulata
STN	SubThalamic Nucleus
TFAM	Mitochondrial Transcription Factor A
TH	Tyrosine Hydroxylase
Tom20	Translocator of the outer mitochondrial membrane 20

TSPO	TranSlocator PrOtein
UPDRS	Unified Parkinson's Disease Rating Scale
UPR	Unfolded Protein Response
VDAC	Voltage Dependent Anion Channel
VSP35	Vacuolar protein Sorting-associated Protein 35
VTA	Ventral Tegmental Area
WT	WildType

CHAPTER 1

General Introduction

1.1 Parkinson's Disease Etiology

Parkinson's disease (PD), the second most common neurodegenerative disease, affects approximately 1% of the population over 60 years of age and up to 4% of the population over 80 years old (de Rijk et al., 1995; Bower et al., 1999; de Lau and Breteler, 2006; Alves et al., 2008). The first medical description of the disease came from James Parkinson, who termed it 'shaking palsy', however this disease has been mentioned even earlier, by Leonardo da Vinci in the late 13th or early 14th century and even in 1350-1200 BCE by Egyptians (Parkinson, 1817; Forno, 1996). In the almost 200 years since the initial medical characterization, the complexity of this disease has been revealed – with patients showing variability in age of onset, symptoms, and responsiveness to therapies. As such, official diagnosis of this disease does not occur until autopsy, although a skilled neurologist can detect over 90% of cases (Hughes et al., 2002). Additionally, treatment is limited to symptomatic relief, due to the multifactorial nature of PD combined with an unknown cause in the majority of cases.

1.1.1 Idiopathic PD

Approximately 90% of all cases of PD are of unknown cause (idiopathic) and are most likely due to environmental factors (Alves et al., 2008). Numerous studies have suggested age as the number one risk factor for developing PD (Tanner and Langston, 1990; de Rijk et al., 1995; Bower et al., 1999; de Lau and Breteler, 2006). Although correlative at best, studies indicate that pesticide exposure, heavy metal exposure, well water consumption and rural living may contribute to idiopathic PD (Tanner and Langston, 1990; Gorell et al., 1998; Priyadarshi et al., 2001; Dick et al., 2007).

Interestingly, both cigarette smoking and coffee consumption have been linked to decrease incidence of PD (Ross et al., 2000; Hernán et al., 2002; Ritz et al., 2007).

Additionally, certain epigenetic changes, such as DNA methylation, chromatin remodelling and histone modification, may mediate susceptibility to these environmental factors (Urduingio et al., 2009; Portela and Esteller, 2010; Jakovcevski and Akbarian, 2012; Feng et al., 2014). Most likely, pathogenesis of the disease occurs due to a combination of environmental and genetic factors.

1.1.2 Familial PD

Almost 20 years ago, the first study showing familial linkage in cases of PD emerged (Polymeropoulos et al., 1997). The development of stronger tools has allowed for identification of numerous genes linked with either autosomal dominant (AD) or autosomal recessive (AR) PD as well as several susceptibility genes (Hardy, 2010; Peeraully and Tan, 2012; Bras et al., 2015). Through the use of these genetic tools, 11 genes have been identified as having a causative role in development of monogenic typical or atypical PD (Table 1.1) (Klein and Westenberger, 2012; Bonifati, 2014; Bras et al., 2015). Genes including *α-synuclein*, *leucine-rich repeat kinase 2 (LRRK2)*, *vacuolar protein sorting-associated protein 35 (VPS35)*, *Parkin*, *PTEN-induced putative kinase 1 (PINK1)*, and *DJ-1* have been shown to be involved in familial PD.

Table 1.1. Summary of confirmed genes having a causative role in Parkinson's disease (PD). Here the confirmed genes responsible for familial PD are summarized with locus, onset, type of inheritance and classification of symptoms. Onset varies in familial PD, with juvenile (<20 years old), early (<40 years old), and late (>50 years old) types. There are two methods of inheritance encountered - autosomal dominant (AD) and autosomal recessive (AR). Genetic forms of PD can either be classified as classical, in which symptoms are similar to idiopathic PD, or atypical, in which additional symptoms may exist.

Gene (Locus)	Onset	Inheritance	Type	References
<i>α-SYNUCLEIN</i> (<i>PARK1,4</i>)	Early to late	AD	Aggressive	(Polymeropoulos et al., 1997)
<i>PARKIN</i> (<i>PARK2</i>)	Early	AR	Slow	(Kitada et al., 1998)
<i>PINK1</i> (<i>PARK6</i>)	Early	AR	Slow	(Valente et al., 2004)
<i>DJ-1</i> (<i>PARK7</i>)	Early	AR	Slow	(Bonifati et al., 2003)
<i>LRRK2</i> (<i>PARK8</i>)	Late	AD	Typical	(Zimprich et al., 2004)
<i>ATP13A2</i> (<i>PARK9</i>)	Juvenile	AR	Atypical	(Ramirez et al., 2006)
<i>PLA2G6</i> (<i>PARK14</i>)	Juvenile	AR	Atypical	(Paisán-Ruíz et al., 2009)
<i>FBXO7</i> (<i>PARK15</i>)	Juvenile	AR	Atypical	(Shojaee et al., 2008)
<i>VPS35</i> (<i>PARK17</i>)	Late	AD	Typical	(Vilariño-Güell et al., 2011; Zimprich et al., 2011)
<i>DNAJC6</i> (<i>PARK19</i>)	Juvenile	AR	Atypical	(Edvardson et al., 2012)
<i>SYNJ1</i> (<i>PARK20</i>)	Juvenile	AR	Atypical	(Krebs et al., 2013)

The well-characterized *α-synuclein* and *LRRK2*, as well as the more recently discovered *VPS35*, show AD inheritance, in which only one mutated allele is required to elicit an effect. Mutations in *α-synuclein* include point mutations as well as gene multiplication events (two or three copies) and account for ~2% of all familial PD cases (Polymeropoulos et al., 1997; Krüger et al., 1998; Chartier-Harlin et al., 2004; Ibáñez et al., 2004; Ibáñez et al., 2009; Nuytemans et al., 2010). There appears to be a dosage effect with *α-synuclein*, as individuals with four copies of the gene show early-onset PD (<50 years old at age of onset) and faster disease progression, compared to individuals with three copies who show late-onset PD (Chartier-Harlin et al., 2004; Fuchs et al., 2007). Mutations in *LRRK2* occur in 2-40% of both the late-onset AD as well as sporadic PD, depending on the population (Lesage et al., 2006; Ozelius et al., 2006). Over 80 mutations in *LRRK2* have been identified, with 6 of them showing pathological involvement in PD (Zimprich et al., 2004; Nuytemans et al., 2010). Individuals with these mutations typically show mid-to-late onset with slow disease progression, and some mutations show an age-dependent penetrance (Healy et al., 2008). Mutations in *VPS35* were identified by two separate groups concurrently (Vilariño-Güell et al., 2011; Zimprich et al., 2011). Both groups demonstrated that these patients have a missense mutation in *VPS35* that results in typically late-onset of the disease (Vilariño-Güell et al., 2011; Zimprich et al., 2011). Further investigation has shown relatively similar symptoms to idiopathic PD but with increased incidence of depression, although the sample size is quite limited (Struhal et al., 2014).

Parkin, *Pink1*, and *DJ-1* mutations resulting in PD are all inherited in an AR manner. The second identified gene to cause PD and the first to be AR-associated was

Parkin (Kitada et al., 1998). Mutations in this gene are responsible for ~10-20% of all early-onset PD and up to 77% of cases with age of onset <30 years old (Lücking et al., 2000; Klein and Lohmann-Hedrich, 2007). An impressive 887 mutations in *Parkin* have been identified, resulting in 147 unique changes to the protein (Klein and Westenberger, 2012). *Parkin* mutations typically result in PD that is early-onset and with slow disease progression (Kitada et al., 1998; Lücking et al., 2000; Lohmann et al., 2003; Klein and Lohmann-Hedrich, 2007). The second most common gene associated with early-onset PD is *Pink1*, with approximately 1-9% of this group carrying mutations for this gene (Rogaeva et al., 2004; Valente et al., 2004; Bonifati et al., 2005). Mutations in *DJ-1* are by far the most rare mutations for early-onset PD, counting for only 1-2% of these cases (Abou-Sleiman et al., 2003; Bonifati et al., 2003; Pankratz et al., 2006). These mutations of *DJ-1* will be more thoroughly discussed in Section 1.7.2.

Additional loci have been linked to PD, however no specific genes within these regions have been identified as yet (Bras et al., 2015). Additionally, one risk gene and 24 risk loci have been identified (Bras et al., 2015). The risk gene, *β -glucocerebrosidase* (*GBA*), is particularly interesting, as over 300 mutations in it are associated with the lysosomal storage disorder Gaucher disease (Hruska et al., 2008). Homozygous or heterozygous mutations in *GBA* are also found in up to 15% of autopsy-confirmed PD cases (Goker-Alpan et al., 2004; Lwin et al., 2004; Sidransky et al., 2009). *GBA* mutations occur 5 times more frequently in PD patients than controls (Sidransky et al., 2009). While mutations in this gene and other loci are associated with a medium to low risk of developing PD, they help give insight into the potential various pathways involved in the disease pathogenesis.

1.2 Parkinson's Disease Phenotypes

1.2.1 Motor Symptoms

The hallmark symptoms of PD include resting tremor, rigidity of limbs, akinesia and postural instability (Parkinson, 1817; Hoehn and Yahr, 1967; Lang and Lozano, 1998; Samii et al., 2004; Jankovic, 2008; Massano and Bhatia, 2012). Resting tremor is an involuntary rhythmic oscillatory movement that occurs during rest and disappears with active movement (Samii et al., 2004; Jankovic, 2008; Massano and Bhatia, 2012). It is the most easily identifiable and most common symptom in PD, with at least 70% of patients experiencing it (Hoehn and Yahr, 1967; Hughes et al., 1993; Samii et al., 2004; Jankovic, 2008). Resting tremor in PD typically occurs in extremities, especially the hands in a “pill rolling” type of movement (Samii et al., 2004; Jankovic, 2008; Massano and Bhatia, 2012). It occasionally involves the jaw, chin and lips but never the head/neck in PD patients (Jankovic, 2008; Massano and Bhatia, 2012). Rigidity of limbs refers to increased resistance and stiffness that persists throughout a range of movements involving both distal and proximal joints (Samii et al., 2004; Jankovic, 2008; Massano and Bhatia, 2012). A “cogwheel” motion is often observed in PD patients, where muscles respond with jerky movements due to the force used to move limbs (Samii et al., 2004; Jankovic, 2008; Massano and Bhatia, 2012). Akinesia (or bradykinesia) is the slowness in movement, particularly in planning, initiating and executing movement (Berardelli et al., 2001; Samii et al., 2004; Jankovic, 2008; Massano and Bhatia, 2012). Considered to be the most disabling of the cardinal symptoms, at least in early stages of PD, akinesia affects fine motor tasks such as handwriting and doing up buttons (Samii et al., 2004). Postural instability is an impairment in balance due to loss of properly functioning

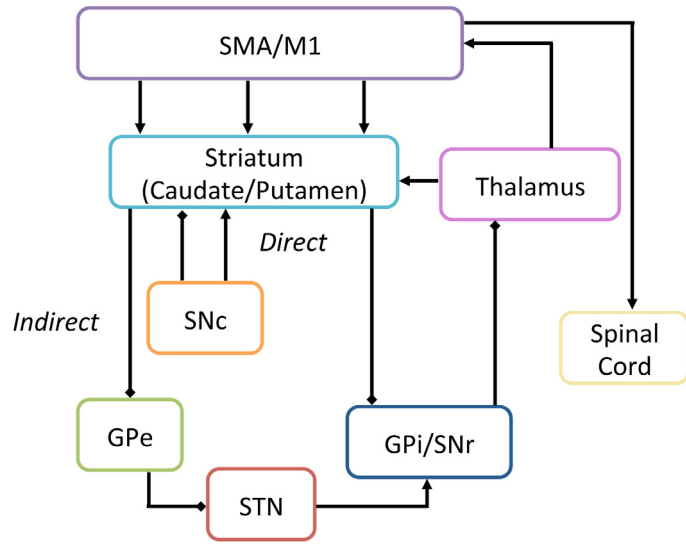
postural reflexes (Samii et al., 2004; Jankovic, 2008; Massano and Bhatia, 2012). It is often absent in early stages of PD, particularly in younger patients (Samii et al., 2004; Jankovic, 2008). Postural instability leads to an increased risk of falling, and the frequency of falls is linked to disease severity (Koller et al., 1989; Samii et al., 2004; Williams et al., 2006; Jankovic, 2008; Massano and Bhatia, 2012).

These symptoms are thought to arise due to the selective loss of dopaminergic neurons in the *substantia nigra pars compacta* (SNc) and thus disruption of basal ganglia circuitry. These neurons are important in motor control, particularly in initiation of voluntary movement. The *substantia nigra* is part of the basal ganglia-thalamocortical circuitry, in which “direct” and “indirect” signalling pathways from the SNc lead to activation of the primary motor cortex and supplementary motor area via the thalamus (Figure 1.1).

Figure 1.1. Effect of Parkinson's disease on basal ganglia signalling. Simplified overview of signalling involved in both “direct” and “indirect” circuits originating from substantia nigra *pars compacta* (SNc). Loss of dopaminergic neurons in the SNc ultimately leads to enhanced inhibition of the thalamus by the globus pallidus internal segment (GPI), loss of cortical activation and loss of initiation of voluntary movement. Thickness of arrow indicates strength of transmission. SMA, supplementary motor area; M1, primary motor cortex; STN, subthalamic nucleus; GPe, globus pallidus external segment; SNr, substantia nigra *pars reticulata*.

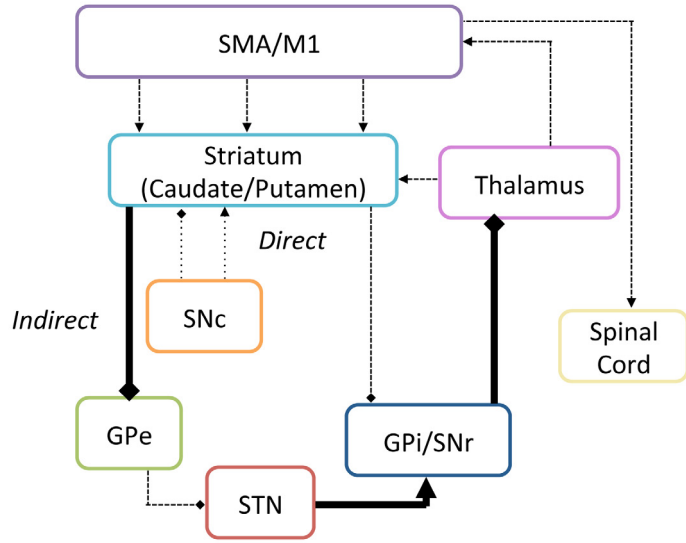
A

Normal Basal Ganglia Signaling



B

PD Basal Ganglia Signaling



→ Excitatory
 —→ Inhibitory

The striatum, made up of the putamen and caudate, consists mostly (~95%) of medium spiny neurons that are rich in dopamine receptors (Kringelbach et al., 2007). In the “direct” circuit, a subset of these striatal neurons are activated by the dopaminergic transmission from the SNc, which in turn inactivate the globus pallidus internal segment (GPi), allowing for activation of the primary motor cortex (M1) and supplementary motor area (SMA) as the thalamus is no longer inhibited. In the “indirect” circuit, a separate subset of the striatal neurons are inhibited by the dopaminergic transmission from the SNc, which prevents the inhibition of the globus pallidus external segment (GPe), and stops the activation of the GPi via the subthalamic nucleus (STN). Loss of input from the SNc leads to an overall increase in inhibition of the thalamus, via loss of inhibition of the GPi by the direct pathway and inhibition of the GPe by the indirect pathway. Loss of thalamus signalling leads to loss of cortical activation and consequently loss of initiation of voluntary movement.

1.2.2 Non-Motor Symptoms

PD patients exhibit various non-motor symptoms throughout the stages of their disease. These symptoms include alterations in neuropsychiatric, sleep, autonomic, and sensory functions (Samii et al., 2004; Chaudhuri and Naidu, 2008; Jankovic, 2008; Poewe, 2008). Almost 40% of PD patients have dementia, with a 2-6 times higher risk versus the general population (Marder et al., 1995; Aarsland et al., 2001). Approximately 30-40% of PD patients suffer from depression (Poewe, 2008; Blonder and Slevin, 2011). The majority of PD patients encounter night time awakenings, at a rate three times higher than the general population (Stacy, 2002; Porter et al., 2008). A wide range of autonomic

symptoms are encountered by PD patients, such as constipation, bladder hyperactivity, erectile dysfunction and excessive sweating, which worsen with disease progression (Edwards et al., 1991; Singer et al., 1992; Sakakibara et al., 2001; Swinn et al., 2003; Verbaan et al., 2007; Jankovic, 2008; Poewe, 2008). Olfactory dysfunction affects anywhere from 70-100% of PD patients (Chaudhuri and Naidu, 2008; Simuni and Sethi, 2008).

Two early occurring symptoms, gastro-intestinal dysfunction and anosmia (loss of sense of smell), are thought to occur years before motor symptoms (Doty et al., 1988; Abbott et al., 2001; Braak et al., 2003; Braak et al., 2004; Ponsen et al., 2004; Poewe, 2008; Haehner et al., 2011). Additionally, rapid eye movement (REM) sleep behaviour disorder is frequently encountered and even considered to be a risk factor for PD (Schenck et al., 1996; Gagnon et al., 2006). With some non-motor symptoms occurring before the motor symptoms, they are ideal early indicators of the disease.

1.3 Pathology

1.3.1 Substantia Nigra Pars Compacta (SNc)

The most visible hallmark of PD in the post-mortem human brain is the striking loss of pigmented cells in the SNc, located in the basal ganglia (Parkinson, 1817; Greenfield and Bosanquet, 1953; Hoehn and Yahr, 1967; Bernheimer et al., 1973; Gaspar and Gray, 1984; Hughes et al., 1993). It is proposed that at least 30% of these neurons are lost by the time clinical symptoms arise (Fearnley and Lees, 1991; Hilker et al., 2005; Greffard et al., 2006). These dopaminergic neurons contain melanin, a naturally dark substance and hence are easily identifiable and their absence is quickly detected visually

during post-mortem analysis (Hughes et al., 1993; Lang and Lozano, 1998). Additionally, loss of dopamine terminals and decreased dopamine levels in the striatum have been observed (Foix and Nicolesco, 1925; Bernheimer et al., 1973; Nyberg et al., 1983; Scherman et al., 1989; Wilson et al., 1996).

Fritz Heinrich Lewy first described the presence of intracytoplasmic protein aggregates called Lewy Bodies (LBs) and Lewy Neurites (LNs) in PD post-mortem brains (Greenfield and Bosanquet, 1953; Okazaki et al., 1961; Forno, 1996; Lang and Lozano, 1998; Holdorff, 2002). These aggregates appear to have a dense core, surrounded by filamentous material and contain α -synuclein and ubiquitin (Okazaki et al., 1961; Forno, 1996; Spillantini et al., 1997; Baba et al., 1998). It is unclear as to whether these aggregates are a protective mechanism or damage-inducing in the cell. It is proposed that oligomers and fibrils of α -synuclein as well as the aggregation process itself are neurotoxic, whereas LBs are protective (Maries et al., 2003; Ross and Poirier, 2005).

1.3.2 Locus Coeruleus (LC)

There is also select degeneration in non-dopaminergic areas such as the *locus coeruleus* (LC) (Greenfield and Bosanquet, 1953; Gaspar and Gray, 1984; Cash et al., 1987; Chan-Palay and Asan, 1989; German et al., 1992; Zarow et al., 2003), which may account for some of the non-motor symptoms observed in many patients. The LC is responsible for the physiological response to stress or panic and therefore its degeneration is thought to be responsible for sleep disturbances, especially during the REM sleep cycle of PD patients (García-Lorenzo et al., 2013).

1.3.3 Ventral Tegmental Area (VTA)

Adjacent to the SNc is a group of dopaminergic neurons termed the ventral tegmental area (VTA). There are mixed reports on the involvement of the VTA in PD pathology, however the consensus appears to be that this area is significantly less affected than the SNc in PD (Uhl et al., 1985; German et al., 1989; German et al., 1992; Dymecki et al., 1996; Alberico et al., 2015). Interestingly, some of the non-motor symptoms such as depression and anxiety found in some PD patients could be related to VTA dysfunction (Russo and Nestler, 2013; Alberico et al., 2015).

1.3.4 Braak Hypothesis

Thorough investigation of the central nervous system (CNS) for the presence of LBs demonstrated a progressive invasion of these proteinaceous inclusions that start in lower brain regions and spread upwards (Braak et al., 2002; Braak et al., 2004). Studying the areas of the brain and nervous system that exhibit LB pathology, together with the timing in which these LBs appeared in accordance to the progression of the disease, led Dr. Heiko Braak to propose a staging system to PD (Braak et al., 2002; Braak et al., 2004). As such, the Braak hypothesis suggests that in PD, the SNc is actually affected at the mid-way point of the disease, at which point the patients are clinically diagnosed (Braak et al., 2002; Braak et al., 2004). In the earlier stages, more caudal parts of the brain are affected by LB pathology and the disease progresses rostrally (Braak et al., 2002; Braak et al., 2004). It is proposed that only once LBs reach the midbrain, do patients become symptomatic (Braak et al., 2002). The more areas affected by LB

pathology, the higher the stage and thus the more severe the stage of the disease (Braak et al., 2002; Braak et al., 2004).

1.3.5 Disease Scale in Parkinson's Disease

PD is a degenerative disease, and as time passes, the symptoms of the disease worsen. Hoehn and Yahr were first to propose a scale in which severity of PD was ranked on a scale of 1-5, with 1 being the least and 5 being the most severe (Hoehn and Yahr, 1967). They did so to highlight the differences in symptoms between patients, in what seemed to be a fairly homogeneous disease population (Hoehn and Yahr, 1967). This study was the first to demonstrate how widely varied symptoms (and severity of these symptoms) were within the PD population. Numerous staging models have since been created and employed, making it difficult to compare assessments between the different models (Disease, 2003). As such, a more universal scale was created, termed the Unified Parkinson's Disease Rating Scale (UPDRS) (Disease, 2003). The UPDRS is comprised of four components – providing a comprehensive assessment of both motor and non-motor symptoms as well as additional complications with these symptoms (Disease, 2003). The stage of PD and identification of the most predominant symptoms often dictates the direction in which treatment is taken.

1.4 Current Therapies

Current therapy for PD consists of managing symptoms caused by the loss of dopaminergic neurons – while effective short-term, there is no long-term single medical

therapy for PD. The complexity of this disease leads to increasing difficulties in treatment, as one therapy could work for one patient but not another.

1.4.1 Dopamine Replacement

The most common drug administered for treatment of PD is levodopa (3,4-dihydroxyphenylalanine; L-DOPA), a precursor of dopamine (Lang and Lees, 2002; Goetz et al., 2005; Connolly and Lang, 2014). Dopamine cannot be administered directly as it does not cross the blood brain barrier. By increasing the amount of precursor available, the remaining dopaminergic neurons can produce more dopamine and thus the SNc neurons can compensate for the loss of cortical activation by the thalamus. Other pharmacological strategies that revolve around boosting available dopamine levels include dopamine agonists and monoamine oxidase inhibitors, which prevent degradation of dopamine (Lang and Lees, 2002; Goetz et al., 2005; Jankovic, 2008; Connolly and Lang, 2014).

PD patients go through “ON” and “OFF” phases in which they experience relief and subsequently no relief from the symptoms despite pharmacological treatment (Lang and Lees, 2002; Goetz et al., 2005; Connolly and Lang, 2014). Over time, the amount of “OFF” time increases as the effectiveness of treatment decreases (Chase, 1998; Ahlskog and Muenter, 2001; Jankovic, 2005; Jankovic, 2008; Connolly and Lang, 2014). Dosages can be adjusted to accommodate patients; however, within a few years of initial treatment, motor fluctuations as well as dyskinesia, or involuntary movement, develop and can become severely debilitating (Chase, 1998; Ahlskog and Muenter, 2001; Lang and Lees, 2002; Goetz et al., 2005; Jankovic, 2005; Jankovic, 2008; Connolly and Lang,

2014; Sharma et al., 2015). These unwanted motor symptoms are most likely partially due to the fact that physiological levels of dopamine transmission are not restored, and go through constant fluxes (Chase, 1998), nonetheless, the full molecular mechanism of L-DOPA-induced dyskinesia is not fully understood (Jenner, 2008; Sharma et al., 2015). Typically within 10 years of L-DOPA treatment, the negative side effects outweigh the benefits from the pharmacological treatment and the patient must seek alternative treatment options (Lang and Lees, 2002; Goetz et al., 2005; Cenci, 2007; Jenner, 2008; Connolly and Lang, 2014; Sharma et al., 2015).

1.4.2 Surgical Treatments

During the 1940s-1960s, specific lesioning techniques were employed to treat a variety of neurological issues, including PD (Meyers, 1940; Cooper, 1956). While the technique of lesioning the thalamus in PD patients proved to be successful, it was often marred by unwanted side effects from the invasiveness of the procedure, or from accidental lesioning of non-target tissue (Matsumoto et al., 1984; Tasker, 1998). The irreversible nature of this procedure also contributed to the possible negative outcome of this technique. It was in the late 1980s that a reversible lesioning technique was introduced in this context – deep brain stimulation (DBS) (Benabid et al., 1987). This technique opened the door for a safer option for treating PD outside of pharmacological methods.

The results from the first DBS procedure for treatment of PD was published by Dr. Benabid in 1987 and involved placement of electrodes in the ventral intermediate thalamic nucleus of the patient (Benabid et al., 1987). It had been discovered that

applying a frequency over 100Hz actually caused *inhibition* of the surrounding tissue, versus activation when the frequency was below 100Hz (Benabid et al., 1987; Kringelbach et al., 2007). This discovery led to the development of a reversible lesioning technique in which tissue did not have to be physically destroyed. Numerous targets in the basal ganglia that had previously been the focus of permanent lesioning techniques were now the main focus for the development of DBS to treat PD.

Unfortunately it still remains that only treatment, but no cure, exists for PD. In order to cure and even prevent this degenerative disease, we need to better understand the causes of the disease itself.

1.5 Parkinson's Disease Pathogenesis

1.5.1 Protein Aggregation

Proteinaceous bodies found throughout the cell body (LBs) and neurites (LNs) were found to contain aggregated α -synuclein and ubiquitin, amongst other proteins (Okazaki et al., 1961; Forno, 1996; Spillantini et al., 1997; Baba et al., 1998). The endoplasmic reticulum (ER) is responsible for the proper folding of proteins following their translation (Kaufman, 1999). The Unfolded Protein Response (UPR) is an ER stress mechanism, activated typically when an accumulation of unfolded and/or misfolded proteins occurs (Kaufman, 1999). Activation of this pathway leads to an overall reduction in translation and therefore less protein burden on the ER, while specifically upregulating translation of stress-response proteins (Kaufman, 1999). Various experimental models of PD have shown ER stress and activation of the UPR *in vitro* (Ryu et al., 2002). Post-mortem analysis of PD patients has also shown an increase in markers of ER stress and

induction of the UPR – specifically increased levels of phosphorylated pancreatic ER kinase (PERK) and its downstream target eukaryotic initiation factor 2 α (eIF2 α) in the SNc (Hoozemans et al., 2007).

Additionally, the PD-related Parkin is an E3 ubiquitin ligase that mediates proteasomal degradation of its targets following ubiquitination (Imai et al., 2000). The UPR increases levels of both Parkin mRNA and protein and overexpression of Parkin can protect against UPR-induced death (Imai et al., 2000). Loss of Parkin leads to an accumulation of its target proteins and this could play a role in the pathogenesis of the disease (Imai et al., 2000). The protein product of another PD gene, α -synuclein, is shown to aggregate, especially when mutated (Narhi et al., 1999). Expression of mutant α -synuclein *in vitro* increases ER stress and leads to significantly higher cell death compared to WT α -synuclein (Smith et al., 2005). Interestingly, transplant of embryonic nigral neurons to PD patients results in LB-like pathology of the transplanted tissue years later (Alves et al., 2008; Kordower et al., 2008). These findings suggest that PD-like pathology can propagate from the host tissue to the donor tissue, possibly via α -synuclein (Alves et al., 2008; Kordower et al., 2008). There are recent studies that indicate aggregated α -synuclein may indeed cause aggregation of soluble α -synuclein, in a similar fashion to the prion protein in prion disease (Volpicelli-Daley et al., 2011; Angot et al., 2012; Luk et al., 2012).

1.5.2 Inflammation

In addition to the proteinaceous inclusions throughout the brain, post-mortem studies of PD patients have found increased markers of inflammation and activated

microglia specifically localized to the *substantia nigra* and striatum (McGeer et al., 1988; Mogi et al., 1994; Mogi et al., 1996; Banati et al., 1998; Hunot et al., 1999; Imamura et al., 2003). The central nervous system was considered “immune privileged” due to the strict regulations of the blood brain barrier – limiting entry of molecules via tight junctions and monitoring by specific astrocytes and microglia (Hanisch and Kettenmann, 2007; Heneka et al., 2014). In the brain, microglia are considered the resident macrophages and are constantly surveying their environment (Hanisch and Kettenmann, 2007; Heneka et al., 2014). When activated, microglia are responsible for clearing dead or dying cells, as well as releasing various trophic factors (Batchelor et al., 1999; Hanisch and Kettenmann, 2007; Heneka et al., 2014). While a moderate level of activation is beneficial, extended periods of microglial activation can be harmful to otherwise healthy cells, due to the generation of reactive oxygen species (ROS) and cytokines (Hanisch and Kettenmann, 2007; Heneka et al., 2014).

Additionally, induction of inflammation either locally or systemically by the bacterial endotoxin lipopolysaccharide, causes specific loss of dopamine neurons in the *substantia nigra* (Herrera et al., 2000; Qin et al., 2007). The proof of concept that suppression of the immune system can be protective in an animal model of PD was shown by our group in two different studies, in which loss of components required for an immune-mediated inflammation response protects dopaminergic neurons in the *substantia nigra* against oxidative stress (Mount et al., 2007; Lira et al., 2011). It has been proposed that early stages of microglial activation is protective however over time this activation can become dysfunctional – it is this aberrant and extended activation of microglia that can cause neuronal death (Mosley et al., 2012; Heneka et al., 2014).

1.5.3 Oxidative Stress and Mitochondrial Dysfunction

It has been suggested that oxidative stress plays a role in dopaminergic cell death, with the finding that there is a decrease in the electron transport chain (ETC) complex I activity in addition to the presence of ROS-damaged end products in the *substantia nigra* of post-mortem PD patients (Dexter et al., 1989; Schapira et al., 1989; Lang and Lozano, 1998). As well, post-mortem examination of the frontal cortex of PD patients shows mitochondrial respiratory impairments, a modest decrease in complex I activity and an increase in oxidation products of protein and phospholipids (Navarro et al., 2009). While these findings are supportive of the notion of the role of oxidative stress in PD, they do not determine if in fact ROS is a cause for degeneration or simply a consequence. Interestingly, Parkinson-like symptoms have been observed in numerous patients following the administration of the heroin analogue 1-methyl-4-phenyl-4-propionoxy piperidine (MPPP) contaminated with 1-methyl-4-phenyl-1,2,5,6-tetrahydropyridine (MPTP) (Davis et al., 1979; Langston et al., 1983). Similarly, administration of MPTP to rodents results in the loss of dopamine and its metabolites in the nigrostriatal pathway as a result of dopaminergic cell death (Heikkila et al., 1984; Heikkila et al., 1985). Importantly the metabolite of MPTP, 1-methyl-4-phenylpyridinium ion (MPP⁺), is a substrate for the dopamine transporter where it is targeted to mitochondria and inhibits complex I (Betarbet et al., 2000).

Another complex I inhibitor, rotenone, often found in pesticides, can cause progressive nigrostriatal dopaminergic degeneration in rats (Heikkila et al., 1985; Betarbet et al., 2000). Inhibition of complex I can lead to deregulated Ca²⁺ levels as well as decreased ATP synthesis (Sherer et al., 2002). Disruption of the ETC can also result

in increased levels of ROS that lead to oxidation of lipids, DNA and proteins (Sherer et al., 2002). An increase in ROS can induce damage to mitochondria when antioxidant defenses have been exhausted (Choi et al., 2006). Through a cycle of mitochondria dysfunction, decreased antioxidant potential, and increased ROS production, cell death is inevitable (Sherer et al., 2002; Choi et al., 2006).

Of the familial PD genes identified, DJ-1, Parkin and Pink1 all have strong association with mitochondria. DJ-1 is a multi-functional protein, most notably involved in sensing reactive oxygen species (Canet-Avilés et al., 2004; Shendelman et al., 2004). DJ-1 partially localizes to mitochondria upon induction of stress and this localization protects cells against further damage (Canet-Avilés et al., 2004; Junn et al., 2009). DJ-1 deficient mice are hypersensitive to oxidative stress and have fragmented mitochondria that produce higher levels of reactive oxygen species (Kim et al., 2005b; Aleyasin et al., 2010; Krebiehl et al., 2010). A more in depth look at DJ-1 will be discussed in section 1.7. Loss of Parkin in mammalian cells causes mitochondrial dysfunction (Palacino et al., 2004). Pink1 is a serine/threonine kinase that contains a mitochondrial targeting motif (Valente et al., 2004; Silvestri et al., 2005; Zhou et al., 2008). Pink1 deficient mammalian cells have dysfunctional mitochondria and are hypersensitive to oxidative insult (Haque et al., 2008; Wood-Kaczmar et al., 2008; Dagda et al., 2009; Liu and Lu, 2010).

There is much controversy surrounding the link between mitochondrial dysfunction and PD – whether the damage to mitochondria is a cause or result of the disease, and if it is a cause, why are only specific areas of the brain affected? There are other diseases in which mitochondrial dysfunction is a key factor. For example, Leber's hereditary optic neuropathy (LHON) is characterized by decreased complex I activity

(Parker et al., 1989). This decrease is most often caused by one of three single point mutations in mitochondrial-encoded subunits of complex I (Schrier and Falk, 2011). Individuals with LHON develop progressive blindness most likely due to thickening of the retinal nerve fibres as well as loss of retinal ganglion cells in the optic nerve (Schrier and Falk, 2011). Despite this complex I dysfunction, there is no apparent correlation between this disease and risk of Parkinson's disease, however it is interesting to note the specificity of degeneration also observed in LHON.

In contrast, mutations leading to defects in the ETC (most commonly in subunits of complex I) in Leigh's disease lead to necrotizing lesions in the basal ganglia, brain stem, diencephalon or cerebellum (Finsterer, 2008). While typically early childhood-onset, it can also develop in young adults however most patients die by 5 years of age (Finsterer, 2008). Some of these patients have lesions involving the substantia nigra (Medina et al., 1990), which supports the role of mitochondrial dysfunction in neurodegeneration. However, this disease has a much more rapid onset compared to PD, and not all the same areas in the brain are affected.

Interestingly, mice in which an essential component of mitochondrial function, mitochondrial transcription factor A (TFAM), was removed from dopaminergic neurons, exhibit a slow degeneration of these neurons as well as progressive motor deficits (Ekstrand and Galter, 2009). TFAM is essential in maintaining the integrity of mitochondrial DNA (mtDNA), and its loss increases the rate of mutations occurring in the mtDNA, thereby affecting the function of mitochondria (Larsson et al., 1998; Ekstrand and Galter, 2009). This mouse model further implicates the role of mitochondrial dysfunction in the pathology of PD. However it does not explain why

dopaminergic neurons in the substantia nigra degenerate while neighbouring dopaminergic neurons in the VTA are relatively spared.

Interestingly, it has been shown that neurons in the SNc are constantly firing, even in absence of synaptic input (Chan et al., 2007; Chan et al., 2010). The SNc pacemaking is rather unique as it uses Ca^{2+} channels, specifically the L-type Ca^{2+} channel $\text{Ca}_v1.3$ (Chan et al., 2007; Chan et al., 2010). It is proposed that this ATP-dependent process results in accelerated aging of these neurons, compared to neighbouring neurons, such as in the VTA, that do not use $\text{Ca}_v1.3$ channels for pacemaking (Chan et al., 2010). In further support of the idea that these $\text{Ca}_v1.3$ channels cause the selective vulnerability of SNc neurons, blockade of these channels using the Ca^{2+} channel inhibitor isradipine prevents cell death in two *in vivo* rodent models of PD (Chan et al., 2007; Chan et al., 2010). Additionally, SNc neurons seem to have more oxidative stress than VTA neurons, and treatment with isradipine considerably reduces these levels (Guzman et al., 2010). Given these findings, a newly discovered inhibitor specific to $\text{Ca}_v1.3$ channels is a potential therapeutic option for PD patients (Kang et al., 2012). By reducing Ca^{2+} mediated pacemaking activity of these neurons, there is less demand for ATP production and therefore less stress on mitochondria, which could in turn prevent the early aging of these neurons (Chan et al., 2010; Kang et al., 2012).

1.6 Mitochondria

1.6.1 Structure and Function

Believed to have originated as engulfed prokaryotes and establishing an endosymbiotic relationship in eukaryotes, mitochondria exist in most eukaryotic cells and

are considered the “power house” of the cells (Gray et al., 1999, 2001). With its own genetic code, mitochondria are able to produce a major source of energy in a cell, ATP, via oxidative phosphorylation. Additionally, mitochondria store and regulate Ca^{2+} and are essential in many signalling pathways, such as cell death (Duchen, 1999; Butow and Avadhani, 2004; Duchen, 2004; Green and Kromer, 2004).

Mitochondria are double membrane bound organelles, with an outer mitochondrial membrane (OMM), inner mitochondrial membrane space (IMS), inner mitochondrial membrane (IMM) and matrix. Invaginations of the inner membrane, termed cristae, largely increase the overall surface area of the IMM and are the site for oxidative phosphorylation.

Embedded within and on the surface of the IMM are the five complexes – termed the electron transport chain (ETC) due to the shuttling of electrons along these complexes. The shuttling of electrons facilitates ATP production via metabolism of glucose and other sugars. Also known as oxidative phosphorylation, this process uses pyruvate (sourced from glucose breakdown by glycolysis) and succinate (mainly sourced from the citric acid cycle) as substrates. Electrons travel through the complexes in a series of redox reactions to finally be accepted by O_2 to create H_2O , driving protons from the matrix across the IMM to the IMS. This drive creates an electrochemical gradient in which the IMS has a higher concentration of protons versus the matrix. ATP synthase, the final complex of the ETC, uses the proton-motive force of this gradient to pump protons back into the matrix, thus driving ATP synthesis.

1.6.2 Dynamics

Mitochondria are not static organelles – they are highly dynamic, undergoing constant fission (breaking apart) and fusion (joining together). This process is mediated by numerous factors, including the fission protein dynamin-related protein 1 (Drp1) and the fusion proteins mitofusins 1 and 2 (Mfn1, 2) and optic atrophy 1 (Opa1) (Chen and Chan, 2004; Detmer and Chan, 2007; Lackner, 2014). Fission occurs when Drp1 is recruited to the OMM and forms a ring-like structure at the site to be fissioned.

Mitochondrial fission protein 1 (Fis1) and mitochondrial fission factor (Mff) actively target Drp1 to the OMM. This site is also in contact with the endoplasmic reticulum (ER), which marks the site for the actual break in the mitochondrion. Fusion of the OMM is regulated by mitofusin-1 (Mfn1) and mitofusin-2 (Mfn2) while IMM fusion is mediated by optic atrophy 1 (OPA1). Mfn1/2 act as tethers – they bind with other Mfn1/2 on the OMM of other mitochondria to initialize fusion.

The dynamic changes of mitochondria allow for mixing of genomic and matrix content and dilution of oxidized and/or damaged proteins and mtDNA (Fischer et al., 2012). Furthermore, fusion enhances ER-mitochondria communication and allows for more efficient movement of mitochondria throughout the cell (Csordás et al., 2006; Rowland and Voeltz, 2012). Disruption of the balance between fission and fusion, more notably towards a fragmented state, is indicative of mitochondrial stress/damage and is implicated in numerous diseases (Chen and Chan, 2006; Chen and Chan, 2009; Archer, 2013; Lackner, 2014).

1.6.3 Reactive Oxygen Species (ROS)

Mitochondria are a major source of energy for cells by oxidative phosphorylation. A by-product of cellular respiration is the creation of ROS, mainly by complex I and III of the ETC (Muller, 2000; Turrens, 2003; Murphy, 2009; Zorov et al., 2014). Multiple components of the cell produce ROS, and the exact contribution of mitochondrial-produced ROS is difficult to determine, but this contribution is accredited to numerous diseases (Halliwell and Whiteman, 2004; Balaban et al., 2005; Beal, 2005; Lin and Beal, 2006; Rhoads et al., 2006; Chinta and Andersen, 2008; Zorov et al., 2014). High levels of ROS can be detrimental to the cell, however there are multiple processes by which the cell can remove excess oxidative stress by converting harsher radicals to less damaging forms (Sherer et al., 2002; Chinta and Andersen, 2008).

One source of ROS is superoxide ($O_2^{\cdot-}$), which is formed by the addition of an electron to molecular oxygen, mainly at the site of the ETC in mitochondria. Manganese superoxide dismutase (mnSOD) converts superoxide to hydrogen peroxide (H_2O_2) in the mitochondrial matrix and catalase can then convert the H_2O_2 to H_2O . Glutathione cycles between a reduced state (GSH) and oxidized state (GSSG), and during this cycling allows for conversion of H_2O_2 to H_2O . Superoxide is highly reactive, and can reduce Fe^{2+} to catalyze the Fenton reaction, in which H_2O_2 is converted to the hydroxyl radical (OH^{\cdot}). Excessive ROS can eventually cause DNA damage and lipid peroxidation (Sherer et al., 2002; Chinta and Andersen, 2008).

It is important to note that ROS plays a physiological role in the cell, and cannot be eliminated completely, without detrimental effects (Sena and Chandel, 2012). Low levels of ROS can serve to activate cell signalling pathways and immune responses (Sena

and Chandel, 2012). However, sustained levels of oxidative stress can be damaging to mitochondria, especially when anti-oxidant defenses have been exhausted (Chinta and Andersen, 2008). Additionally, damaged mitochondria can release ROS, further contributing to oxidative stress in the cell (Chinta and Andersen, 2008). Mitochondrial DNA is especially sensitive to oxidative damage, which leads to loss of essential components of the electron transport chain (Larsson et al., 1998). Damaged, dysfunctional mitochondria inefficiently produce energy, have disrupted regulation of dynamics, and can induce apoptosis (Detmer and Chan, 2007; Mattson et al., 2008).

1.6.4 Mitochondrial Quality Control (MQC)

Mitochondrial quality control (MQC) exists at various levels, depending on the degree of damage in the cell. Regulation occurs at the molecular, organellar and cellular level (Tatsuta and Langer, 2008; Ashrafi and Schwarz, 2012; Fischer et al., 2012). Maintenance of the ETC minimizes excessive ROS production and is achieved by proteolytic and protein regulation (Detmer and Chan, 2007; Tatsuta and Langer, 2008; Ashrafi and Schwarz, 2012; Fischer et al., 2012). Damaged mitochondria can be selectively degraded through a type of autophagy, termed mitophagy.

Two PD genes, Parkin and Pink1, have been recently implicated in mediating mitophagy. Parkin, an E3 ubiquitin ligase, translocates to damaged mitochondria to facilitate their clearance via mitophagy (Narendra et al., 2008; Geisler et al., 2010). Recent findings have also implicated Parkin-mediated ubiquitination of outer mitochondrial membrane proteins as a signal for degradation by mitophagy (Geisler et al., 2010; Narendra et al., 2010a; Poole et al., 2010). Additionally, upon induction of

stress, Pink1 is stabilized in the mitochondria – a process required for Parkin recruitment (Kim et al., 2008; Geisler et al., 2010; Narendra et al., 2010b).

This process allows for mitochondria to be removed in order to prevent further damage to the mitochondrial network (Tatsuta and Langer, 2008; Ashrafi and Schwarz, 2012; Fischer et al., 2012). If damage is too severe to fix, mitochondria can signal for apoptosis and this prevents the damaged cell from adversely affecting surrounding cells (Tatsuta and Langer, 2008; Ashrafi and Schwarz, 2012; Fischer et al., 2012).

The existence of Parkin-mediated MQC in neurons, especially *in vivo*, is still highly debated. The major issue is the fact that the majority of studies investigating MQC employ overexpression techniques and harsh, non-physiological stressors (Grenier et al., 2013). Notably, one group did not observe *in vivo* Parkin-mediated MQC in a dopaminergic neuron-specific mitochondrial damage model (Sterky et al., 2011). It is important to note that this mitochondrial damage model has not been fully characterized, and there may be complications in the model, in which Parkin is unable to localize to mitochondria (Grenier et al., 2013). Despite this, MQC is still argued to have an essential function in neurons (Rugarli and Langer, 2012).

1.7 DJ-1

1.7.1 Structure

The human *PARK7* gene consists of 8 exons over a span of 24 kilo base pairs (Kb), located on chromosome 1p36. It encodes for a 189 amino acid protein called DJ-1. Human DJ-1 tertiary structure consists of a six-strand parallel β -sheet flanked by α -helical arrangements, and is typically found in dimeric form (Abou-Sleiman et al., 2003;

Honbou et al., 2003; Huai, 2003; Macedo et al., 2003; Tao and Tong, 2003; Wilson et al., 2003). This structure places DJ-1 in the highly conserved DJ-1/ThiJ/PfpI superfamily of proteins. The archetypical bacterial ThiJ and PfpI proteases contain similar structural domains to DJ-1. Interestingly, DJ-1 has a warped catalytic triad and a blocked putative active site, thus rendering it non-proteolytic (Abou-Sleiman et al., 2003; Honbou et al., 2003; Huai, 2003; Wilson et al., 2003; Shendelman et al., 2004).

DJ-1 undergoes a shift in its isoelectric point during oxidative stress, becoming more acidic (Mitsumoto et al., 2001; Taira et al., 2004). Based on its structure, DJ-1 has two highly reactive cysteine residues – at position 53 and 106. It is believed that oxidation of one residue in particular, cysteine 106 (C106), is responsible for the shift in its isoelectric point (Canet-Avilés et al., 2004). Some studies have suggested that C53 also plays a role in this shift (Taira et al., 2004). The cysteine residue can be oxidized to sulfinic acid (via sulfenic acid) or even to sulfonic acid with prolonged exposure to oxidative stress (Abou-Sleiman et al., 2003; Canet-Avilés et al., 2004; Zhou et al., 2006). Highly oxidized DJ-1 has been found in both sporadic PD and Alzheimer's disease patients' brains (Choi et al., 2006).

1.7.2 Mutations Causing Parkinson's Disease

Over 10 years ago, two loss of function mutations in *PARK7* were linked to early-onset PD. The first mutation was identified in a Dutch family, where exons 1-5 of the gene as well as 4Kb of the promoter were deleted (Bonifati et al., 2003). This deletion mutation led to no detectable protein level (Macedo et al., 2003; Irrcher et al., 2010). The second mutation was identified in an Italian family, where a single point mutation in exon

7 lead to leucine 166 becoming a proline (L166P) (Bonifati et al., 2003). This substitution leads to loss of dimerization and consequently destabilization of the protein (Macedo et al., 2003). Additional PD-causing mutations that alter amino acid sequence have been identified, including M26I (exon 2), E64D (exon 3), E163K (exon 7), A104T (exon 5), and D149A (exon 7) (Abou-Sleiman et al., 2003; Clark et al., 2004; Hering et al., 2004; Annesi et al., 2005). It is estimated that mutations in *PARK7* account for approximately 1-2% of early-onset PD (Abou-Sleiman et al., 2003; Pankratz et al., 2006).

1.7.3 Functions

1.7.3.i Oncogene

DJ-1 was originally identified as an oncogene, as in co-operation with H-ras or C-myc, it can transform mouse cells (Nagakubo et al., 1997). While able to minimally transform cells by itself, a combination of DJ-1 and ras or myc causes exponential transformation (Nagakubo et al., 1997). Additionally, DJ-1-expressing cells induce significantly more tumour formation in nude mice (Kim et al., 2005b). Notably, increased levels of DJ-1 have been observed in various types of cancer. In breast cancer, even in early detected cases, DJ-1 expression is increased and thought to be a potential biomarker for this cancer (Le Naour et al., 2001). Additionally, elevated levels of DJ-1 have been detected in lung cancer and are correlated to poor outcome (Kim et al., 2005b; Fan et al., 2015). In astrocytomas, loss of DJ-1 localized to the nucleus is suggestive of poor prognosis (Miyajima et al., 2010).

1.7.3.ii Chaperone

The *Escherichia coli* molecular chaperone Hsp31 is also a member of DJ-1/ThiJ/PfpI superfamily of proteins, and shares structural resemblance to DJ-1 (Abou-Sleiman et al., 2003). This similarity suggests that DJ-1 too could possess a chaperone-like activity, which has been confirmed by various studies (Shendelman et al., 2004; Zhou et al., 2006). The chaperone function of DJ-1 is redox-dependent as this function is lost in a reducing environment (Shendelman et al., 2004; Zhou et al., 2006). This chaperone activity depends on the highly reactive C53 but not C106 in one study (Shendelman et al., 2004) and C106 but not C53 in another study (Zhou et al., 2006). Additionally, the PD-mutant L166P does not possess any chaperone activity (Shendelman et al., 2004). Moderately oxidized DJ-1, but not the L166P mutant, is able to prevent aggregation of α -synuclein (Shendelman et al., 2004; Zhou et al., 2006). Interestingly, highly oxidized DJ-1 is unable to prevent fibrillation of α -synuclein (Zhou et al., 2006).

1.7.3.iii Transcription Regulator

DJ-1 has been implicated as a co-factor in regulation of numerous genes. The first interactor of DJ-1 identified was the protein inhibitor of activated signal transducers and activators of transcription (PIAS) α (Takahashi et al., 2001). DJ-1 positively regulates the androgen receptor (ARe) by binding PIAS α , which normally inhibits this receptor – a process dependent on sumoylation of DJ-1 at lysine 130 (Takahashi et al., 2001; Shinbo et al., 2006). Overexpression of DJ-1 increases ARe activity ~20-fold whereas DJ-1

knockdown decreases the activity by ~5-10-fold (Tillman et al., 2007). Furthermore, DJ-1 increases tyrosine hydroxylase (TH) transcription via the ARe (Jeong et al., 2006). Notably, the PD-associated mutant L166P does not interfere with binding to PIASx- α (Macedo et al., 2003). However both this mutant as well as the K130R mutant show improper sumoylation and can not protect cells against UV radiation-induced death (Shinbo et al., 2006).

Pyrimidine tract-binding protein-associated splicing factor (PSF), which has a co-repressor function on the TH promoter, interacts with DJ-1 (Tanner et al., 2005; Ishikawa et al., 2010). This interaction prevents the inhibitory effect on TH transcription by stopping the sumoylation of PSF and thus preventing recruitment of histone deacetylase 1 (HDAC1) (Zhong et al., 2006; Ishikawa et al., 2010). PD-associated mutants M26I, D149A and L166P as well as the exon 1-5 deletion DJ-1 demonstrate higher levels of PSF sumoylation (Zhong et al., 2006). PSF also inhibits transcription of peroxisome proliferator-activated receptor- γ co-activator 1 α (PGC-1 α), a master regulator of mitochondrial biogenesis and stress response (Zhong and Xu, 2008). DJ-1 prevents sumoylation of PSF, thereby releasing inhibition of PGC-1 α and allowing for transcription of MnSOD (Zhong and Xu, 2008). Interestingly, highly oxidized DJ-1 is unable to prevent sumoylation of PSF and therefore MnSOD levels are reduced (Zhong and Xu, 2008).

Overexpressed DJ-1 protects dopaminergic neuronal cultures against oxidative stress by upregulating biosynthesis of glutathione (Kim et al., 2005b). DJ-1 increases both glutamate cysteine ligase transcription and activity (Kim et al., 2005b). Blocking glutathione synthesis abolishes the protective effects of DJ-1 overexpression (Kim et al.,

2005b). In addition, DJ-1 regulates the stability of a master anti-oxidant transcription factor, nuclear factor erythroid 2-related factor (Nrf2) (Clements et al., 2006). DJ-1 binds to Nrf2, preventing interaction with Kelch-like ECH-associated protein 1 (Keap1), its inhibitor protein that leads to Nrf2 ubiquitination and subsequent degradation (Clements et al., 2006).

1.7.3.iv Pro-Survival

Previous research in our laboratory has shown that loss of DJ-1 leads to hypersensitization to MPTP and oxidative stress and that its reintroduction can promote survival in the same paradigms (Kim et al., 2005a). Overexpressed WT DJ-1, but not PD-associated mutant L166P, protects against various stressors in numerous cell models (Junn et al., 2005; Kim et al., 2005b; Shinbo et al., 2006). A study showed that part of this pro-survival role of DJ-1 is through the Akt pathway, as DJ-1 negatively regulates phosphatase and tensin homolog (PTEN) (Kim et al., 2005b). Overexpressed DJ-1 was able to protect against PTEN-induced cell death, but interestingly DJ-1 provides protection in a PTEN-dependent manner (Kim et al., 2005b). Akt phosphorylation, and thus activation, is reliant on DJ-1 (Kim et al., 2005b; Aleyasin et al., 2010). Our group further explored this link, demonstrating that Akt requires DJ-1 in order to be activated during times of stress, and DJ-1 is only protective in the presence of Akt (Aleyasin et al., 2010). Additionally, there is noticeably less Akt activation with the PD-associated L166P mutant (Aleyasin et al., 2010).

Another study demonstrated that DJ-1, but not L166P mutant DJ-1, interacts with the cell death-inducing protein Daxx (Junn et al., 2005). Upon stimulation, Daxx

translocates from the nucleus to the cytoplasm to activate apoptosis signal-regulating kinase 1 (Ask1). DJ-1 binds to Daxx, sequestering it into the nucleus and thus preventing activation of Ask1 and halting the subsequent cell death pathway (Junn et al., 2005).

1.7.3.v Oxidative Stress Sensor

It has been speculated that DJ-1 acts directly as an anti-oxidant, and the C53A and C106S cysteine mutants, as well as the PD-associated L166P mutant, lack this ability (Taira et al., 2004; Andres-Mateos et al., 2007). It was also demonstrated that WT DJ-1 but not C53A, C106S/A or L166P mutants could undergo a shift in isoelectric point and additionally protect against cell death (Canet-Avilés et al., 2004; Taira et al., 2004; Blackinton et al., 2009). This role is controversial, as a study has shown DJ-1 to have too low of a direct anti-oxidant function to be protective (Shendelman et al., 2004; Yang et al., 2005; Andres-Mateos et al., 2007). It is instead suggested that oxidation of DJ-1 serves to indicate increased levels of oxidative stress in the cell (Canet-Avilés et al., 2004).

1.7.3.vi Role in Mitochondrial Health

Previous studies demonstrate that DJ-1 can localize to mitochondria to exert its antioxidant effects (Canet-Avilés et al., 2004; Blackinton et al., 2005; Zhang et al., 2005; Shinbo et al., 2006; Andres-Mateos et al., 2007; Hayashi et al., 2009; Junn et al., 2009; Xiong et al., 2009). It is believed that oxidation of one residue in particular, cysteine 106 (C106) is essential for it to translocate to mitochondria and exert its protective role (Canet-Avilés et al., 2004). Some studies question the necessity of C106 oxidation (Maita

et al., 2013), however DJ-1 targeted specifically to mitochondria provide the highest protection against oxidative stress, compared to nuclear targeted or WT DJ-1 (Junn et al., 2009).

More recent work in our laboratory, as well as others, has demonstrated that DJ-1 deficiency both *in vitro* and *in vivo* results in fragmented mitochondria that produce more ROS (Irrcher et al., 2010; Krebiehl et al., 2010). Treatment with the anti-oxidant N-acetyl cysteine (NAC) rescues this mitochondrial morphological effect (Irrcher et al., 2010). Mfn1, one of the regulators of OMM fusion, is decreased with loss of DJ-1 and inhibition of fission by expression of a dominant-negative Drp1 can reverse the hypersensitivity of DJ-1 null neurons *in vitro* (Irrcher et al., 2010). Loss of DJ-1 negatively impacts mitochondrial health.

1.8 Voltage Dependent Anion Channel (VDAC)

1.8.1 Structure and Function

The voltage-dependent anion channel (VDAC) is a pore-forming protein that resides predominantly in the OMM (Colombini, 1980; Roos et al., 1982; Lindén and Gellerfors, 1983; Ludwig et al., 1986; Peng et al., 1992; Rostovtseva et al., 2000). This transmembrane protein is capable of oligomerization and has multiple, distinct isoforms in humans, mice and rats (Colombini, 1980; Lindén and Gellerfors, 1983; Sampson et al., 1997; Shi et al., 2003; Shoshan-Barmatz et al., 2004; Zalk et al., 2005; Shoshan-Barmatz et al., 2006; Bayrhuber et al., 2008; Shoshan-Barmatz et al., 2010). VDAC is approximately 31kDa in size and consists of a single β -barrel that spans the membrane and an α -helix at the N-terminus that sits horizontally in the middle of the pore

(Bayrhuber et al., 2008; Hiller et al., 2008; Ujwal et al., 2008). The diameter of the monomer VDAC channel is estimated at 0.9 – 3nm (Ludwig et al., 1986; Colombini, 1987; Benz, 1994; Bayrhuber et al., 2008; Hiller et al., 2008; Ujwal et al., 2008). The α -helix has a high degree of flexibility and is thought to move in and out of the pore, allowing for either an ‘open’ or ‘closed’ status, which accounts for the larger variability in pore diameter measured (Bayrhuber et al., 2008; Ujwal et al., 2008; Mertins et al., 2012).

This voltage-dependent channel has the highest conductance at low potentials, when it allows for the passage anions such as adenine nucleotides, chloride, phosphate, succinate and pyruvate (Colombini, 1980; Roos et al., 1982; Ludwig et al., 1986; Rostovtseva and Colombini, 1997; Shoshan-Barmatz et al., 2006; Mertins et al., 2012). The size of the channel become reduced with higher positive or negative potentials, and VDAC becomes almost impermeable to ATP and ADP (Ludwig et al., 1986; Benz et al., 1988; Benz et al., 1990; Liu and Colombini, 1992; Gellerich et al., 1993; Lee et al., 1994; Rostovtseva and Colombini, 1997; Shoshan-Barmatz et al., 2006). In this relatively ‘closed’ state, VDAC becomes more preferential to cations and mitochondrial function decreases significantly (Ludwig et al., 1986; Benz et al., 1988; Benz et al., 1990; Liu and Colombini, 1992; Gellerich et al., 1993; Lee et al., 1994).

1.8.2 Ca^{2+} Regulation

The translocation of Ca^{2+} into and out of the mitochondria is partially regulated through VDAC (Gincel et al., 2001; Rapizzi et al., 2002; Bathori et al., 2006). Ca^{2+} is a universal messenger that regulates many cellular processes such as cellular structure,

muscle contraction, synaptic transmission of neurotransmitters and even cell death (Bennett and Weeds, 1986; Trump and Berezsky, 1995; Crompton, 1999; Berchtold et al., 2000; Friel, 2000; Verkhratsky, 2005; Clapham, 2007; Kostyuk, 2007). Cytoplasmic Ca^{2+} levels are significantly lower than extracellular Ca^{2+} levels. A large influx of Ca^{2+} into the cell can occur rapidly and the cell must return cytosolic Ca^{2+} to resting levels in order to prevent activation of various messengers (Pounds and Rosen, 1988; Friel, 2000; Verkhratsky, 2005). Two Ca^{2+} 'sinks' exist to help maintain Ca^{2+} homeostasis in the cytosol – the ER and mitochondria (Bernardi, 1999; Friel, 2000; Verkhratsky, 2005). VDAC contains Ca^{2+} binding sites, and may regulate mitochondria-dependent apoptosis (Gincel et al., 2001). Increased Ca^{2+} levels induce an 'open' conformation of VDAC, which could allow for rapid entry of Ca^{2+} into mitochondria (Bathori et al., 2006). Additionally, VDAC enhances the permeability of Ca^{2+} at mitochondria-ER contact points (Rapizzi et al., 2002). Increased mitochondrial Ca^{2+} levels can enhance metabolism, however sustained high levels of Ca^{2+} can also lead to mitochondrial dysfunction and eventually apoptosis (Hunter and Haworth, 1979; Jouaville et al., 1999; Boustany et al., 2002; Pivovarova and Andrews, 2010). By regulating permeability of Ca^{2+} to mitochondria, VDAC plays a role in regulating various cellular processes (Rapizzi et al., 2002; Bathori et al., 2006).

1.8.3 Role in Cell Death

There are various models in which mitochondria have been implicated in inducing apoptosis, chiefly by releasing the pro-apoptotic factor cytochrome *c* (Green and Reed, 1998; Shoshan-Barmatz et al., 2006). Upon accumulation of excessive mitochondrial

Ca^{2+} , mitochondria can undergo a sudden permeability transition (Massari and Azzone, 1972; Haworth and Hunter, 1979; Hunter and Haworth, 1979; Bernardi, 1999; Bernardi et al., 2006; Shoshan-Barmatz et al., 2008). This change in permeability can cause a loss of mitochondrial membrane potential, efflux of Ca^{2+} into the cytosol, and release of cytochrome *c* (Haworth and Hunter, 1979; Hunter and Haworth, 1979; Newmeyer and Ferguson-Miller, 2003; Green and Kromer, 2004; Ekert and Vaux, 2005; Shoshan-Barmatz et al., 2008). Together with cytochrome *c*, other proteins such as direct inhibitor of apoptosis binding protein with low pI (DIABLO), apoptosis-inducing factor (AIF) and cleaved optic-atrophy 1 (OPA1) are also released from permeabilized mitochondria into the cytoplasm (Li et al., 1997; Susin et al., 1999; Verhagen et al., 2000; Newmeyer and Ferguson-Miller, 2003; Green and Kromer, 2004; Arnoult et al., 2005; Ekert and Vaux, 2005). These proteins trigger a chain of reactions, leading to apoptosis via apoptosis activating factor 1 (Apaf-1) activation and subsequently caspase activation (Green and Kromer, 2004; Ekert and Vaux, 2005; Youle and Strasser, 2008).

The mitochondrial permeability transition pore (mPTP) has been proposed to contain VDAC, adenine-nucleotide transferase (ANT), cyclophilin D (CypD) and translocator protein (TSPO) (Halestrap and Davidson, 1990; Szabó et al., 1993; Szabó and Zoratti, 1993; Baines et al., 2005; Sileikyte et al., 2011). The essential participation of ANT, CypD and TSPO in the mPTP has since been refuted, as cells deficient for each of these components still can undergo mitochondrial permeability (Kokoszka et al., 2004; Basso et al., 2005; Šileikytė et al., 2014). The voltage-dependence and diameter of the mPTP is similar to VDAC, and thus it was suggested that VDAC was in fact the mPTP (Szabó et al., 1993; Szabó and Zoratti, 1993; Bernardi et al., 2006). Despite the

similarities, cells deficient for all three VDAC isoforms can undergo permeabilization of the OMM and are inducible for apoptosis (Baines et al., 2007). While not an essential component, further investigation into VDAC1 specifically, suggests that regulation of its N-terminus can promote either cell-survival or apoptosis, depending on the interactor (Shi et al., 2003; Azoulay-Zohar et al., 2004; Abu-Hamad et al., 2009; Arbel and Shoshan-Barmatz, 2010; Arbel et al., 2012).

1.8.4 Interactors

Hexokinase, a key enzyme in glycolysis, has been shown to localize to mitochondria in an Akt-dependent manner to promote survival (Pastorino et al., 2005). It interacts with VDAC1 to reduce the conductance of the channel and promote survival (Azoulay-Zohar et al., 2004; Abu-Hamad et al., 2008). This interaction and subsequent decrease in channel conductance is reliant on specifically the N-terminus of VDAC1 (Azoulay-Zohar et al., 2004; Abu-Hamad et al., 2009). Interaction of VDAC and hexokinase is also dependent on the phosphorylation status of VDAC – phosphorylated VDAC does not bind hexokinase, thereby losing its protective effect (Pastorino et al., 2005).

VDAC1 has been shown to interact with various members of the B-cell lymphoma-2 (Bcl-2) family of protein. Bcl-2 proteins regulate both cell survival and death (Youle and Strasser, 2008). The anti-apoptotic Bcl-2 protein is the founder protein for the Bcl-2 family of proteins and its deregulation is associated with development of lymphomas (Tsujimoto et al., 1985; Vaux et al., 1988). It interacts with VDAC1, lowering conductance of the channel and preventing cell death (Arbel and Shoshan-

Barmatz, 2010). This interaction is dependent on several domains of VDAC1, including its N-terminus (Abu-Hamad et al., 2009; Arbel and Shoshan-Barmatz, 2010).

Another family member, B-cell lymphoma-extra large (Bcl-x_L), resides in mitochondria and prevents apoptotic cell death (Boise et al., 1993). Bcl-x_L interacts with VDAC1, however the functional outcome of this interaction is controversial. One group demonstrated that this interaction induced closing of VDAC1 and prevented cytochrome *c* release into the cytosol (Shimizu et al., 1999). However another group showed that the interaction promoted the open state of VDAC, allowing for passage of metabolites (Vander Heiden et al., 2001). Additional studies have shown that Bcl-x_L interacts specifically within the N-terminal region of VDAC1, causing reduced conductance of the channel and preventing apoptosis (Shi et al., 2003; Arbel et al., 2012). More recently it has been suggested that this interaction appears to allow for increased Ca²⁺ uptake into the mitochondrial matrix (Huang et al., 2013).

The pro-apoptotic proteins Bax and Bak, also Bcl-2 family members, have both been implicated in an alternative mechanism for mediating release of cytochrome *c* from mitochondria following membrane permeabilization (Kluck et al., 1999; Kuwana et al., 2002; Green and Kromer, 2004; Youle and Strasser, 2008). It has been proposed that Bax and/or Bak can oligomerize and form a pore that allows for release of proteins from the OMM such as cytochrome *c* (Kuwana et al., 2002). Additionally, Bax appears to interact with VDAC1 and enhances the opening of this channel, leading to increased release of cytochrome *c* (Shimizu et al., 1999; Shi et al., 2003). This interaction appears to depend on the N-terminus of VDAC1 (Shi et al., 2003).

In collaboration with the laboratory of Dr. Daniel Figeys (Institute of Systems Biology, University of Ottawa), an interaction screen was performed. This screen, in which FLAG-VDAC1 was overexpressed in HEK293 cells, interacting proteins were co-immunoprecipitated and identified by mass spectrometry, showed that DJ-1 interacts with VDAC1 (Dr. Figeys, personal communication). The convergence of both DJ-1 and VDAC1 on promoting survival during oxidative stress via mitochondrial function, together with this possible interaction, has led us to investigate the possible interaction between these two factors.

1.9 Statement of Research Hypothesis and Objectives

The Parkinson's disease-linked DJ-1 is a pro-survival protein that can protect against oxidative stress and inhibit cell death, especially when targeted to mitochondria. The outer mitochondrial membrane protein VDAC1 is also a key factor in regulating cell survival during stress.

We hypothesize that *VDAC1 mediates entry of DJ-1 into mitochondria during stress to promote survival*. To address this theory, we outlined the following objectives to study for this dissertation:

- 1) Assess stress-induced localization of DJ-1 to mitochondria
- 2) Confirm physical/functional interaction between DJ-1 and VDAC1
- 3) Determine effect of VDAC1 deficiency on cortical neuron mitochondrial health
- 4) Elucidate sub-mitochondrial localization of DJ-1
- 5) Identify signal inducing DJ-1 translocation to mitochondria

CHAPTER 2

ROS-dependent regulation of Parkin and DJ-1 localization during oxidative stress

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Statement of Author Contributions

Sarah J. Hewitt and Dr. Alvin P. Joselin designed and conducted all experiments. **Sarah J. Hewitt** carried out all experiments investigating DJ-1 translocation and Dr. Alvin P. Joselin carried out all experiments investigating Parkin translocation. Steve M. Callaghan made all viruses utilized and provided general technical assistance. DJ-1 transgenic mice were made in the laboratory of Dr. Tak W, Mak, by Dr. Raymond H. Kim. Pink1 transgenic mice were made in the laboratory of Dr. Jie Shen. Dr. Young Hwa-Chung gave insight into experimental design. **Sarah J. Hewitt**, Dr. Alvin P. Joselin and Dr. David S. Park analyzed data, wrote the manuscript and edited the manuscript.

**ROS-dependent regulation of Parkin and DJ-1 localization during oxidative stress
in neurons**

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Abstract

Mutations in several genes, including *Parkin*, PTEN-induced kinase 1 (*Pink1*) and *DJ-1*, are associated with rare inherited forms of Parkinson's disease (PD). Despite recent attention on the function of these genes, the interplay between DJ-1, Pink1 and Parkin in PD pathogenesis remains unclear. In particular, whether these genes regulate mitochondrial control pathways in neurons is highly controversial. Here we report that Pink1-dependent Parkin translocation does occur in mouse cortical neurons in response to a variety of mitochondrial damaging agents. This translocation only occurs in the absence of antioxidants in the neuronal culturing medium, implicating a key role of reactive oxygen species (ROS) in this response. Consistent with these observations, ROS blockers also prevent Parkin recruitment in mouse embryonic fibroblasts. Loss of DJ-1, a gene linked to ROS management, results in increased stress-induced Parkin recruitment and increased mitophagy. Expression of wild-type DJ-1, but not a cysteine-106 mutant associated with defective ROS response, rescues this accelerated Parkin recruitment. Interestingly, DJ-1 levels increase at mitochondria following oxidative damage in both fibroblasts and neurons, and this process also depends on Parkin and possibly Pink1. These results not only highlight the presence of a Parkin/Pink1-mediated pathway of mitochondrial quality control (MQC) in neurons, they also delineate a complex reciprocal relationship between DJ-1 and the Pink1/Parkin pathway of MQC.

Introduction

Parkinson's disease (PD), a neurodegenerative movement disorder, is characterized by loss of dopaminergic (DA) neurons in the substantia nigra *pars compacta* (Dauer and Przedborski, 2003). Growing evidence has implicated mitochondrial quality control (MQC) pathways. Mitochondrial defects have been noted in PD patients (Schapira et al., 1989; Navarro and Boveris, 2009). Moreover, exposure to drugs that inhibit mitochondrial complex I mimic certain aspects of PD (Greenamyre et al., 1999; Betarbet et al., 2000; Jenner, 2001). Interestingly, a number of recessive, early-onset PD genes are implicated in the maintenance of mitochondrial homeostasis. Pink1 is a serine/threonine kinase containing an N-terminal mitochondrial-targeting motif (Valente et al., 2004). Pink1 localizes to mitochondria (Valente et al., 2004; Silvestri et al., 2005; Zhou et al., 2008) and its loss leads to increased oxidative stress and sensitization to death (Haque et al., 2008; Wood-Kaczmar et al., 2008). Parkin, another PD gene, possesses E3 ligase activity (Rankin et al., 2001). At least in select tumor lines in response to carbonyl cyanide m-chloro phenyl hydrazone (CCCP)-induced mitochondrial depolarization, Parkin translocates to mitochondria and participates in clearance of dysfunctional mitochondria (Narendra et al., 2008) in a Pink1-dependent manner (Kim et al., 2008; Vives-Bauza et al., 2010). Whether this is true in primary neurons is unclear. Critically, recent reports have indicated that neither CCCP (Van Laar et al., 2010), nor mitochondrial damage caused by mitochondrial transcription factor A (TFAM) loss (Sterky et al., 2011) induce Parkin translocation in neurons, seriously undermining the relevance of the Pink1/Parkin mitochondrial quality control pathway in neurodegeneration.

DJ-1, a third PD recessive PD gene, is critical in oxidative stress response (Mitsumoto et al., 2001; Canet-Avilés et al., 2004; Kim et al., 2005a) and modulates various survival pathways (Yang et al., 2005; Görner et al., 2007; Aleyasin et al., 2010). We and others have shown that DJ-1 loss results in hypersensitization of neurons to oxidative damage (Kim et al., 2005a; Manning-Boğ et al., 2007). How this sensitivity occurs is unclear. Recently, we demonstrated that DJ-1 deficiency leads to a fragmented mitochondrial phenotype, which can be rescued, by Parkin or Pink1 (Irrcher et al., 2010). However, while DJ-1 consistently appears to modulate oxidative stress responses (Mitsumoto et al., 2001; Kim et al., 2005a), Parkin translocation is reported to not involve ROS (Narendra et al., 2008). These inconsistencies led us to more carefully examine whether DJ-1 participates in the Pink1/Parkin mitochondrial quality control pathway. In summary, two central questions have emerged: a) does DJ-1 interact with the Pink1/Parkin mediated pathway of mitochondrial quality control and b) are these pathways relevant in primary neurons.

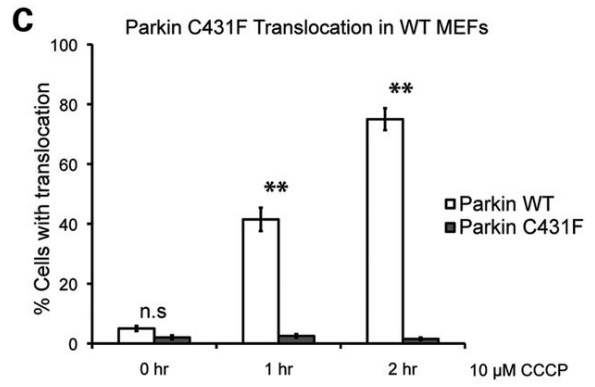
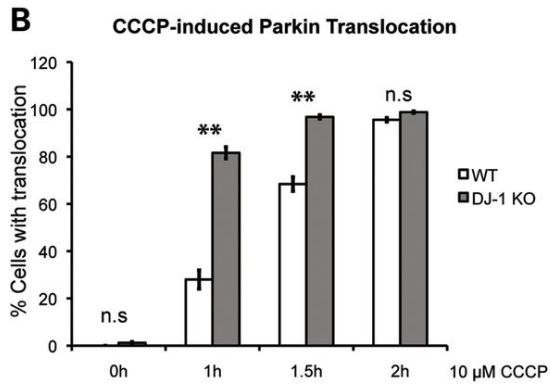
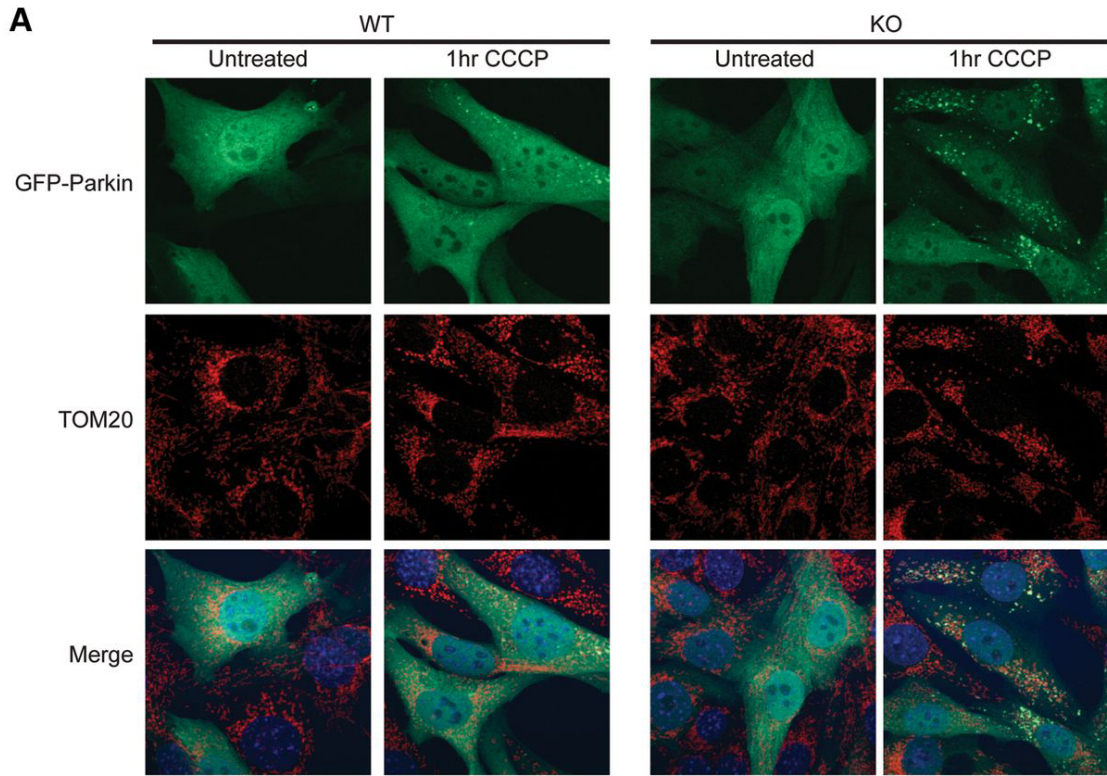
Presently, we show that DJ-1 integrates into the classical Pink1/Parkin pathway by both modulating Parkin translocation/mitophagy and responding to Pink1/Parkin by increasing its level at mitochondria during oxidative stress. Moreover, we provide critical evidence that Parkin translocation to mitochondria does occur in primary neurons in a ROS-dependent manner. Taken together, we provide a model by which DJ-1 acts in a complementary fashion to regulate a ROS-dependent Pink1/Parkin-mediated mitochondrial quality control pathway in neurons.

Results

Loss of DJ-1 results in earlier Parkin recruitment to mitochondria in MEFs

Specific Parkin recruitment to mitochondria has been documented in response to mitochondrial depolarization following CCCP (Narendra et al., 2008) or valinomycin (Rakovic et al., 2010) treatment and hydrogen peroxide treatment (Rakovic et al., 2010) in a number of cell lines. Previous reports from our lab (Irrcher et al., 2010) and others (Canet-Avilés et al., 2004) have also established a role for DJ-1 in the regulation of ROS and maintenance of mitochondrial dynamics. Accordingly, we first examined if the loss of DJ-1 affects Parkin recruitment to the mitochondria. DJ-1 deficient mouse embryonic fibroblasts (MEFs) were transfected with GFP-Parkin and treated with the mitochondrial uncoupler CCCP for various durations and analyzed for formation of Parkin puncta as previously described (Narendra et al., 2008). Within 1h of 10 μ M CCCP treatment, we observed noticeable mitochondrial translocation of wild-type (WT) Parkin (Figure 2.1A and 2.1B) but not the PD-related mutant C431F (Figure 2.1C) in WT MEFs. In the absence of DJ-1, however, the amount of cells displaying Parkin translocation was significantly higher after 1hr of CCCP treatment (Figure 2.1A and Figure 2.1B). This data demonstrates that DJ-1 deficient mitochondria are hypersensitized to depolarization-induced stress and recruit Parkin earlier.

Figure 2.1: Parkin translocation occurs earlier in the absence of DJ-1. (A) DJ-1 wildtype (WT) and knockout (KO) MEFs were transfected with GFP-Parkin and were either left untreated or treated with 10 μ M CCCP for 1h. Following treatment, cells were fixed, permeabilized and the mitochondria labeled using TOM20 antibody. Representative confocal images are presented. (B) Quantification of CCCP-induced Parkin translocation in DJ-1 WT and KO MEFs. GFP-Parkin transfected DJ-1 WT and KO MEFs were treated with 10 μ M CCCP for the indicated duration. Fixed cells were stained using TOM20 antibody and the number of cells displaying Parkin co-localization with mitochondrial staining quantified. (C) WT MEFs were infected with AAV encoding either WT GFP-Parkin or the C431F mutant. Cells were treated with 10 μ M CCCP and samples prepared for confocal analysis as mentioned before. (B and C) Results show the mean \pm SEM values of triplicates with an average of 200 cells counted per condition. n.s., not significant; ** P <0.01; t -test for related samples.

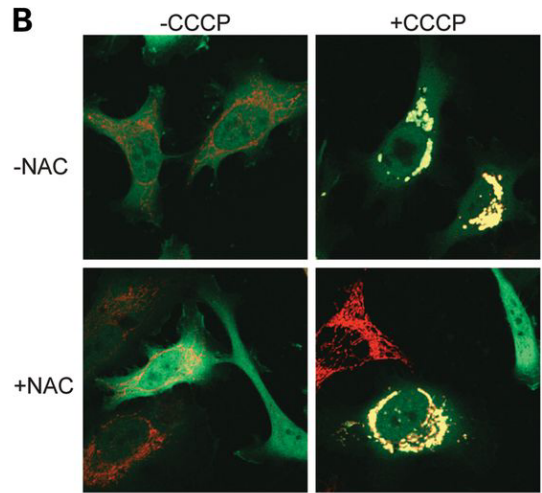
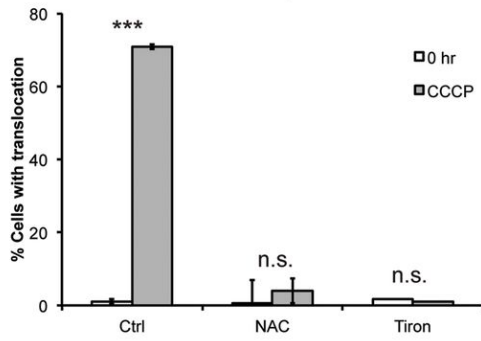


DJ-1 is known to regulate ROS (Mitsumoto et al., 2001; Canet-Avilés et al., 2004). In addition, absence of DJ-1 leads to increased ROS under a number of conditions (Irrcher et al., 2010; Thomas et al., 2011). Accordingly, a plausible explanation for the observed earlier recruitment of Parkin to mitochondria in the absence of DJ-1 is increased oxidative stress. However, previous reports in HeLa cells indicated that ROS was not involved in mediating Parkin translocation (Narendra et al., 2008). We questioned whether there was something unique about HeLa cells that made them unresponsive to ROS. To address this discrepancy, we more carefully examined the requirement of ROS in our present studies in MEFs. WT MEFs were pre-treated with the antioxidants N-acetyl cysteine (NAC; 2mM) or TIRON (100 μ M) for 3h before the addition of CCCP. As evident from Figure 2.2A, Parkin translocation was noticeably inhibited by both NAC and TIRON even after 2h of CCCP treatment. Consistent with previous reports, we observed that NAC treatment, however, failed to prevent Parkin translocation in HeLa cells (Figure 2.2B, 2.S1). To further support the importance of ROS in Parkin translocation, we tested whether WT DJ-1 or a cysteine-106 (C106A) mutant of DJ-1, known to be deficient in response to oxidative stress, could alter Parkin translocation kinetics. Importantly, earlier translocation of Parkin observed in DJ-1 deficient MEFs was restored to WT levels by exogenously expressing WT DJ-1, but not the mutant C106A DJ-1 (Figure 2.2D). Consistent with previous reports in other cell types, Parkin translocation in MEFs was observed to be Pink1-dependent since Parkin translocation did not occur in a Pink1 deficient background (Figure 2.2E). Finally, in line with previously published results (Rakovic et al., 2010), Parkin translocation was also induced by 5h of 100 μ M hydrogen peroxide (H₂O₂) treatment in WT MEFs (Figure 2.S2). Taken together,

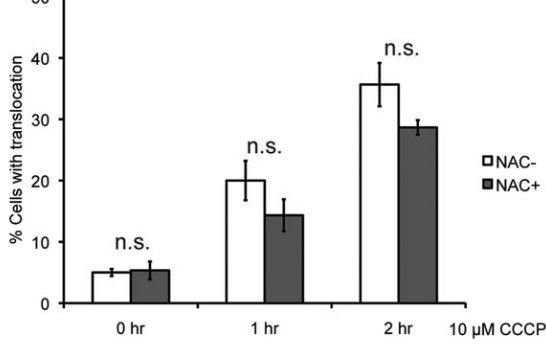
our results indicate that the ROS environment (known to be regulated by DJ-1) is an essential regulator of Pink1-mediated Parkin translocation, at least in non-transformed cell types.

Figure 2.2: Parkin translocation is ROS dependent in MEFs. GFP-Parkin transfected WT MEFs (A) or HeLa cells (B and C) were pretreated with either 2mM NAC or 100 μ M TIRON in the case of MEFs and only NAC in the case of HeLa cells, for 3h before treating the cells with 10 μ M CCCP for 2h. Cells were fixed, stained and the number of cells displaying Parkin translocation quantified (A and C). (D) DJ-1 WT or KO MEFs were co-transfected with GFP-Parkin and either vector control (Empty Vector), WT-DJ-1, or DJ-1 C106A (C106A) and were treated with vehicle (0h) or 10 μ M CCCP for 2h. GFP-positive cells were scored for the presence of Parkin puncta. (E) GFP-Parkin transfected WT or Pink1 deficient MEFs (Pink1 KO) were treated with 10 μ M CCCP for the indicated duration and Parkin translocation quantified. Bar graphs A, C, D and E show the mean \pm SEM values of triplicates with an average of 200 cells counted per condition. * P <0.05 and *** P <0.001; n.s., not significant; t -test for related samples.

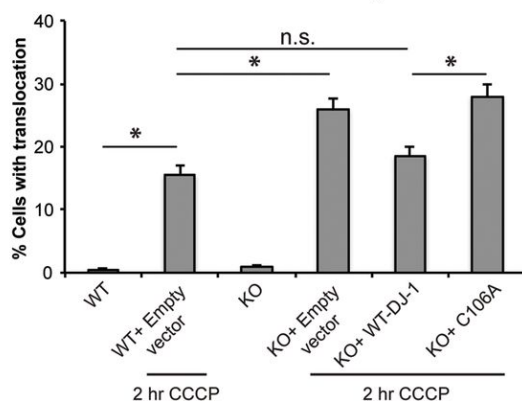
A Parkin Translocation in the presence of Antioxidants



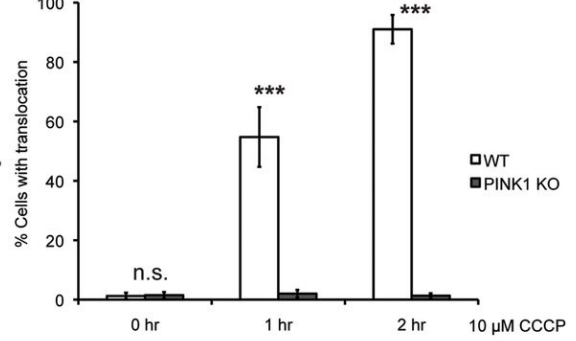
C Parkin Translocation in HeLa cells



D Parkin translocation rescue by WT-DJ-1



E Parkin Translocation in PINK1 KO MEFs



It has been reported previously (Narendra et al., 2008) that once recruited to mitochondria, Parkin selectively mediates the clearance of these damaged mitochondria by activating mitophagy. To test if mitochondrial clearance was also heightened in DJ-1 knockout (KO) MEFs, we analyzed the total mitochondria per cell, both in Parkin-overexpressing WT and DJ-1 KO MEFs after treatment with 10 μ M CCCP for 6h (Figure 2.3). Compared to vehicle treated cells (0h), a noticeable decrease in the number of mitochondria was observed after 6h of CCCP treatment both in WT and DJ-1 KO MEFs. Interestingly, mitochondrial-staining intensity after CCCP treatment was significantly lower in DJ-1 deficient MEFs compared to WT MEFs (Figure 2.3B). These results suggest that earlier recruitment of Parkin in DJ-1 deficient cells is also accompanied by faster clearance of the damaged mitochondria.

Figure 2.3: Mitochondrial clearance is enhanced in DJ-1 deficient MEFs. (A)

Representative confocal photomicrographs of GFP-Parkin transfected WT or DJ-1 KO

MEFs treated with 10 μ M CCCP for 6h. Fixed cells were stained for mitochondrial

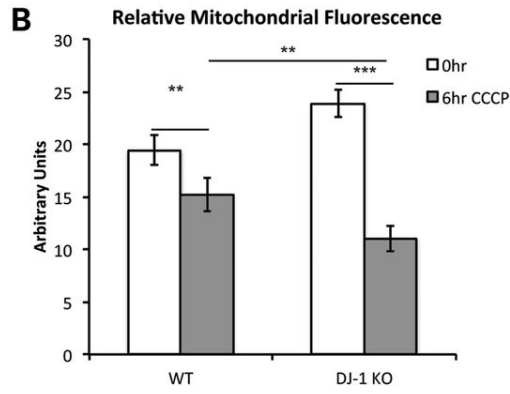
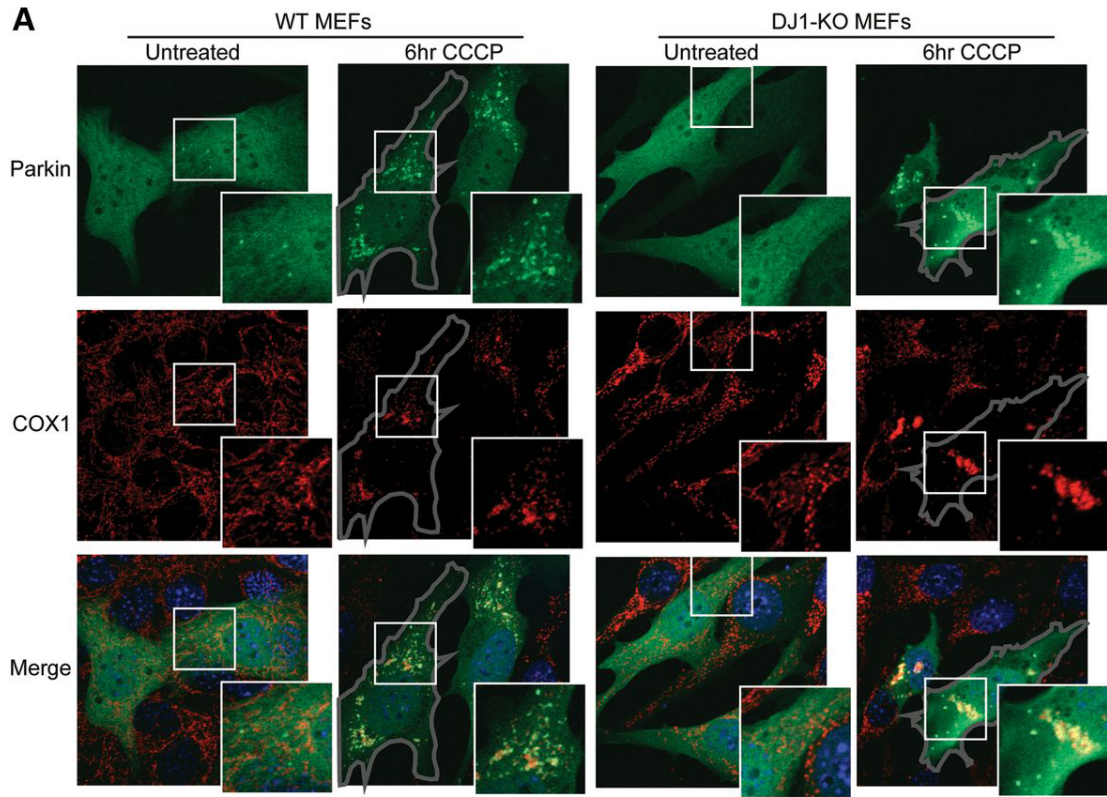
marker COX 1. (B) Quantification of mitochondrial fluorescence intensity. Mitochondrial

fluorescence of GFP positive cells was measured using ImageJ from confocal

photomicrographs, as described in materials. Bar diagram represent \pm SEM values of at

least 25 cells per conditions. Results are representative of two independent experiments.

** P <0.01 and *** P <0.001; t -test for related samples.

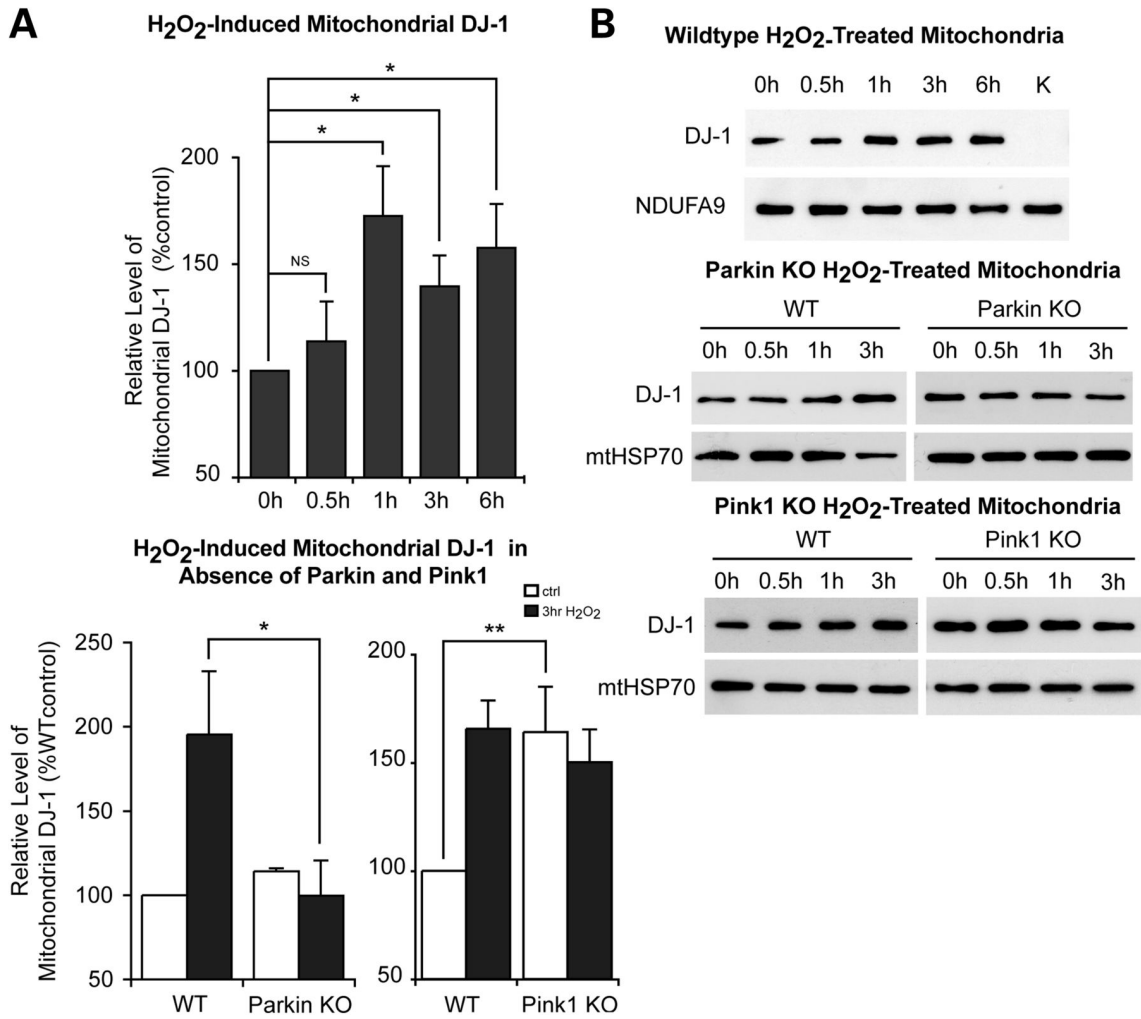


Stress-induced increase of mitochondrial DJ-1 is dependent upon Parkin/Pink1 in MEFs

The results above indicate that DJ-1 loss leads to earlier Parkin translocation, suggesting a critical role for DJ-1-mediated ROS regulation in Parkin function. We next determined whether the converse may be true, i.e. whether any function of DJ-1 may be impacted by Parkin/Pink1. Previous evidence indicated that the level of mitochondrial DJ-1 increases in response to H₂O₂-induced oxidative stress in SK-N-BE(2)C human neuroblastoma cells (Junn et al., 2009) and paraquat-induced stress in M17 neuroblastoma cells (Canet-Avilés et al., 2004). Accordingly, we explored how this increase may be impacted by Parkin/Pink1 deficiency. To determine levels of DJ-1 at mitochondria upon induction of oxidative stress in our present system, WT MEFs were treated with 100μM H₂O₂ for up to 6h and the cytoplasmic and mitochondrial-enriched fractions were separated by sub-cellular fractionation for analysis by immunoblot (Figure 2.4). Equal amounts (10μg) of mitochondrially-enriched fractions from each time point were loaded and a whole cell lysate from DJ-1 KO MEFs was included as a negative control. Following 1h of H₂O₂ treatment, a significant increase (Figure 2.4A) in the level of DJ-1 was observed at mitochondria and this augmented level was maintained at both 3h and 6h post-treatment. Immunoblotting against the 39kDa subunit of Complex I (NDUFA9) or mitochondrial heat shock protein 70 (mtHSP70) was performed as a loading control. Additionally, we noted no substantial increase in whole cell levels of DJ-1 with H₂O₂ treatment indicating that the observed increased levels of DJ-1 in the mitochondrial-enriched fraction is not simply due to increased global levels of DJ-1 in the cell (Figure 2.S3A). We also noticed endoplasmic reticulum (ER) contamination, as observed by the ER marker calnexin in our mitochondrial-enriched fractions (Figure

2.S4A). Accordingly, we could not rule out DJ-1 at the ER (however see data for neurons below). We next determined whether oxidative stress-mediated increase in mitochondrial DJ-1 might in turn be mediated by Parkin and/or Pink1. Importantly, the stress-induced increase of mitochondrial DJ-1 in WT MEFs is absent with Parkin deficiency (Figure 2.4A). This lack of increase in mitochondrial DJ-1 indicates that Parkin is required for stress-induced response of DJ-1 to mitochondria increase. While Pink1 deficiency resulted in higher basal DJ-1 levels at the mitochondria, mitochondrial DJ-1 level did not further increase with oxidative stress (Figure 2.4). Pink1 or Parkin deficiency did not induce any notable change in total basal DJ-1 levels (Figure 2.S3D). Taken together, this evidence indicates that the relationship of DJ-1 and Parkin is reciprocal; DJ-1 modulates stress-induced Parkin recruitment while Parkin and Pink1 activity is required for stress-induced increase of mitochondrial DJ-1.

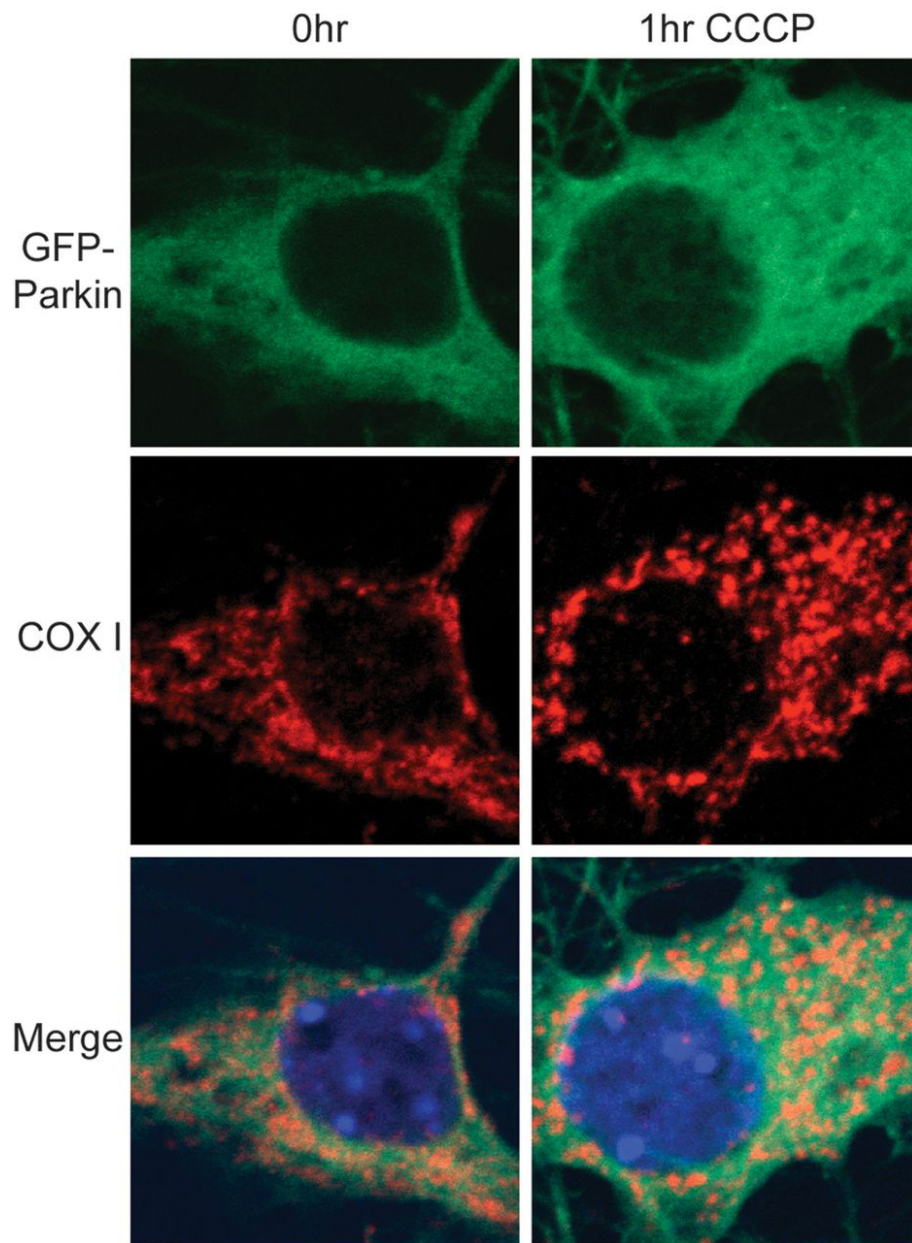
Figure 2.4: Oxidative stress-induced increase in mitochondrial DJ-1 is dependent upon Parkin and Pink1 in MEFs. Wild-type (WT), Pink1-null and Parkin-null MEFs were treated with 100 μ M H₂O₂ for indicated time points. Mitochondria-enriched fractions were obtained through sub-cellular fractionation and were analyzed by immunoblot. (A) Quantification of densitometry using Image J software (NIH). Data represent mean \pm SEM (n=3-4). n.s, not significant; * P <0.05 and ** P <0.01; t -test for related WT samples; two-way ANOVA for WT vs. KO samples. (B) Representative blots for DJ-1 and mitochondrial loading control (NDUFA9 or mtHSP70). K, DJ-1 KO sample.



Punctate Parkin staining in neurons in response to CCCP, rotenone and MPP⁺ treatment

As stated previously, Parkin translocation to mitochondria is well established in HeLa cells, in other cultured cell types, and as presently reported in MEFs. In neurons however, Parkin translocation in the presence of classic Parkin-recruiting stimuli such as CCCP (Van Laar et al., 2010) or in the absence of TFAM (Sterky et al., 2011) does not appear to occur in neurons. This is a critical issue when it comes to determining whether or not MQC may be involved in degeneration observed in PD. Under routine culture conditions in media containing B27 supplement used for cortical neurons, we also failed to observe any Parkin translocation following induction of mitochondrial damage. To analyze for this translocation in neurons, we infected E15.5 mouse cortical neurons with an Adeno-associated virus (AAV) encoding the human *Parkin* gene fused to emerald-GFP. Parkin expression, observable as diffuse GFP fluorescence throughout the neuronal cell body, could be seen after 6 to 7 days of infection. With extended time courses and dosing ranges of CCCP, 1-methyl-4-phenylpyridinium (MPP⁺) or rotenone, we could not observe any Parkin translocation. Interestingly, however, we could detect mitochondrial fragmentation within 1h of CCCP treatment or 9h of MPP⁺ treatment indicating that the agents utilized were having an effect on mitochondria (Figure 2.5).

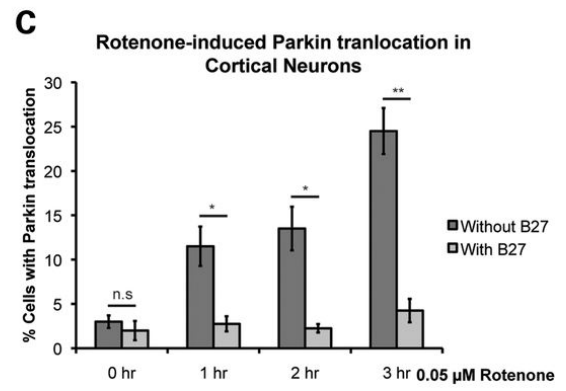
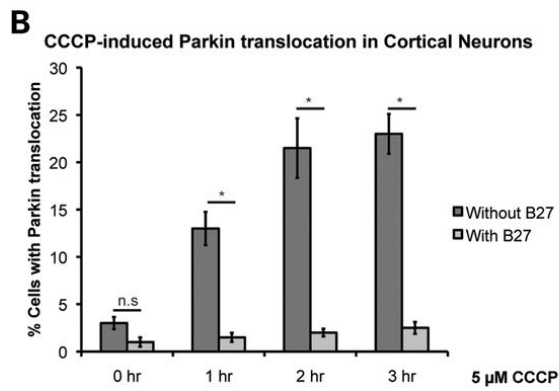
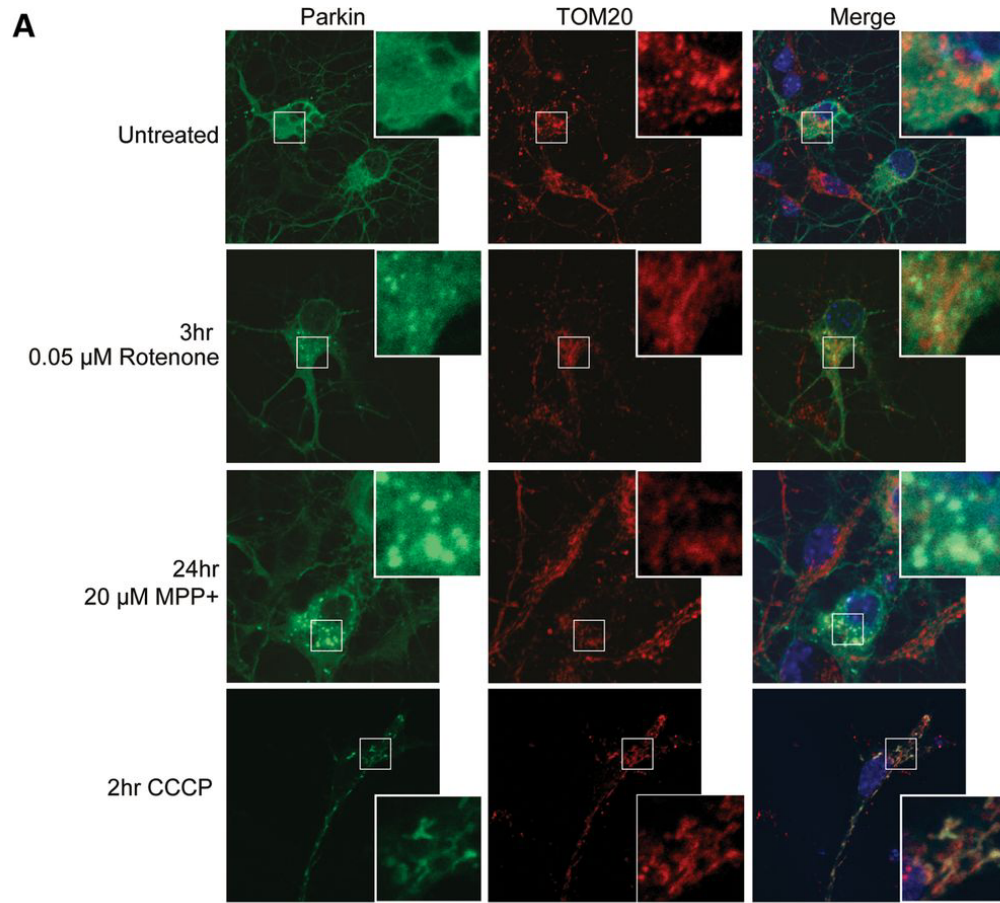
Figure 2.5: Antioxidant-dependent Parkin translocation in mouse primary cortical neurons. Representative confocal photomicrographs of primary cortical neuronal cultures infected with GFP-Parkin AAV were cultured under routine cortical culture conditions in the presence of B27. Cells were either treated with vehicle (0h) or with 5 μ M CCCP for 1h. GFP-Parkin localization was analyzed after staining for mitochondria.



Our previous data in MEFs, however, suggested that ROS is a critical mediator of Parkin translocation. The supplement B27 contains numerous antioxidants including reduced glutathione, vitamin E (dl- α -tocopherol), catalase and superoxide dismutase. Accordingly, we reasoned that perhaps translocation was not observed in neurons because of the antioxidant-enriched media. To test this, we compared cells cultured in the presence or absence of B27 supplement. Initial experiments using poly-D-lysine only coated coverslips resulted in detachment of majority of neurons during drug treatments and subsequent staining procedure. For this reason, cortical neurons derived from WT CD-1 E15.5 mice embryos were plated on acid-treated coverslips, coated with poly-D-lysine and laminin. Indeed, a comparison of Parkin localization in cortical neurons cultured in the presence or absence of B27 revealed appearance of intense punctate Parkin staining in the cell bodies of the neurons after 5 μ M CCCP, 0.05 μ M rotenone or 20 μ M MPP⁺ treatment (Figure 2.6A). Quantification of the number of neurons displaying punctate Parkin staining revealed a statistically significant increase in cells displaying Parkin puncta after oxidative stress (Figure 2.6B and 2.6C). We should note that the time course of CCCP and MPP⁺-induced Parkin translocation differs likely due to delayed mitochondrial damage as observed by fragmentation. These observations not only demonstrate a change in Parkin translocation following oxidative damage in neurons, but also suggest that Parkin translocation is ROS-dependent.

Figure 2.6: Differential Parkin translocation in CCCP-treated mouse cortical

neurons. (A) GFP-Parkin AAV infected cortical neurons were changed to media without B27 (-B27). Cells were either treated with vehicle (0h) or treated with 0.05 μ M rotenone for 3h or 20 μ M MPP+ for 24h or 5 μ M CCCP for 3h. Fixed and permeabilized cells were co-stained to label mitochondria using TOM20 antibody. (B and C) Quantification of number of neurons displaying GFP-Parkin translocation. Primary mouse cortical cultures infected with GFP-Parkin AAV were either changed to fresh media with or without B27 at least 24h before treating with 5 μ M CCCP or 0.05 μ M rotenone for the indicated durations. Neurons displaying punctate Parkin staining were quantified under fluorescence microscope. Bar graph represents the mean \pm SEM values of triplicates with an average of 200 cells counted per condition. Quantification is representative of at least 3 independent experiments. n.s, not significant; * P <0.05 and ** P <0.001; t -test for related samples.



Parkin translocation in cortical neurons and mitophagy

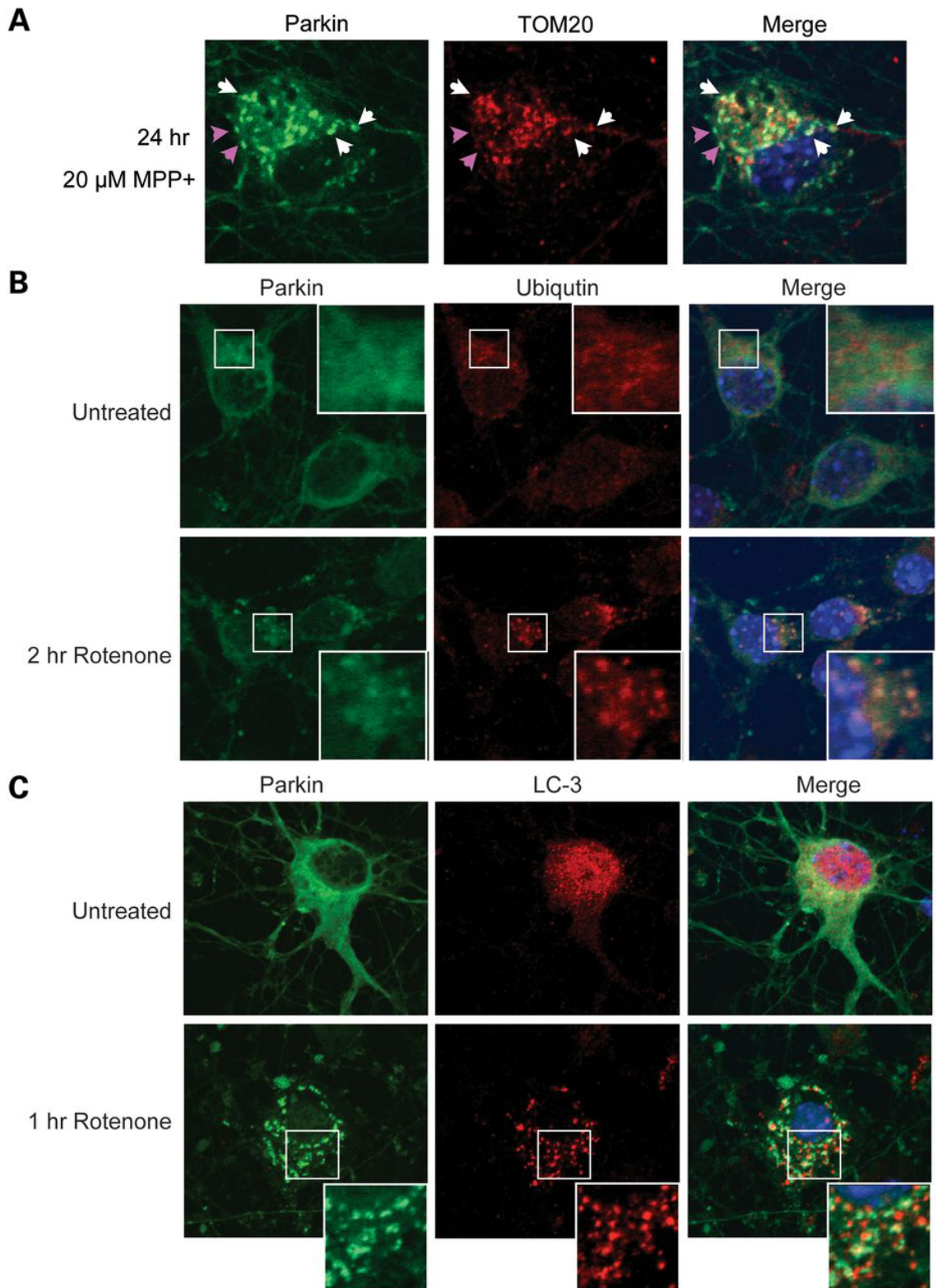
To analyze the localization of the Parkin puncta, we performed co-labeling immunofluorescence studies. Cortical neurons from E15.5 mouse embryos were infected with GFP-Parkin encoding AAV and treated with 0.05 μ M rotenone after 7 days of culture. We first tested whether these puncta co-localized with mitochondrial markers. All mitochondrial markers used, such as TOM20, Complex IV subunit 1, Complex V and an artificial mitochondrial matrix cargo Oct4-dsRed (data not shown) all exhibited partial co-localization with the Parkin puncta in cells treated with MPP⁺ (Figure 2.7A). However, the co-localization pattern was clearly different than that observed in CCCP-treated neurons (compare Figure 2.6A rotenone and MPP⁺-treated with CCCP-treated), those previously shown in MEFs (Figure 2.1), and those reported in other cell types where there was more prominent overlap with mitochondrial staining.

Parkin is an E3-ubiquitin ligase and translocated Parkin has been shown to enhance ubiquitination at the clustering mitochondria in HeLa cells (Geisler et al., 2010; Matsuda et al., 2010). We were curious as to whether the punctate Parkin observed in the neurons overlap in any way with ubiquitination. To test this, we co-stained rotenone-treated, Parkin over-expressing cortical neurons with an antibody recognizing ubiquitin (Figure 2.7B). A diffuse cytoplasmic staining of ubiquitin was observed in control cells. Interestingly, rotenone-treated cells exhibited notable overlap of ubiquitin staining with Parkin puncta consistent with enhanced ubiquitination reported previously (Ding et al., 2010; Geisler et al., 2010; Matsuda et al., 2010).

We also performed co-staining for endogenous LC-3 as a marker for autophagy. LC-3 attaches to early autophagic vesicles during autophagosome biogenesis and is

widely used as a marker for autophagy induction (Klionsky et al., 2008). Since previous reports (Narendra et al., 2008) had demonstrated that in cell lines, Parkin translocation precedes mitochondrial clearance by autophagic vesicles by a process termed mitophagy, we investigated if the Parkin puncta observed in cortical neurons could also be mitophagic in nature. Some overlap of Parkin puncta with the endogenous LC-3 staining was observed (Figure 2.7C). These observations indicate that there are indeed MQC processes occurring in primary neurons in a ROS-dependent fashion. However, this process appears to be qualitatively quite different than those observed in other cell types.

Figure 2.7: Parkin co-localization with cellular organelle markers. (A) Confocal photomicrographs of GFP-Parkin infected primary cortical neurons treated with 20 μ M MPP⁺ for 24h in the absence of B27 co-stained with TOM20. (White arrowheads, co-localized; purple arrowheads, not co-localized.). (B) and (C) Primary cortical neurons treated with 0.05 μ M rotenone were analyzed for co-localization with ubiquitin (B) and LC3 (C).



Parkin translocation in DJ-1 or PINK1 deficient neurons

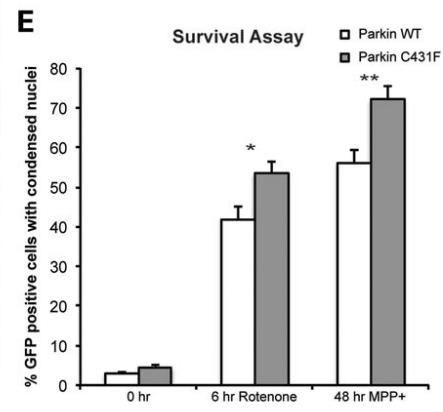
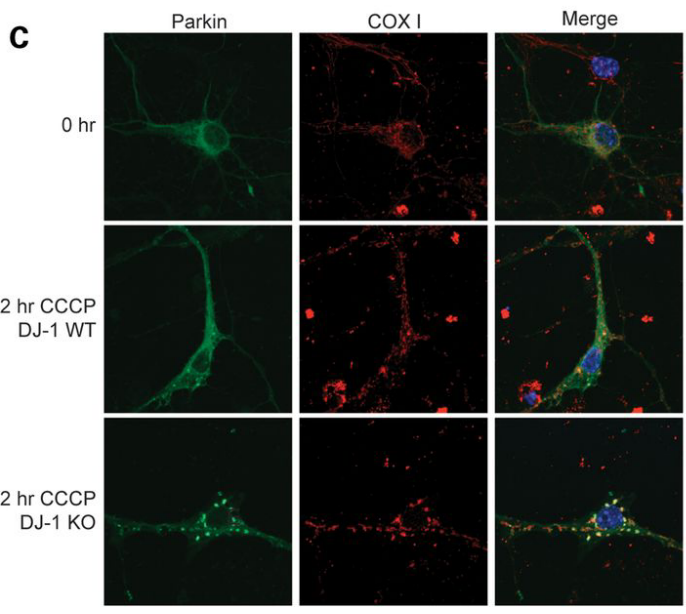
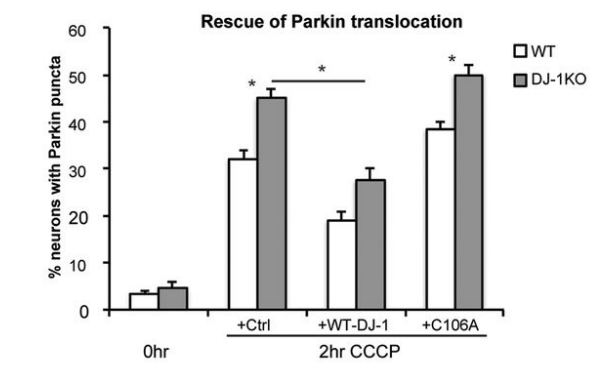
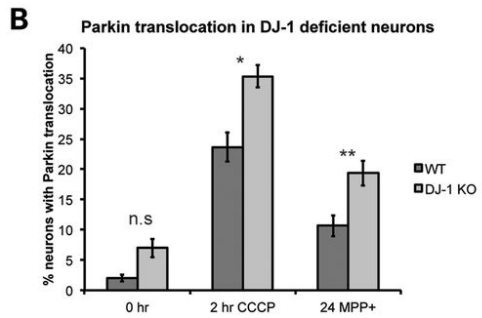
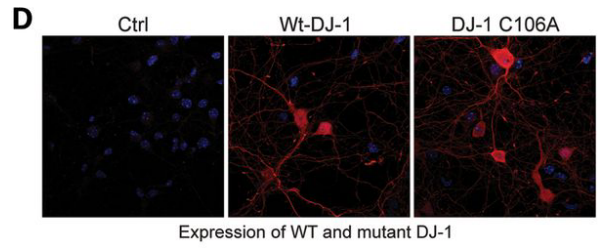
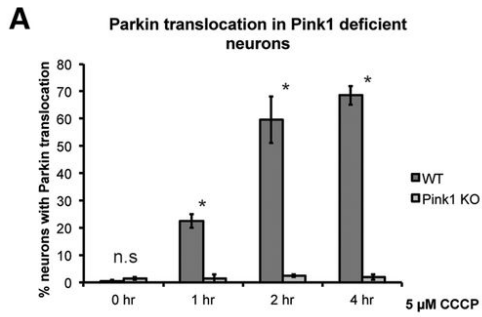
We next determined whether the observed aggregation of Parkin in primary neurons was dependent upon Pink1 and DJ-1, as we have explored in MEFs. Cortical neurons derived from WT and Pink1 deficient E15.5 mice embryos were plated on acid-treated coverslips, coated with poly-D-lysine and laminin. The neurons were infected with GFP-Parkin expressing AAV at the time of plating. Seven days post-plating, the media was changed to fresh growth media lacking B27, as mentioned before, followed by drug treatments. Within 2h of 5 μ M CCCP treatment, significant increase in cells displaying mitochondrially-translocated Parkin could be observed (Figure 2.8A) in WT cortical neurons. However, consistent with observations in Pink1 KO MEFs, no punctate Parkin staining was observed in Pink1 deficient neurons, even after 4h of CCCP treatment. These results indicate the presence of an active Pink1/Parkin pathway in primary neurons in response to mitochondrial damage.

Furthermore, similar experiments were performed in primary cortical neuronal cultures from DJ-1 deficient mice. We observed that, in comparison to WT neurons, Parkin translocation was accelerated in the absence of DJ-1, following treatment with either 5 μ M CCCP or 20 μ M MPP⁺ (Figure 2.8B). We also investigated whether the observed Parkin translocation phenotype in DJ-1 deficient neurons could be rescued by overexpressing WT-DJ-1 (Figure 2.8D). Similar to MEFs, exogenously expressed WT-DJ-1 but not C106A mutant could restore CCCP-induced Parkin translocation levels to those observed in WT neurons. These results provide further evidence of sensitization of DJ-1 deficient cells to mitochondrial damage and therefore suggest an earlier activation of the Pink1/Parkin pathway of mitochondrial damage control.

An important consequence of the activation of the Pink1/Parkin pathway of mitochondrial clearance would be increased survival of cells that can more efficiently clear damaged mitochondria. To test if Parkin overexpression and therefore increased MQC does confer a survival advantage to cells under oxidative stress conditions, we analyzed the survival status of cells overexpressing WT Parkin or the E3-ubiquitin ligase mutant C431F after 6h of 0.05 μ M rotenone or 48h of 20 μ M MPP⁺ treatment (Figure 2.8E). Under both oxidative stress conditions, overexpression of wild type Parkin offered a modest but significant increase in survival when compared to the C431F mutant. These observations provide further support for a functional Pink1/Parkin pathway in neurons. However, care must be taken in interpreting these survival results since the E3 ligase activity of Parkin may have other functions than regulating MQC.

Figure 2.8: Parkin translocation in Pink1 and DJ-1 deficient cortical neurons.

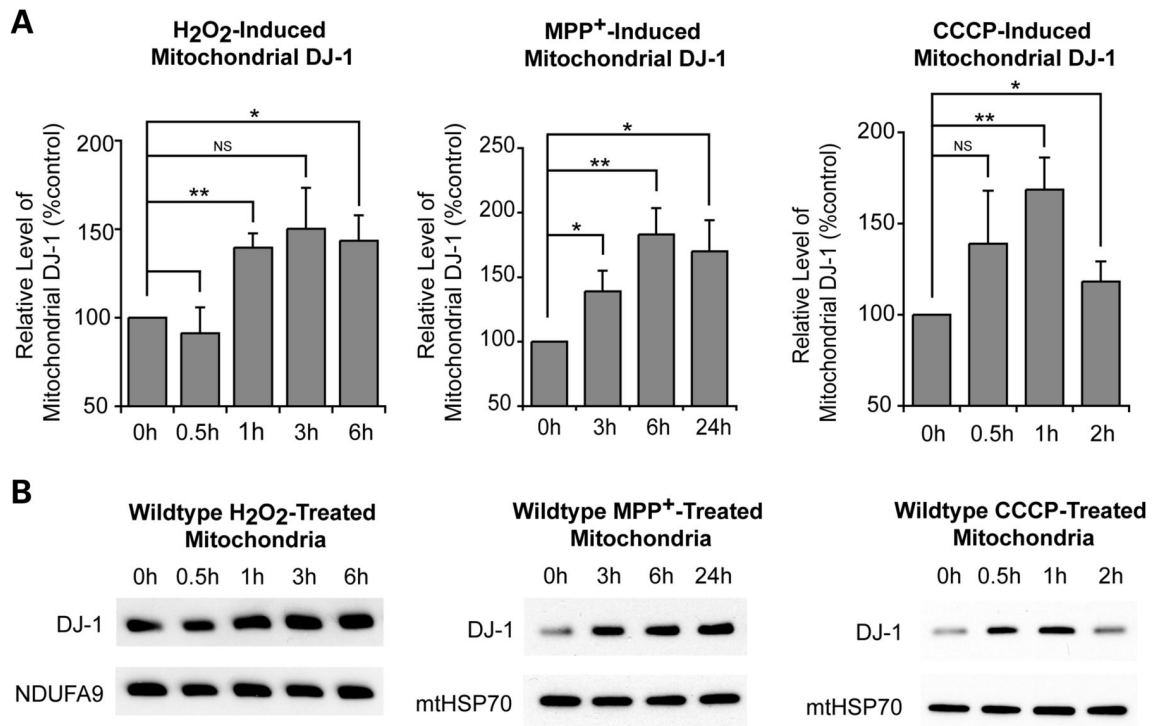
Primary mouse cortical cultures from wild-type (WT) or Pink1 deficient (Pink1 KO) (A) or DJ-1 deficient (DJ-1 KO) (B) embryos infected with GFP-Parkin AAV were treated with 20 μ M MPP⁺ for the indicated durations. Number of cells displaying Parkin puncta were quantified. (C) Representative confocal images of Parkin translocation in CCCP-treated wild-type (DJ-1 WT) and DJ-1 knockout (DJ-1 KO) cortical neuronal cultures. (D) WT or DJ-1 deficient (DJ-1 KO) cortical neurons were infected with GFP-Parkin and either control (Ctrl) or FLAG-WT DJ-1 or FLAG-C106A DJ-1 AAV at the time of plating. Upper panel; expression levels of WT and C106A DJ-1 as illustrated by FLAG staining. Lower panel; Quantification of cells displaying Parkin puncta. (E) Survival of primary cortical neurons from CD1 embryos infected with either GFP- Parkin or GFP-C431F Parkin AAV after treatment with 20 μ M MPP⁺ for 48h. All bar graphs are mean \pm SEM vales of triplicates with an average of 200 cells counted per condition. * P <0.05 and ** P <0.001; t -test for related samples and representative of at least 2 independent experiments.



Increase of mitochondrial DJ-1 in primary neurons with oxidative stress

The above results further implicate DJ-1 in MQC. We next explored whether increased mitochondrial DJ-1 also occurs in primary neurons and whether this was dependent upon Pink1 similar to that observed in MEFs. WT primary cortical neurons from E14.5-15.5 were treated with 30 μ M H₂O₂, 10 μ M MPP⁺, or 10 μ M CCCP in absence of antioxidants on DIV 6 (Figure 2.9). Equal amounts (10 μ g) of mitochondrially-enriched fractions from each time point were loaded. At 1h of H₂O₂ treatment, a significant increase (Figure 2.9A) in the level of DJ-1 at mitochondria was observed in cortical neurons. Sustained maintenance of these DJ-1 levels was also observed until 6h of H₂O₂ treatment. Similarly, by 3h treatment with MPP⁺ and 1hr treatment with CCCP, the level of mitochondrial DJ-1 was significantly increased (Figure 2.9). Similar to MEFs, we also noted no significant increase in whole cell levels of DJ-1 with any treatment (Figure 2.S3B, C). These results demonstrate increased levels of DJ-1 at mitochondria in primary cortical neurons in response to oxidative stress by various agents, most notably the PD-linked drug MPP⁺.

Figure 2.9: The PD-related MPP⁺ as well as other oxidative stressors increase level of DJ-1 at mitochondria in cortical neurons. Wild-type (WT) cortical neurons harvested from E14.5-15.5 embryos were treated with 30 μ M H₂O₂, 10 μ M MPP⁺ or 10 μ M CCCP for indicated time points in absence of antioxidants. Mitochondrial-enriched fractions were obtained through sub-cellular fractionation and were analyzed by immunoblot. A) Quantification of densitometry using Image J software (NIH). Data represent mean \pm SEM (n=3-4 H₂O₂ and CCCP; n=6 MPP⁺). n.s, not significant; * P <0.05 and ** P <0.01 B) Representative blots for DJ-1 and mitochondrial loading control (either NDUFA9 or mtHSP70).

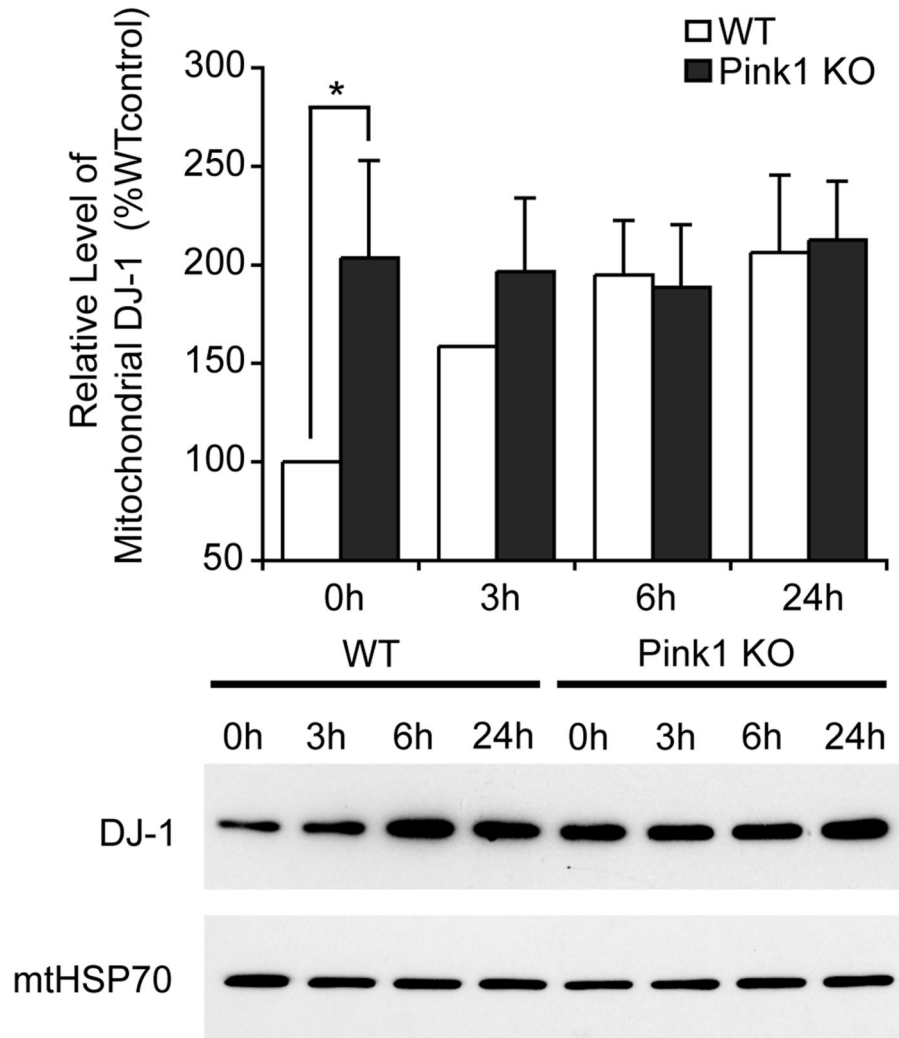


To further confirm DJ-1 increase at the mitochondria and to rule out changes in DJ-1 levels due to contaminating ER (Figure 2.S4B), we investigated changes in mitochondrial DJ-1 using immunofluorescence. WT cortical neurons obtained as previously mentioned were plated onto poly-D-lysine-coated coverslips at a density of 100,000 cells per well of a 24-well dish. These neurons were treated, in absence of antioxidant supplementation, on DIV 6 with either 10 μ M MPP⁺ (6h) or 10 μ M CCCP (1h). Neurons were stained for endogenous DJ-1 and a mitochondrial marker, mtHSP70. Control neurons exhibited mostly ubiquitous staining for DJ-1 while neurons treated with either MPP⁺ or CCCP showed punctate DJ-1 staining that partially co-localizes with mitochondrial staining (Figure 2.S5, white arrows). Due to the large amount of cytoplasmic staining of DJ-1 as well as the large amount of mitochondria in the cell body, we focused on the neuronal processes for demonstrating DJ-1 punctate staining. These observations further support our previous findings using cellular fractionation that DJ-1 levels increase at mitochondria following oxidative stress in neurons.

Importantly, increased mitochondrial DJ-1 was dependent upon Pink1 just as observed in MEFs (Figure 2.10). It is also important to note that again, basal DJ-1 seems to be higher at mitochondria with Pink1-deficiency (Figure 2.10), perhaps due to an increase in basal ROS known to occur with Pink1 deficiency (Wood-Kaczmar et al., 2008). Unlike in the MEFs, Pink1 deficiency increased basal levels of total DJ-1 in cortical neurons, perhaps accounting for the increased basal level of mitochondrial DJ-1 in this cell type (Figure 2.S3E). Unfortunately, we could not obtain breeding from Parkin KO mice pairings required to test for Parkin involvement in DJ-1 translocation in neurons.

Figure 2.10: MPP⁺-induced increase in mitochondrial DJ-1 is dependent upon Pink1 in primary cortical neurons. Wild-type (WT) and Pink1 cortical neurons harvested from E14.5-15.5 embryos were treated with 10 μ M MPP⁺ for indicated time points in absence of antioxidants. Mitochondrial-enriched fractions were obtained through sub-cellular fractionation and were analyzed by immunoblot. A) Quantification of densitometry using Image J software (NIH). Data represent mean \pm SEM (n=2-4). * P <0.05; two-way ANOVA for WT vs. KO samples. B) Representative blots for DJ-1 and mitochondrial loading control (mtHSP70).

MPP⁺-Induced Mitochondrial DJ-1 in Absence of Pink1



Discussion

Numerous recent studies have reported the individual roles of DJ-1, Parkin, and Pink1 in the regulation of mitochondrial function (Narendra et al., 2008; Hao et al., 2010; Vives-Bauza et al., 2010; Thomas et al., 2011). However, how these proteins relate to each other under situations of oxidative stress and the relevance of this interplay in PD pathogenesis is not completely clear.

Our present work addresses two critical questions in relation to the molecular and functional interactions between these PD-associated genes, namely: does DJ-1 have any significance in the Pink1/Parkin mitochondrial quality control pathway; and secondly, is oxidative stress central to Parkin translocation?

Although the role of Pink1 and Parkin in mitochondrial quality control has been well described, the role of DJ-1 at mitochondria remains less certain. Previous work from our laboratory (Irrcher et al., 2010) and others (Thomas et al., 2011) has shown that loss of DJ-1 leads to basally increased levels of ROS and deregulated mitochondrial dynamics suggesting a loss of mitochondrial quality control. Furthermore, loss of mitochondrial integrity would cause cells to be sensitized to additional oxidative stress, which we have previously observed with DJ-1 deficiency both *in vitro* and *in vivo* (Kim et al., 2005a). However, how and whether DJ-1 associates to mitochondrial quality control pathways is unknown.

Presently, we provide critical evidence that DJ-1 does indeed impact the Parkin translocation-mediated pathway of MQC both in MEFs and neurons in response to CCCP. DJ-1-deficiency enhances Parkin translocation. Interestingly, this result is dissimilar from a previous report in which transient knockdown of DJ-1 in HeLa cells did

not have any significant effect on Parkin translocation (Vives-Bauza et al., 2010). Although the reason for this is unclear, it may involve the peculiarities of HeLa cells in regards to what we have observed with their response to ROS. Interestingly, HeLa cells usually lack endogenous levels of Parkin and may have activation of compensatory mechanisms to deal with damaged mitochondria.

The potential reason for DJ-1 regulation of Parkin translocation in response to abrupt depolarization is unclear. While there are a number of functions attributed to DJ-1 including transcription regulation and chaperone abilities (Nagakubo et al., 1997; Hod et al., 1999; Quigley et al., 2003; Tao and Tong, 2003), the most prominent is the ability of DJ-1 to manage ROS. Mitochondria deficient in DJ-1 are reported to produce more ROS (Irrcher et al., 2010). This increase occurs through numerous potential mechanisms including regulation of Nrf2 (Clements et al., 2006), a master antioxidant regulator, and the pro-survival Akt pathway (Aleyasin et al., 2010). It is possible that increased ROS leads to increased mitochondrial damage, which increases the need for Parkin-initiated MQC. This would also suggest that ROS plays a central role in signaling and/or mediating mitochondrial damage resulting in specific Parkin activation. Indeed our present work would support this hypothesis.

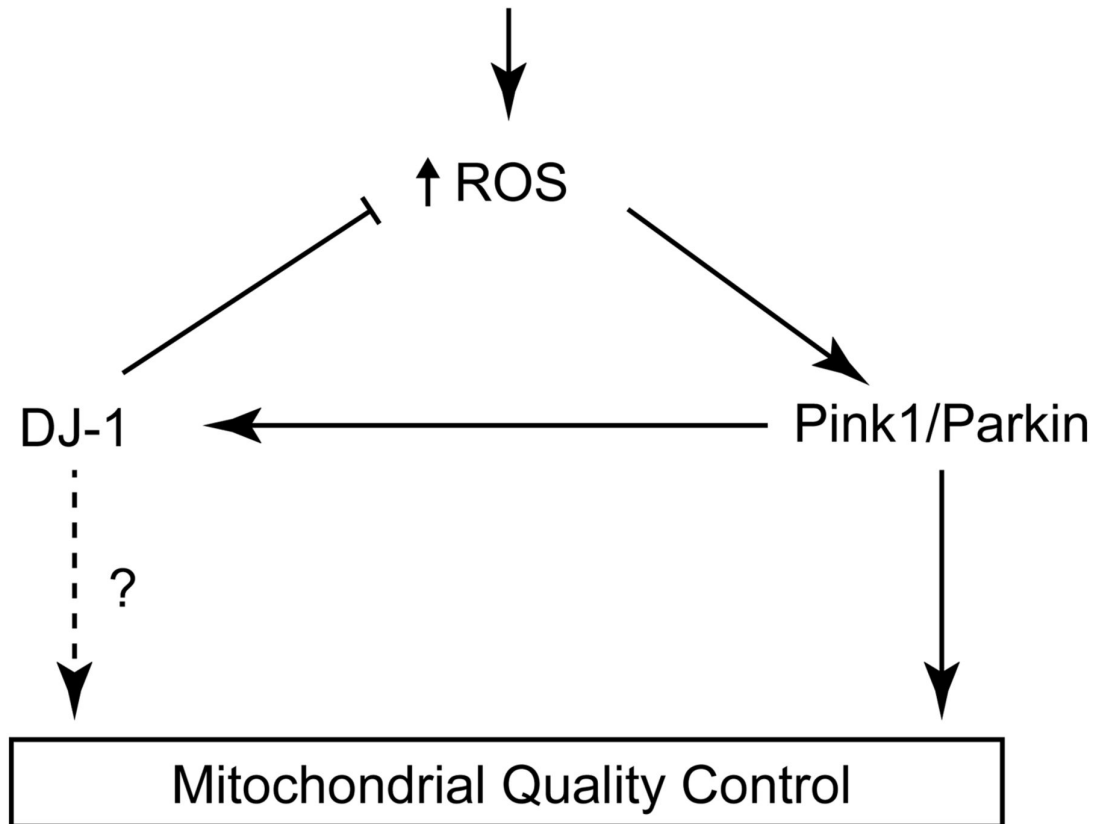
While the evidence above suggests that DJ-1 influences Parkin recruitment, the reciprocal also appears to be true, i.e., stress-induced increase of mitochondrial DJ-1 is mediated by Parkin. Whether this is dependent upon Parkin recruited at mitochondria or Parkin in the cytoplasm, is unknown. Additionally, it is important to note that in this scenario, the role of Pink1, while clear for Parkin translocation, is less clear for DJ-1. While no oxidative stress-induced increase in DJ-1 at mitochondria was detected with

Pink1 loss, increased total DJ-1 expression and increased level of mitochondrial DJ-1 was observed under basal conditions. This basal increase of DJ-1 is reasonable given that Pink1 loss is also reported to increase the ROS environment (Wood-Kaczmar et al., 2008) and perhaps accounts for the increased levels of DJ-1 at the mitochondria. Stress-mediated increase in mitochondrial DJ-1, however, appears to also involve Pink1 since no further increase in DJ-1 levels was observed following oxidative stress in Pink1 deficient cells. Finally, it is important to note that we have not ascertained the source of the increased mitochondrial DJ-1. However, our data suggest that it is not due to a global increase in DJ-1.

What is the potential role of mitochondrial DJ-1? Previous work has demonstrated that this mitochondrial translocation promotes survival of cells in response to oxidative stress (Junn et al., 2009). How survival is affected is unknown. Our unpublished data suggests that DJ-1 loss reduces PGC1- α levels, a key mediator of mitochondria biogenesis, which was shown to be regulated by DJ-1 activity (Zhong and Xu, 2008). In addition, DJ-1 deficiency decreases fusion rates, which predisposes cells to death (Irrcher et al., 2010). Whether these mechanisms are facilitated by only mitochondrial DJ-1 is unclear. Taken together, these data fit a model by which a Parkin-mediated signal induced by oxidative damage initiates a survival response of increased DJ-1 at mitochondria, perhaps to limit oxidative damage - although this has yet to be directly tested. Presumably, as our data would suggest, cells lacking DJ-1 would not be able to initiate this survival response at mitochondria, and the resulting increased mitochondrial damage would promote an even greater translocation of Parkin to further activate mitochondrial quality control (see Figure 2.11 for summary).

Figure 2.11: Schematic representation of DJ-1 and Pink/Parkin interplay during oxidative stress. The Pink1/Parkin MQC pathway is activated by increased ROS levels due to oxidative stress and/or mitochondrial damage in order to maintain mitochondrial health. Stress-induced DJ-1 requires Pink1/Parkin to help maintain mitochondrial health, possibly through inhibiting ROS directly or through other unknown MQC pathways in parallel to Pink1/Parkin.

Oxidative Stress/
Mitochondrial Depolarization/
Mitochondrial Damage



While the above evidence presents a model of reciprocal relationship between DJ-1 and Parkin, its physiological relevance is unclear. There is controversy at least on two levels. First, most work on Parkin translocation has focused on CCCP. How biologically relevant this artificial and robust method of rampant and complete depolarization of mitochondria is to the neurodegenerative process remains unknown. Second, whether this translocation occurs in any robust fashion in neurons is also unclear. Previous reports indicate that it does not, at least with CCCP (Van Laar et al., 2010) and TFAM loss (Sterky et al., 2011). In support of this, we initially had difficulty detecting any Parkin translocation with CCCP or any other mitochondrial-damaging agents in cultured neurons under routine culture conditions. However, we observed that treatment with these agents did induce depolarization and massive mitochondrial fragmentation (Figure 2.5). These results indicated that the lack of Parkin translocation was not due to lack of biological effect of these agents and that Parkin translocation can be separated from fission events. The latter is particularly interesting since recent reports suggest an active role for Parkin in maintaining mitochondrial morphology (Gegg et al., 2010; Ziviani et al., 2010). Importantly, it has been shown that Parkin can ubiquitinate Mitofusin 1 and 2 (Gegg et al., 2010), key molecules regulating mitochondrial fusion, leading to the degradation of these molecules and increasing mitochondrial fission. Results presented here, however, suggest that recruitment of Parkin to mitochondria occurs after induction of mitochondrial fission. It is therefore unlikely that fission events are directly related to Parkin translocation.

Based on our observations of ROS-dependency in MEFs, we reasoned that perhaps the lack of translocation in neurons might be due to the presence of antioxidants in the culture media. Indeed we showed that depletion of such supplements revealed

translocation induced by mitochondrial toxins including CCCP, MPP⁺ and rotenone. These results suggest that Parkin translocation mediated by depolarization of mitochondria or inhibition of mitochondrial complex I require, at least in neurons (and in MEFs), the generation of ROS. However, care must be taken in interpreting the specifics of the ROS mediated signal. Indeed, the source and localization of ROS is known to be critical for any particular biological outcome (Valko et al., 2007; Novo and Parola, 2008).

Interestingly, CCCP treatment induced qualitatively different translocation than that with H₂O₂ in MEFs or MPP⁺ or rotenone in neurons, which produced only partial Parkin translocation to mitochondria. Why this difference occurs is unknown. However, CCCP induces complete depolarization of mitochondria while MPP⁺ is known to activate multiple death pathways both mitochondrial and independent of its role as a mitochondrial complex I inhibitor (Choi et al., 2008). It should be noted that Parkin puncta observed in neurons are characteristically similar to those observed in other cell types (Geisler et al., 2010; Matsuda et al., 2010) in that these aggregates are also positive for ubiquitin. It is, however, difficult to distinguish whether enhanced ubiquitination in these aggregates is a result of Parkin's E3 ligase-mediated ubiquitination of downstream targets (Geisler et al., 2010) or a result of Parkin's auto-ubiquitination function (Matsuda et al., 2010).

Finally, we have shown that the regulatory relationships between Parkin, Pink1 and DJ-1 in primary neurons are similar, if not identical, to those observed in MEFs. This includes the fact that Pink1 is absolutely required for Parkin translocation and that DJ-1 regulates Parkin translocation and is in turn regulated by Pink1 and Parkin. It is important to note that not all modes of damage activate the Parkin-specific mitochondrial quality

control pathway. For example, TFAM deletion induced mitochondrial damage does not result in any evidence of Parkin translocation *in vivo*. In fact, multiple pathways of mitochondrial quality control have been proposed to exist (Andrade-Navarro et al., 2009).

In summary, we have clarified at least three critical issues in this report. First, we show that primary neurons can activate mitochondrial quality control-related Parkin translocation to mitochondria. Second, we demonstrate that ROS plays a central role in this process. Third, we provide evidence that DJ-1 regulates this process. Loss of DJ-1 leads to enhancement in Parkin translocation and conversely both Parkin and Pink1 deficiency block stress-mediated increase in mitochondrial DJ-1, an event previously shown to be critical for cell survival (Junn et al., 2009). Taken together, we propose that in neurons, mitochondrial health and consequent sensitivity to environmental stress is regulated by at least two interrelated and parallel pathways that are in turn regulated via feedback from mitochondrial health. These pathways include: a) the classic pathway of mitochondrial quality control involving Parkin translocation to damaged mitochondria, which are then eliminated via downstream clearance mechanisms and b) Pink1/Parkin-regulated increase in mitochondrial DJ-1. In this latter case, we hypothesize that this may limit oxidative stress-induced damage at mitochondria to improve mitochondrial health.

Materials and Methods

Transgenic mice

The generation and genotype of the Parkin, DJ-1, and Pink1 deficient mice have previously been described in detail, respectively (Itier et al., 2003; Kim et al., 2005a; Kitada et al., 2007). All procedures involving animals were approved by the University of Ottawa Animal Care Committee and were maintained in strict accordance to the Guidelines for the Use and Treatment of Animals put forth by the Animal Care Council of Canada and endorsed by the Canadian Institute of Health Research.

Cell Culture

Mouse embryonic fibroblasts (MEFs) were derived from E14.5-15.5 transgenic DJ-1 (C57BL/6), Pink1 (C57BL/6) and Parkin (mixed background) mice (Charles River Laboratories) of either sex and maintained in Dulbecco's Modified Eagle Media (DMEM) (Sigma) supplemented with 10% fetal bovine serum (FBS) (Sigma) and antibiotic/antimycotic (Sigma). All MEFs were immortalized as previously described (Aleyasin et al., 2010). Fractionation experiments were performed on near confluent (90-95%) 100mm plate and were treated with 100 μ M H₂O₂ for up to 6hr to induce oxidative stress. Cortical neurons were derived from E14.5-15.5 wildtype (WT) CD1 mice or C57BL/6 WT/transgenic Pink1/transgenic DJ-1 mice (Charles River Laboratories) of either sex and maintained in Neurobasal media (Invitrogen) supplemented with B27 with antioxidants (Gibco), N2 (Gibco), 0.5 mM L-glutamine (Sigma), and penicillin/streptomycin (Gibco) as previously reported (Kim et al., 2005a). For DJ-1 studies of mitochondrial-enriched fractions, neurons were plated on poly-D-lysine-coated (Sigma)-100mm plates at a density of 4-5 x10⁶ cells/100mm plate. For immunofluorescence of

endogenous DJ-1, neurons were plated on poly-D-lysine-coated coverslips in 24-well plates at a density of 100,000 cells per well. For all DJ-1 studies, on DIV5, media was completely changed to media identical to initial plating, with the exception of including B27 without antioxidants (Gibco). Neurons were treated with 30 μ M H₂O₂ for up to 6hr, 10 μ M MPP⁺ (Sigma) for up to 24hr, or 10 μ M CCCP (Sigma) for up to 2hr to induce oxidative stress. All treatments finished on DIV6.

Antibodies, Plasmids and Virus

The following antibodies were used: rabbit anti-DJ-1 (Abcam), mouse anti-parkin (Santa Cruz), mouse anti-NDUFA9 (MitoSciences), mouse anti-mtHSP70 (Abcam, mouse anti-COX V (MitoSciences), mouse anti-COX I (MitoSciences), rabbit anti-TOM20 (Santa Cruz), rabbit anti-LC3 (Novus Biologicals), rabbit anti-calnexin (Abcam), mouse anti-actin (Sigma), rabbit anti-ubiquitin (Abcam), rabbit anti-Raf-1 (Santa Cruz) and anti-mouse and anti-rabbit horse radish peroxidase-conjugated secondary antibody (Bio-Rad). Construction of the FLAG-DJ-1 pcDNA3.1 has been described before (Kim et al., 2005a). FLAG-C106A mutant was generated by site directed mutagenesis of the FLAG-DJ-1. emGFP-Parkin Adeno-associated virus was generated and purified as described (Zolotukhin et al., 2002).

Infection/Transfection

For infection of mouse cortical neurons, cortical cultures were prepared as described above. 5 x 10⁵ neurons were plated into 24-well plates containing coverslips that were acid treated with 1N Nitric acid and 1N HCl and pre-coated with 1X Poly D-Lysine (PDL) and Lamminin. Cultures were infected with GFP-Parkin Adeno-associated virus at the time of plating at an MOI of 5. Fresh growth media was added to the conditioned

media at the ratio of 1:1 every 3 days of culture. On DIV7, media from the wells were aspirated and replaced with fresh growth media similar to that used at the time of plating with the exception of B27. Treatments were performed on DIV8 using 10X working stocks of CCCP, rotenone (Sigma) or MPP⁺.

For MEFs, 5×10^4 cells were seeded into 24-well plates containing poly-D-lysine pre-coated coverslips one day before the day of transfection. GFP-Parkin-pEGFP construct was transfected into the cells using Lipofectamine (Invitrogen) following manufacturer's recommendations. For co-transfections GFP-Parkin-pEGFP was co-transfected with either empty vector, WT DJ-1-FLAG or C106A-FLAG at a ratio of 1:3 using Effectene Transfection Reagent (Qiagen) as per manufacturer's recommendations. 24 hours after transfection, cells were treated with 10 μ M CCCP or 100 μ M hydrogen peroxide for indicated amounts of time. For antioxidant studies, cells were pre-treated for 3hr with either 100 μ M TIRON (Sigma) or 2mM N-acetyl cysteine (Sigma) prior to oxidative insult.

Immunofluorescence, quantification of Parkin translocation and mitochondrial fluorescence intensity

For endogenous DJ-1, following treatment, cells were fixed in 4% formalin in growth media at 37°C for 15min. The cells were permeabilized and blocked simultaneously using 0.1% Triton X-100 and 5% normal goat serum for 1hr at room temperature.

Hybridizations using the respective primary antibodies were performed overnight at 4°C. Cells were subsequently washed in 5% normal goat serum and stained with the corresponding secondary antibodies. Cells were subsequently washed in 1X PBS, stained with Hoechst, mounted and analyzed by confocal microscopy.

For Parkin translocation experiments, following drug treatments the cells were fixed in 4% formalin in growth media at 37°C for 15min. The cells were permeabilized using 0.2% Triton X-100 for 5min at room temperature, followed by blocking using 2.5% normal goat serum for 1hr at room temperature. Hybridizations using the respective primary antibodies were performed either at 37°C for 30min or at 4°C overnight. Cells were subsequently washed in 1X PBS and stained with the corresponding secondary antibodies. Cells were finally stained with Hoechst, mounted and were analyzed by confocal microscopy. Quantifications of Parkin translocation were performed using an inverted fluorescence microscope. Cells displaying Parkin puncta were scored among the cells that were positive for GFP-Parkin staining.

For quantification of mitochondrial fluorescence intensity, all confocal photomicrographs were taken using identical conditions. Using NIH ImageJ software, an outline of the individual cell was drawn using the GFP staining as a cue. Mitochondrial staining intensity within this region of interest was measured, which is indicative of total mitochondrial staining intensity relative to the total area of the region of interest. At least 25 cells were counted per condition. Bar diagram is representative of two independent experiments.

Mitochondrial Fractionation

Fractionation was performed identically for both MEFs and neurons. Briefly, cells were washed once with PBS and scraped in 1.2mL of PBS into a 1.5mL Eppendorf tube. From each sample, 300uL of cell suspension was saved for whole cell lysate. Harvested cells were centrifuged at 5000rpm for 5min at 4°C in an Eppendorf Centrifuge 5417R. The cell pellet was resuspended in 250-500uL of isolation buffer (0.25M Sucrose, 10mM Tris,

pH7.5, 1mM EDTA, freshly added protease inhibitors) and passed through a 27 gauge insulin syringe 35 times. Samples were then centrifuged at 610g for 10min at 4°C. The supernatant was then transferred to a new tube and centrifuged at 10,000g for 20min at 4°C. The supernatant (cytosolic fraction) was transferred to a new tube and the pellet (mitochondrial-enriched fraction) was resuspended in 25-50µL of isolation buffer. The whole cell lysis pellet was resuspended in 50-100µL of lysis buffer (50mM Tris-HCl pH 7.5, 100mM NaCl, 1mM EDTA, 0.2% NP-40, and freshly added 1mM DTT and protease inhibitors), vortexed for 10sec at maximum setting, and incubated on ice for 30min. Samples were stored at -80°C.

Immunoblotting

Protein quantification was carried out using traditional Bradford (Bio-Rad) method. For mitochondrial-enriched blots, 10µg of each sample was electrophoresed on 12% sodium dodecyl sulfate polyacrylamide gels and transferred to polyvinylidene fluoride (PVDF) membranes (Millipore). For relative whole cell, mitochondrial-enriched fractions and cytoplasmic fractions comparisons, sample amounts were calculated based on cell number. Membranes were probed with the respective primary antibodies followed by horseradish peroxidase-conjugated secondary antibodies and developed with the Immobilon Western Chemiluminescent HRP Substrate (Millipore).

Survival Assay

For survival assay, primary cortical neurons infected with GFP-Parkin AAV were prepared as mentioned before. Following 48 hr of MPP⁺ treatment, cells were fixed and stained with Hoechst and the number of GFP-positive apoptotic nuclei counted under fluorescence microscope.

Statistical Analysis

Statistical significance was determined using paired Student's t-test for related samples. Two-way ANOVA was used in select immunoblots to determine significance between WT and KO in control and treated conditions. All data are presented as mean \pm standard error of the mean (SEM). Significance at $p < 0.05$ (*), $p < 0.01$ (**) and $p < 0.001$ (***); no significance is denoted by n.s.

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Conflict of Interest Statement

All authors declare no conflict of interest.

Supplementary Information

Figure 2.S1. Parkin expression levels in HeLa cells. HeLa cells transfected with GFP-Parkin were pretreated with 2mM n-acetyl cysteine for 3hr before treating with 10 μ M CCCP for 2h. Cell lysates were then analyzed by western blotting using the indicated antibodies. Images are representative of 3 independent experiments.

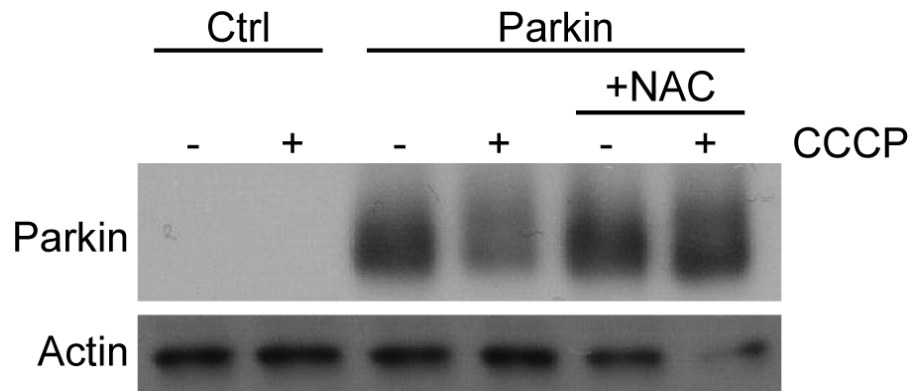


Figure 2.S2. Parkin translocation in response to hydrogen peroxide treatment. A) Representative confocal photomicrographs of WT MEFs either left untreated (0h) or treated with 100 μ M H₂O₂ for 5h. Fixed cells were stained using COX I antibody. White arrowheads highlight co-localized Parkin puncta B) Quantification of number of cells displaying Parkin translocation. Bar graph represents mean \pm SEM with 200 cells counted in duplicates per condition. **** P <0.01**; t -test for related samples.

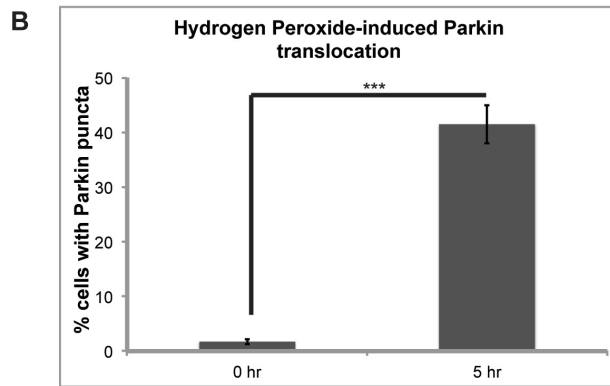
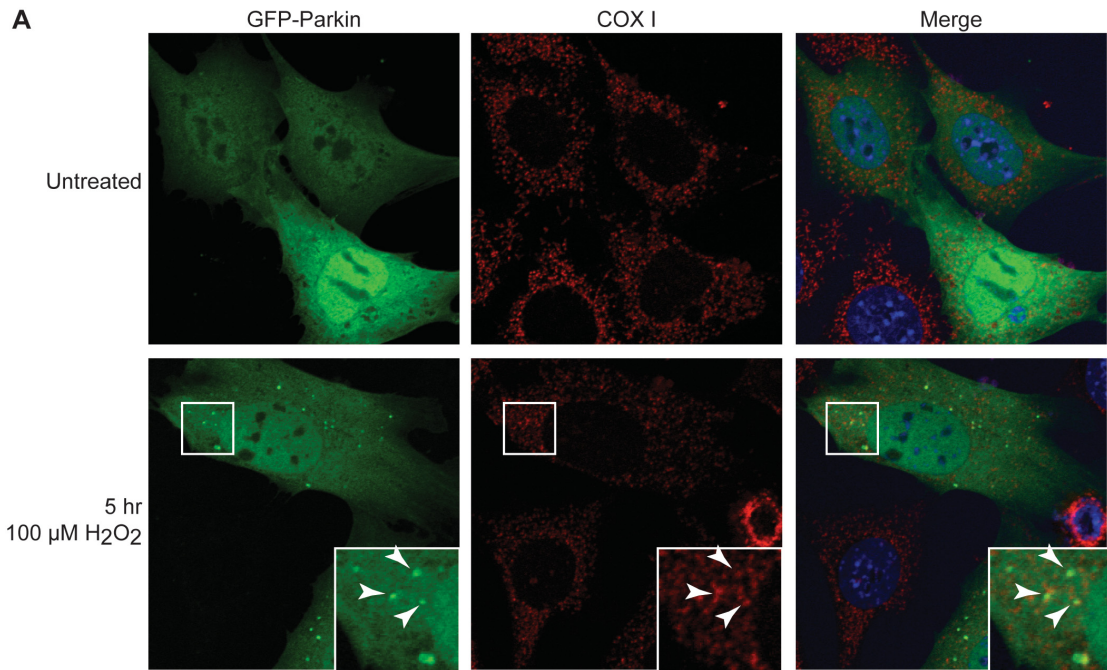
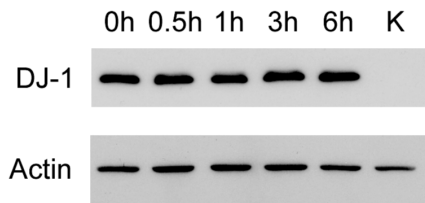
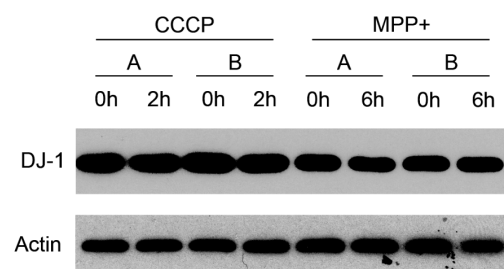


Figure 2.S3. Whole cell level of DJ-1 in mouse embryonic fibroblasts and cortical neurons. A-C) Treatment with H₂O₂, CCCP, and MPP⁺ does not increase whole cell level of DJ-1. D) Pink1 and Parkin deficient MEFs have similar DJ-1 expression level to WT MEFs. E) Pink1 deficient cortical neurons have slightly increased DJ-1 levels compared to WT cortical neurons. All data is representative of n=2. K, DJ-1 KO sample.

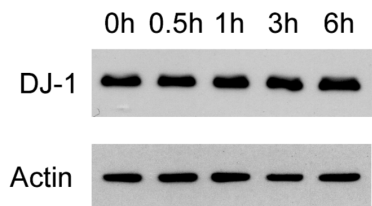
A MEFs - 100 μ M H₂O₂ Treatment



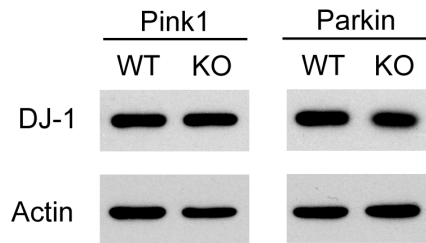
B Cortical neurons - 10 μ M CCCP and 10 μ M MPP⁺ Treatment



C Cortical neurons - 30 μ M H₂O₂ Treatment



D Pink1 and Parkin KO MEFs - no treatment



E Pink1 KO Cortical neurons - no treatment

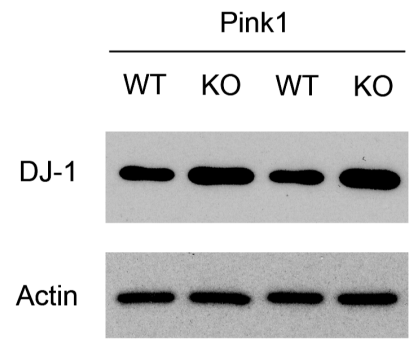
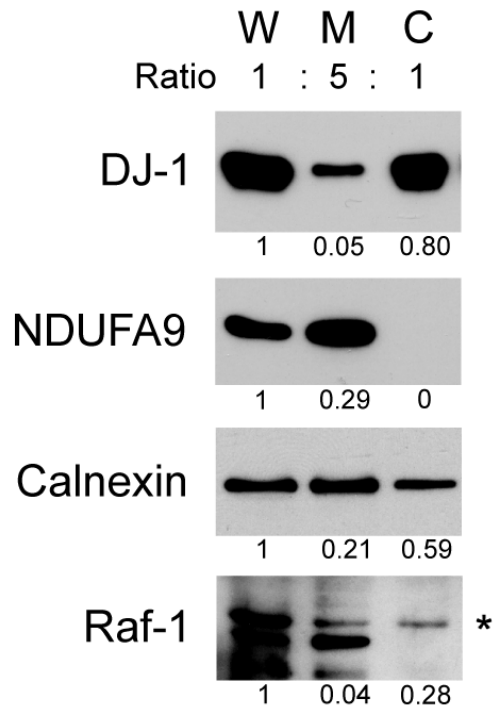


Figure 2.S4. Relative levels of DJ-1, calnexin, and Raf-1 in whole cell lysates, mitochondria and cytoplasm. The relative amount of DJ-1 in the mitochondrial-enriched and cytoplasmic fractions was determined. ER marker calnexin and cytoplasmic marker Raf-1 were assessed to check ER or cytoplasmic contamination respectively. Mitochondrial markers NDFUA9, mtHSP70 and TOM20 were also assessed. Densitometric quantification of the levels of each marker in mitochondria-enriched and cytoplasmic fractions relative to whole cell level is indicated below each blot. A) WT MEF whole cell, mitochondrial and cytoplasmic fractions. Equal amounts of whole cell and cytoplasmic fraction were loaded. 5 times as much mitochondrial enriched fractions was used (as indicated by ratio). B) CD1 whole cell, mitochondrial and cytoplasmic fractions. Equal amount of mitochondria-enriched fraction and cytoplasmic fraction were loaded relative to whole cell lysate (as indicated by ratio). W, whole cell lysate; M, mitochondrial-enriched fraction; C, cytoplasmic fraction. * band of interest.

A

MEFs

**B**

Cortical Neurons

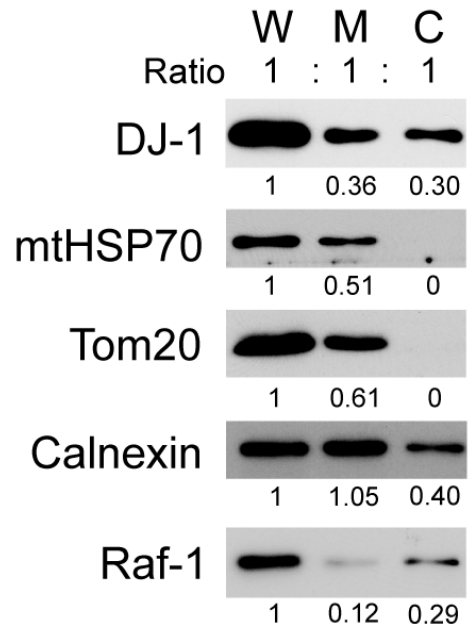
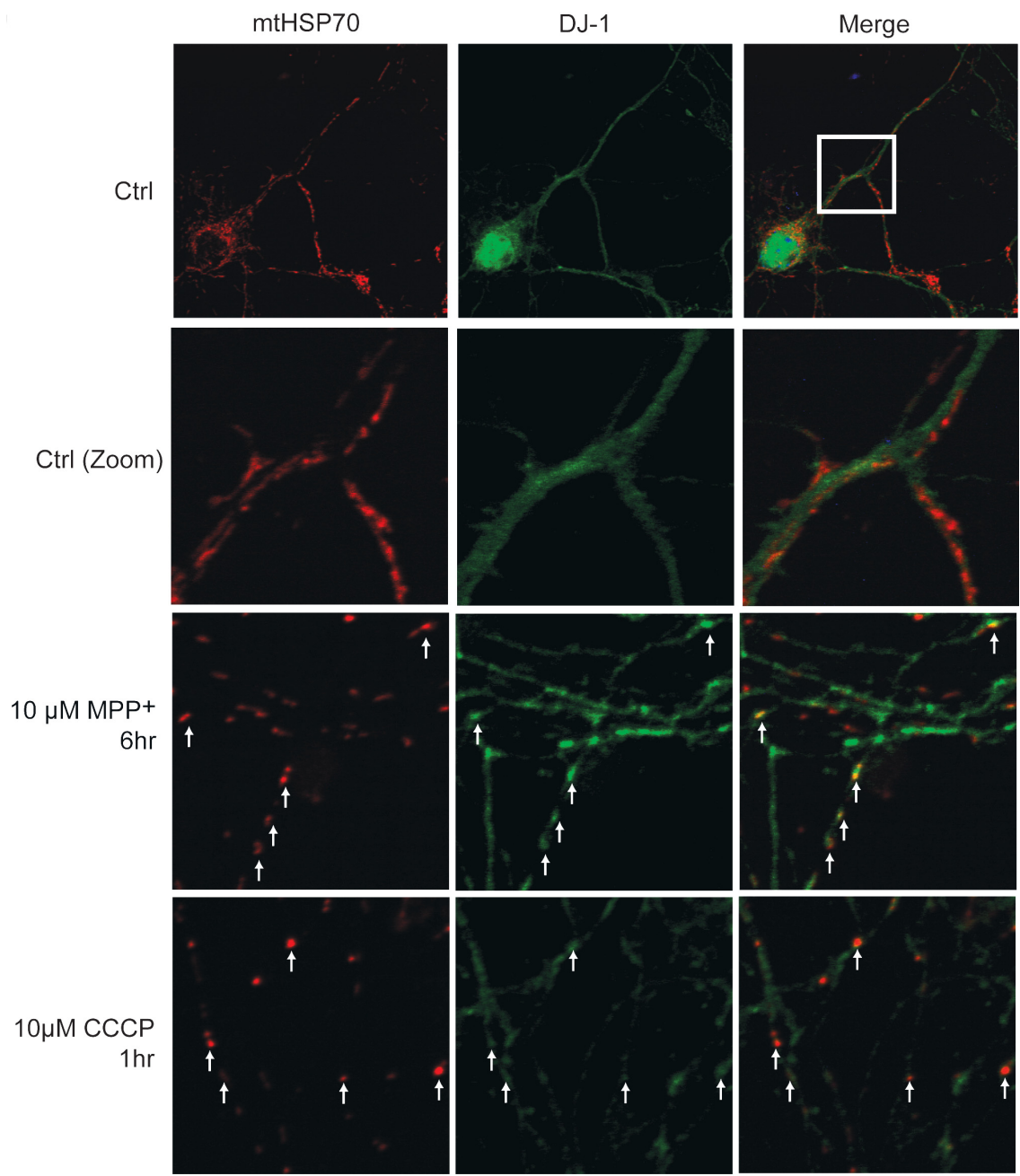


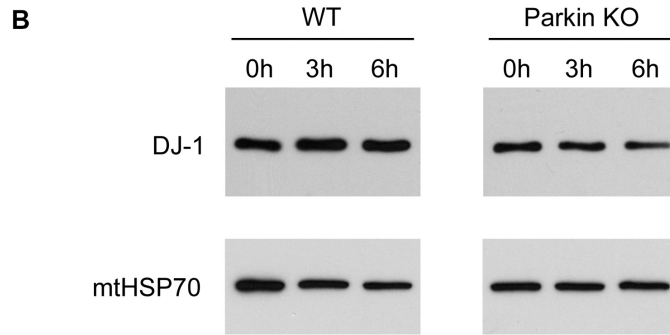
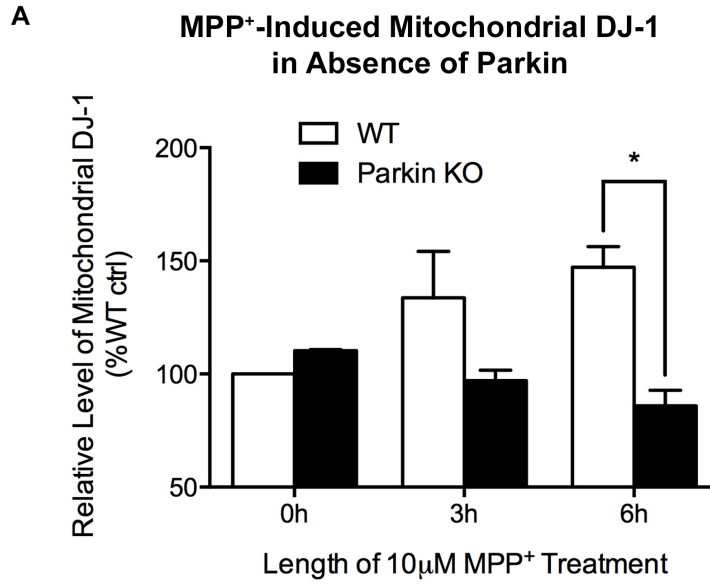
Figure 2.S5. Immunofluorescence of endogenous DJ-1 in cortical neurons. CD1 cortical neurons were treated with vehicle, 10 μ M MPP⁺ (6h) or 10 μ M CCCP (1h) in the absence of antioxidants on DIV6. White box corresponds to zoomed area of interest in control sample. Representative zoomed area of interest of MPP⁺ and CCCP treated samples are shown with specific examples of co-localization demonstrated (white arrows). Images are representative of two independent experiments conducted in quadruplicate.



Unpublished Data Relevant to Manuscript

Following the publication of this manuscript, we were able to examine stress-induced response of DJ-1 translocation to mitochondria in Parkin KO cortical neurons. Parkin WT and KO primary cortical neurons from E14.5-15.5 were treated with 10 μ M MPP⁺, in absence of antioxidants on DIV 6 (Figure 2.12). Equal amounts (10 μ g) of mitochondrial enriched fractions from each time point were loaded. At 1h of MPP⁺ treatment, a significant increase (Figure 2.12B) in the level of DJ-1 at mitochondria was observed in cortical neurons. These findings are similar to what was observed in Parkin KO MEFs and therefore indicate that Parkin is important in stress-induced increase of mitochondrial DJ-1.

Figure 2.12. MPP⁺-induced increase in mitochondrial DJ-1 requires Parkin in cortical neurons. Wild-type (WT) and Parkin KO cortical neurons harvested from E14.5-15.5 embryos were treated with 10 μ M MPP⁺ for indicated time points in absence of antioxidants. Mitochondrial-enriched fractions were obtained through sub-cellular fractionation and were analyzed by immunoblot. A) Quantification of densitometry using Image J software (NIH). Data represent mean \pm SEM (n=2). * P <0.05; two-way ANOVA for WT vs. KO samples. B) Representative blots for DJ-1 and mitochondrial loading control (mtHSP70).



CHAPTER 3

VDAC1 is important for sub-mitochondrial localization of DJ-1

Sarah J. Hewitt, Steve M. Callaghan, Marisa Brini, William J. Craigen, Daniel Figeys,
Ruth S. Slack, David S. Park

This manuscript is in preparation for submission and peer-review

Statement of Author Contributions

Sarah J. Hewitt designed and conducted all experiments under the guidance of Dr. David S. Park. Steve M. Callaghan provided excellent technical support. DJ-1 constructs were a generous gift from Dr. Marisa Brini. VDAC1 MEFs and transgenic mice were a generous gift from Dr. William J. Craigen. Dr. Daniel Figeys performed the interactor screen. Dr. Ruth S. Slack provided insight into the design and implementation of experiments. **Sarah J. Hewitt** and Dr. David S. Park analyzed data and wrote the manuscript.

VDAC1 is important for sub-mitochondrial localization of DJ-1

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Abstract

Loss-of-function mutations in *DJ-1* cause early-onset Parkinson's disease (PD) and are responsible for ~1-2% of all familial cases. Investigation of familial genes involved in PD gives us insight into the mechanism of degeneration, as the majority of cases are of unknown cause. While DJ-1 has many potential functions in the cell, its major role appears to be the handling of oxidative stress. In this regard, DJ-1 loss leads to hypersensitivity to exogenous oxidative insults. Others have shown that an important factor in the mechanism of DJ-1-mediated survival is its mitochondrial localization. In this study we show an interaction between DJ-1 and the mitochondrial protein voltage dependent anion channel 1 (VDAC1). We demonstrate that stress-induced increase in mitochondrial DJ-1 requires VDAC1. We also identify decreased mitochondrial health in VDAC1 deficient cortical neurons, as evidenced by reduced survival, increased ROS production following stress, fragmented mitochondria and decreased ATP production. We also show that DJ-1 requires VDAC1 for its sub-mitochondrial matrix localization. In the absence of VDAC1, DJ-1 localization to the matrix is reduced. Importantly, DJ-1 localization is responsive to reductions in mitochondrial-generated ATP. Taken together our work suggests one potential model by which VDAC1 regulates proper localization of DJ-1 in the mitochondrial matrix to regulate ATP production.

Introduction

Parkinson's disease (PD) is a common neurodegenerative disease that is caused by loss of dopaminergic neurons in the *substantia nigra pars compacta* (SNc). Approximately 90% of cases are of unknown cause, however the remaining 10% have a genetic basis. Understanding the function of these genes will lead to a better understanding of the pathogenesis in PD.

DJ-1 was originally identified as an oncogene (Nagakubo et al., 1997) and since has had a multitude of functions attributed to it, including chaperone (Shendelman et al., 2004), transcription regulator (Takahashi et al., 2001), atypical peroxireductase (Andres-Mateos et al., 2007) and most relevant to our study, oxidative stress sensor (Canet-Avilés et al., 2004). Loss-of-function mutations in *DJ-1* cause early-onset PD (Bonifati et al., 2003).

Given the wide range of functions that DJ-1 appears to regulate, it is unclear which activity(s) are relevant for PD pathogenesis. Previously we have shown that loss of DJ-1 results in hypersensitivity to oxidative stress *in vitro* and *in vivo*, as well as fragmented mitochondria and elevated ROS levels (Kim et al., 2005a; Irrcher et al., 2010). We and others have demonstrated that during oxidative stress, DJ-1 partially localizes to mitochondria (Canet-Avilés et al., 2004; Andres-Mateos et al., 2007; Junn et al., 2009; Joselin et al., 2012). This mitochondrial localization of DJ-1 has been shown to be protective during oxidative stress (Canet-Avilés et al., 2004; Junn et al., 2009). Despite these findings, the mechanism that regulates mitochondrial localization of DJ-1 remains unclear.

One major factor that plays a role in mitigating cell survival is the voltage dependent anion channel (VDAC). Mammalian cells have three isoforms of VDAC, all of which reside in the outer mitochondria membrane (OMM) (Colombini, 1980; Roos et al., 1982; Rostovtseva et al., 2000). This voltage dependent channel allows passage of anions such as pyruvate and adenine nucleotides as well as cations such as Ca^{2+} through the OMM (Shoshan-Barmatz et al., 2006). During times of stress, mitochondria can undergo a sudden permeabilization, in which the mitochondrial permeability pore (mPTP) opens and leads to apoptosis (Massari and Azzone, 1972; Haworth and Hunter, 1979; Green and Reed, 1998). Although not an essential component of the mPTP, VDAC1 can interact with numerous factors such as Bcl-XL and hexokinase to affect mitochondrial permeabilization and therefore influence cell survival (Azoulay-Zohar et al., 2004; Baines et al., 2007; Abu-Hamad et al., 2009; Arbel et al., 2012).

An interaction screen revealed DJ-1 as a potential binding partner of VDAC1. Given their overlapping roles in survival and mitochondrial localization, we investigated the potential role of these two factors regulating mitochondrial function and stress response.

Results

DJ-1 requires VDAC1 for stress-induced localization to mitochondria

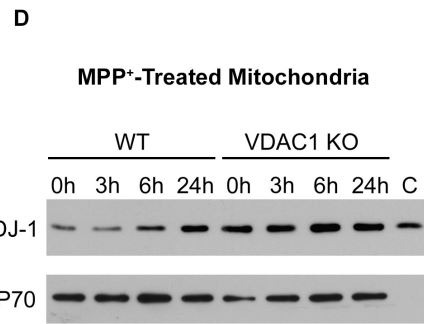
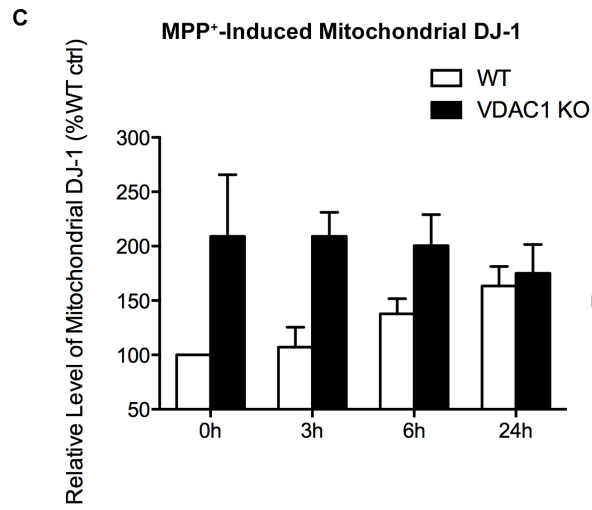
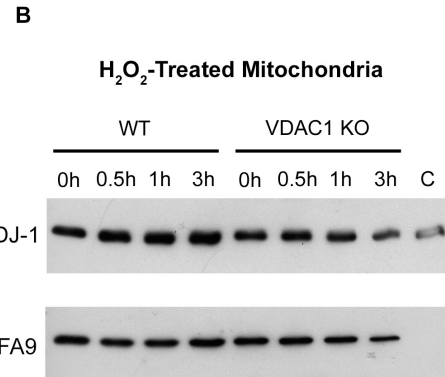
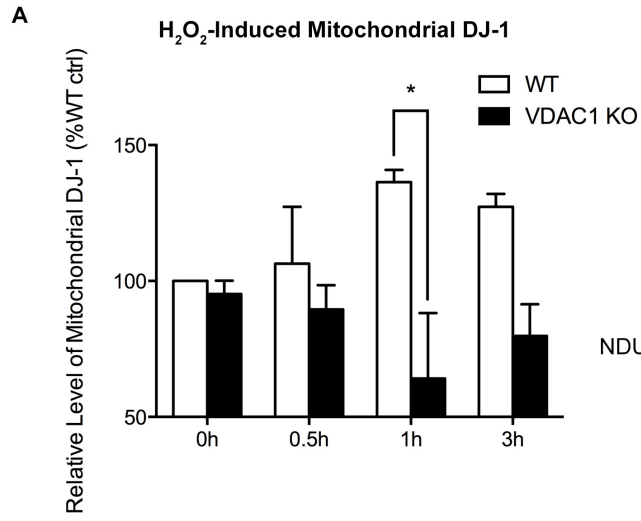
An unbiased screen, that employed mass spectrometry to identify endogenous proteins interacting with overexpressed bait proteins, was performed. This unbiased screen suggests that overexpressed VDAC1 interacts with endogenous DJ-1. We sought to validate this interaction screen to further understand the function of DJ-1 in the cell. Both overexpressed GST-DJ-1 in HEK293 cells and endogenous DJ-1 in murine embryonic fibroblasts (MEFs) show an interaction with endogenous VDAC1 (Figure 3.S1A, B).

Based upon this data, we next investigated the potential role of these two proteins at the mitochondria. In our previous work, we demonstrated that mitochondrial DJ-1 levels increase with oxidative stress, in both MEFs and in primary cortical neurons (Joselin et al., 2012). The signal that regulates this translocation has yet to be determined. As VDAC1 is localized to the OMM and interacts with DJ-1, we investigated how its loss could affect translocation of DJ-1 to mitochondria.

Following up to 3h of 100 μ M H₂O₂ treatment, VDAC1 WT and KO MEFs were subjected to subcellular fractionation via differential centrifugation to obtain mitochondrial enriched fractions. Samples were analyzed by Western blot for levels of DJ-1 and the mitochondrial loading control mitochondrial heat shock protein 70 (mtHSP70). WT MEFs show an increase in mitochondrial DJ-1 levels and this increase does not occur with VDAC1 deficiency (Figure 3.1A, B). We next examined mitochondrial localization of DJ-1 in primary cortical neurons. WT and VDAC1 KO

primary cortical neurons from E14.5-15.5 embryos were cultured *in vitro* for 6 days prior to treatment with 10 μ M MPP⁺ in absence of supplemented antioxidants for up to 24h. Mitochondrial enriched fractions were similarly obtained as mentioned above and subjected to Western blot analysis. Unlike in WT cortical neurons, there is no stress-induced increase in mitochondrial DJ-1 in absence of VDAC1 (Figure 3.1C, D). VDAC1 appears to be necessary for stress-induced increase of mitochondrial DJ-1. Interestingly, the basal level of mitochondrial DJ-1 is increased with VDAC1 deficiency in cortical neurons. This finding is suggestive that VDAC1 KO cortical neurons have increased stress, as increased mitochondrial DJ-1 occurs following exogenous stimulus of oxidative stress (Joselin et al., 2012).

Figure 3.1: Oxidative stress-induced increase in mitochondrial DJ-1 is impaired in VDAC1-deficient MEFs and primary cortical neurons. A, B) Wildtype (WT) and VDAC1 KO MEFs were treated with 100 μ M H₂O₂ for indicated time points. C, D) WT and VDAC1 KO cortical neurons harvested from E14.5-15.5 embryos were treated with 10 μ M MPP⁺ for indicated time points in absence of antioxidants. Mitochondrial enriched fractions were obtained through subcellular fractionation and were analyzed by immunoblot. A, C) Quantification of densitometry using Image J software (NIH). Data represent mean \pm SEM (n=3). **P*<0.05; two-way ANOVA with Tukey post-hoc analysis for WT vs. KO samples. B, D) Representative blots for DJ-1 and mitochondrial loading control (NDUFA9 or mtHSP70).



VDAC1 deficiency causes significantly decreased mitochondrial health

Given that VDAC1 KO appear, at least in neurons, to show increased DJ-1 mitochondrial localization, we sought to determine whether VDAC1 KO neurons display indices of cellular stress. Although the mitochondrial effects of VDAC1 deficiency has been investigated in multiple tissues (Wu et al., 1999; Anflous et al., 2001; Krauskopf et al., 2006; Baines et al., 2007), little work has been done characterizing neurons that lack VDAC1. As such, we question what effect VDAC1 deficiency may have on mitochondria function. Here we sought to determine how VDAC1 KO affected mitochondrial health by examining survival, ROS levels, mitochondrial length, and ATP levels in cortical neurons.

While decreased cell survival can occur via multiple pathways, increased cell death can be indicative of mitochondrial damage (Esposito et al., 1999; Fiskum et al., 2003; Lin and Beal, 2006; Lin et al., 2009). Primary cortical neurons from WT and VDAC1 KO E14.5-15.5 embryos were grown *in vitro* for 6 days prior to treatment with 10 μ M MPP⁺ treatment for up to 6h in absence of supplemented antioxidants. Samples were fixed and nuclei were stained with Hoechst to assess nuclear integrity. Basally, VDAC1 KO cortical neurons exhibit significantly decreased survival that is not further enhanced by 10 μ M MPP⁺ treatment (Figure 3.2A). The decreased survival of these cortical neurons basally suggests increased cellular stress.

Accordingly, we next examined levels of ROS in VDAC1 WT and KO cortical neurons. Increased ROS is also often indicative of mitochondrial dysfunction (Esposito et al., 1999; Fiskum et al., 2003; Lin and Beal, 2006; Chinta and Andersen, 2008; Lin et al., 2009). WT and VDAC1 KO primary cortical neurons were cultured *in vitro* for 6 days

prior to analysis. We employed the cell-permeable probe CM-H₂DCFDA, which fluoresces according to the level of oxidative stress within the cell. With 1h of 10 μ M MPP⁺ treatment (in absence of antioxidants), we see a significantly smaller increase in ROS production with VDAC1 KO, compared to WT (Figure 3.2B). Interestingly, with 3h of 10 μ M MPP⁺ (in absence of antioxidants) we observe a significantly larger increase in ROS production in the VDAC1 KO cortical neurons (Figure 3.2B). These findings suggest that VDAC1 KO cortical neurons are able to compensate with short-term stress, but fail to do so with extended stress and subsequently produce higher levels of ROS.

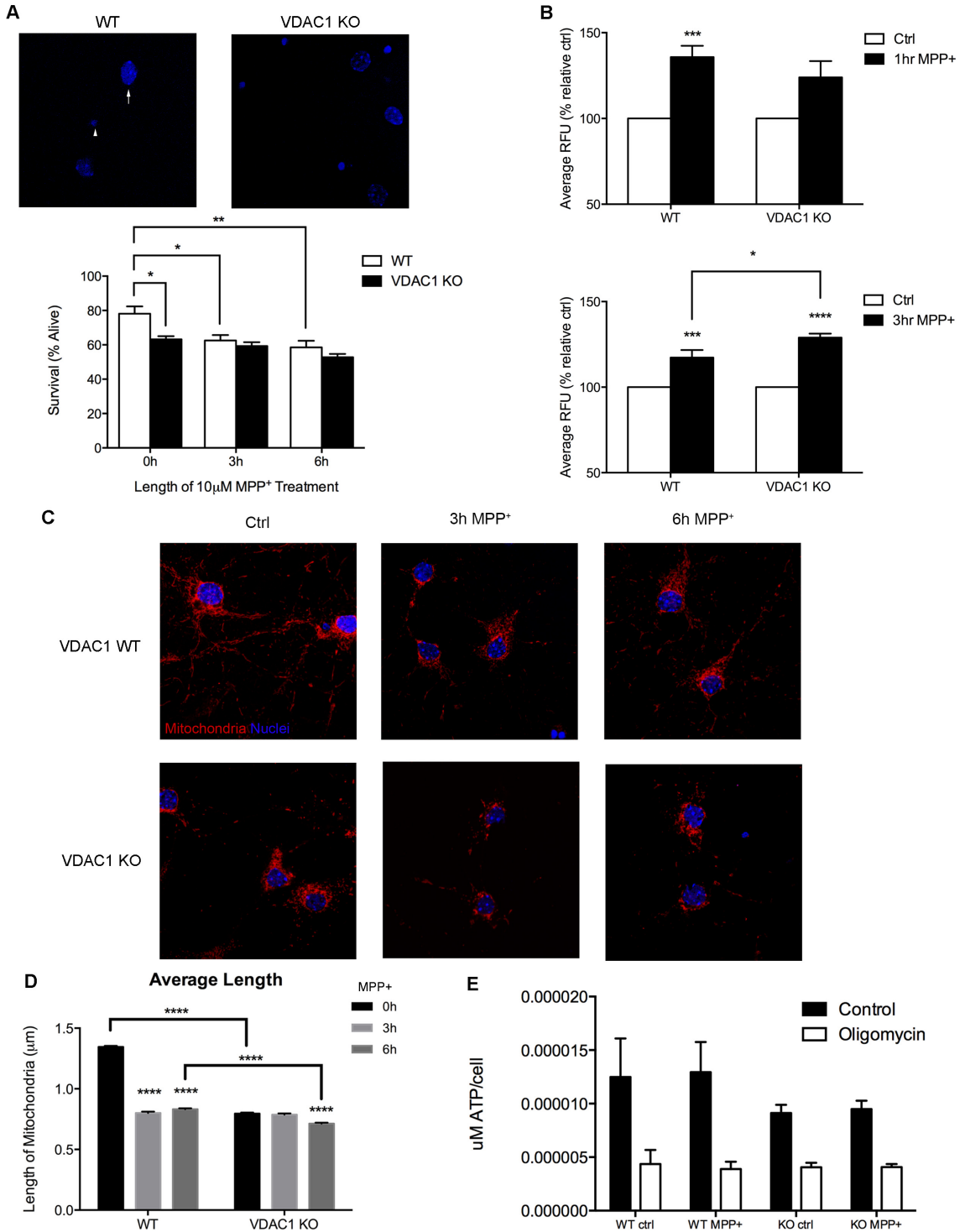
Next we examined mitochondrial length. Healthy mitochondria exist in tubular networks and can undergo fission and fusion. A disruption in the balance between fission and fusion is often indicative of mitochondrial damage (Chen et al., 2006; Detmer and Chan, 2007; Archer, 2013). WT and VDAC1 KO primary cortical neurons were grown *in vitro* for 6 days prior to up to 6h of 10 μ M MPP⁺ in absence of supplemented antioxidants. Samples were fixed and stained for mitochondria (mitochondrial protein Tom20) and nuclei (Hoechst) and analyzed by confocal microscopy. Length was measured using ImageJ software (NIH). With 10 μ M MPP⁺ treatment for 3h, WT mitochondria become more fragmented (Figure 3.2C, D; Figure 3.S2). Basally, VDAC1 KO cortical neurons have shorter mitochondria compared to WT and are further fragmented following 10 μ M MPP⁺ treatment for 6h (Figure 3.2C, D; Figure 3.S2). A shift towards a fragmented pool of mitochondria, as we have observed here, is often indicative of mitochondrial damage (Chen and Chan, 2006; Chen and Chan, 2009; Archer, 2013; Lackner, 2014).

Finally we sought to determine ATP levels, as neurons are highly dependent on mitochondria for ATP production and a decrease would indicate a decrease in

mitochondrial health (Fiskum et al., 2003; Detmer and Chan, 2007; Mattson et al., 2008). Using a luciferase-based assay, we determined ATP levels in VDAC1 WT and KO cortical neurons. Basally, there is less ATP in VDAC1 KO versus WT neurons (Figure 3.2E). Additionally, treatment with the ATP synthase inhibitor oligomycin, which blocks mitochondrial ATP production, decreases ATP levels to similar levels in both VDAC1 WT and KO (Figure 3.2E). This finding suggests that specifically mitochondrial-produced ATP (indicated by the decrease in ATP levels with oligomycin treatment) is decreased in VDAC1 KO neurons. No significant difference was noted in ATP levels following 1h MPP⁺ treatment (Figure 3.2E). VDAC1 deficiency results in decreased mitochondrial-dependent ATP production, which suggests these cortical neurons have dysfunctional mitochondria.

Figure 3.2: VDAC1 deficient cortical neurons have impaired mitochondrial health.

Cortical neurons harvested from WT and VDAC KO E14.5 – E15.5 embryos were cultured 6 days *in vitro* prior to 10 μ M MPP⁺ treatment for 1h, 3h or 6h, in absence of antioxidants. A) Survival was determined by assessment of nuclear integrity, via Hoechst stain. Arrow, live cell; arrowhead, dead cell. Data represent mean \pm SEM (n=3, in quadruplicate). * P <0.05 and ** P <0.01; two-way ANOVA with Tukey post-hoc analysis for WT vs. KO samples. B) Cortical neurons were incubated with the cell permeable CM-H₂DCFDA (10 μ M), to detect ROS production. Data represent mean \pm SEM (n=3-5). * P <0.05, *** P <0.001 and **** P <0.0001; two-way ANOVA with Bonferroni post-hoc analysis. C) Representative confocal images of mitochondria, stained for Tom20, in WT and VDAC1 KO cortical neurons. D) Average length of mitochondria, quantified using ImageJ (NIH). Data represent mean \pm SEM (n=4-5, with minimum 500 mitochondria/n). **** P <0.0001; Two-way ANOVA with Bonferroni post-hoc analysis. E) A luciferase-based assay was used to quantify ATP levels in WT and VDAC1 KO cortical neurons. Oligomycin was used to inhibit mitochondrial-produced ATP. Data represent mean \pm SEM (WT n=2; KO n=4).



VDAC1 KO cortical neurons exhibit reduced basal survival, produce more ROS with prolonged stress and have fragmented mitochondria that produce less ATP. These findings suggest that VDAC1 KO cortical neurons have decreased mitochondrial health, even in absence of an exogenous stressor. However, basally there is more DJ-1 localized to mitochondria - something that has been suggested to be protective in a WT scenario (Canet-Avilés et al., 2004; Junn et al., 2009). These discrepant observations suggest that perhaps DJ-1 is not properly localized to the right mitochondrial compartment critical for survival and regulation of mitochondrial function, in absence of VDAC1. Accordingly we next determined where DJ-1 is localized and how this may be affected with VDAC1 deficiency.

DJ-1 requires VDAC1 for proper sub-mitochondrial localization

While DJ-1 localization to mitochondria has been documented by a number of groups (Canet-Avilés et al., 2004; Junn et al., 2009; Joselin et al., 2012), the function that DJ-1 exerts at mitochondria is still unknown. DJ-1 contains no mitochondrial localization signal and the mechanism by which it localizes to mitochondria is also not well understood. As such, the site DJ-1 resides within mitochondria is not agreed upon, with different groups claiming OMM, IMM and/or matrix (Canet-Avilés et al., 2004; Li et al., 2005; Zhang et al., 2005; Hayashi et al., 2009). In order to better understand the potential function of DJ-1 at mitochondria, we wanted to clarify its sub-mitochondrial localization.

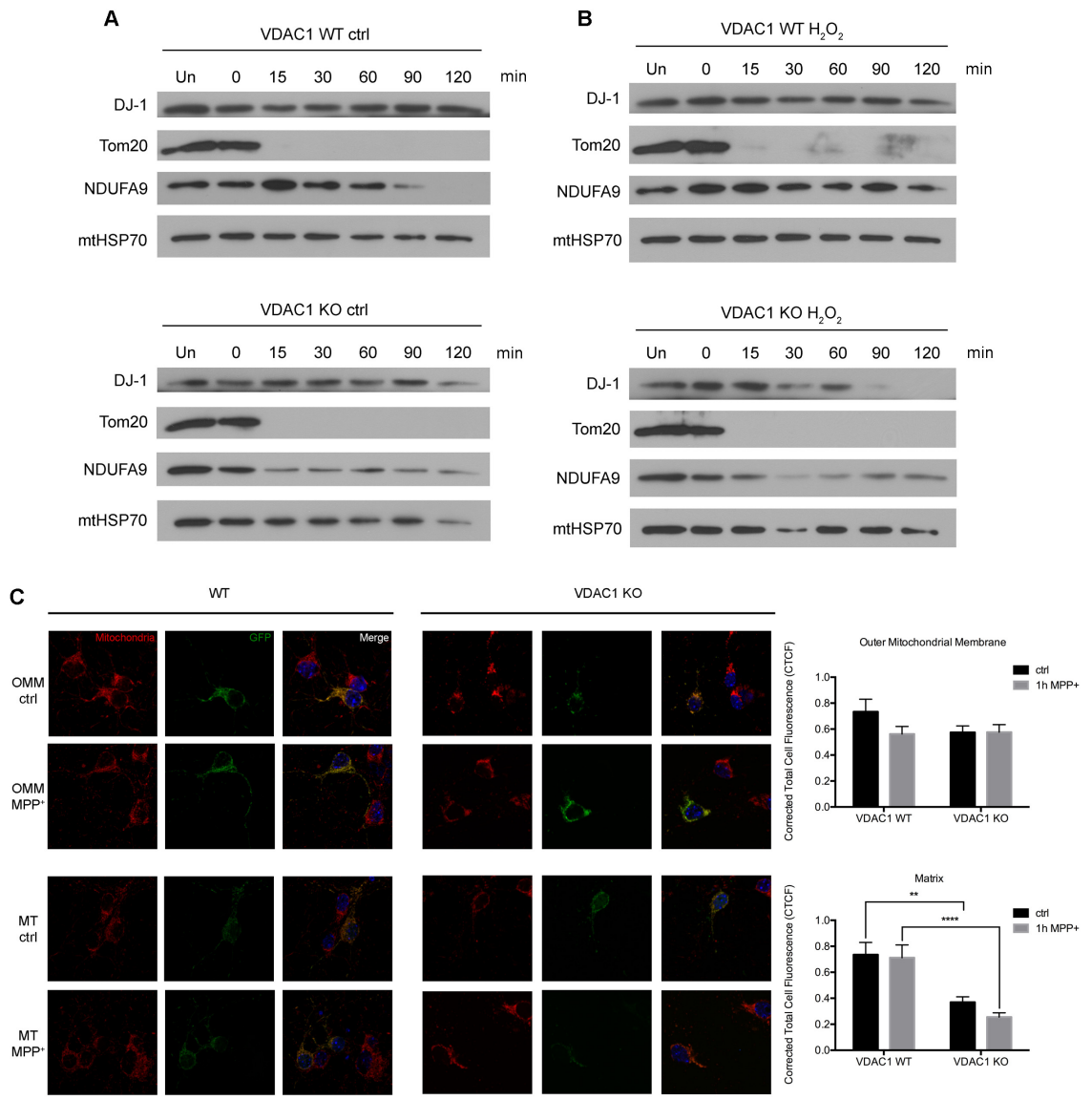
To assess sub-mitochondrial localization of DJ-1, we subjected mitochondrial enriched fractions to proteolytic digestion by trypsin for up to 120min. Proteins localized

at the OMM will be subjected to digestion first, and over time more internally localized proteins are exposed and able to be digested. WT MEFs have mitochondrial DJ-1 that is highly resistant to proteolytic digestion, both in control and H₂O₂-treated conditions (Figure 3.3A). The degree to which DJ-1 is digested is similar to the digestion of matrix marker mtHSP70, which suggests that DJ-1 largely resides in the matrix. VDAC1 KO MEFs appear to have a similar localization for DJ-1 in control conditions, however with H₂O₂ treatment DJ-1 is much more readily digested (Figure 3.3B). This finding suggests that during oxidative stress, in absence of VDAC1, DJ-1 is not localized to the matrix. As a control, to confirm that our proteins of interest can be degraded by proteolysis, we subjected mitochondrial enriched fractions to identical proteolytic digestion in the presence of Triton X-100, which allows for equal digestion regardless of location within mitochondria (Figure 3.S3). All proteins of interest are readily digested by trypsin. In MEFs, VDAC1 is important for sub-mitochondrial localization of DJ-1 during oxidative stress.

To further confirm the changes in DJ-1 sub-mitochondrial localization in cortical neurons, we utilized a recently devised system with bi-fluorescent complementation. In this system, complementation of GFP can occur when DJ-1 is localized either at the OMM or the matrix, depending on the plasmid employed. We analyzed the relative level of GFP fluorescence, and thus level of DJ-1 at either the OMM or matrix, compared to mitochondrial content. WT and VDAC1 KO primary cortical neurons were cultured *in vitro* for 4 days prior to transfection with either WT-DJ1-S11 and OMM-GFP1-10 or WT DJ-1 and matrix-GFP1-10. At 24h post-transfection, cortical neurons were treated with 10 μ M MPP⁺ for 3h in absence of antioxidants. Both control and 10 μ M MPP⁺ treated

VDAC1 WT cortical neurons exhibit strong, and similar levels of both OMM and matrix DJ-1 (Figure 3.3C). While we do not observe a change in either OMM or matrix DJ-1 levels following treatment in WT cortical neurons, this may be due to the over-expression system utilized. Notably, control VDAC1 KO cortical neurons have reduced matrix DJ-1, and this level is further decreased following 10 μ M MPP⁺ treatment (Figure 3.3C).

Figure 3.3: Sub-mitochondrial DJ-1 is altered with VDAC1 deficiency. During oxidative stress, DJ-1 is localized more superficially within mitochondria deficient for VDAC1. Either control (A) or 3h 100 μ M H₂O₂-treated (B) WT and VDAC1 KO MEFs were subjected to trypsin digestion for up to 120min and subsequently analyzed by Western blot to assess degradation of mitochondrial components. Tom20 was used to identify outer mitochondrial membrane (OMM), NDUFA9 was used to identify inner mitochondrial membrane (IMM) and mtHSP70 was used to identify matrix. Blots are representative of n=3. C) Cortical neurons harvested from WT and VDAC KO E14.5 – E15.5 embryos were cultured 4 days *in vitro* prior to transfection. On DIV 5, neurons were treated with 10 μ M MPP⁺ treatment for 3h, in absence of antioxidants. Representative confocal images with mitochondrial (Tom20, red), nuclei (Hoechst, blue) GFP signal. Quantification of corrected total cell fluorescence (as a % of WT ctrl) for ctrl and 10 μ M MPP⁺ treatment. Data represent mean \pm SEM (n=4). ** P <0.01 and **** P <0.0001; two-way ANOVA with Tukey's post-hoc analysis.



Both VDAC1 KO MEFs and cortical neurons have reduced matrix-localized DJ-1 compared to WT cells. This suggests that VDAC1 is important in proper sub-mitochondrial localization of DJ-1. Improper localization of DJ-1 could result in the mitochondrial dysfunction observed in the VDAC1 null cortical neurons.

Mitochondrial DJ-1 is responsive to decreased ATP levels

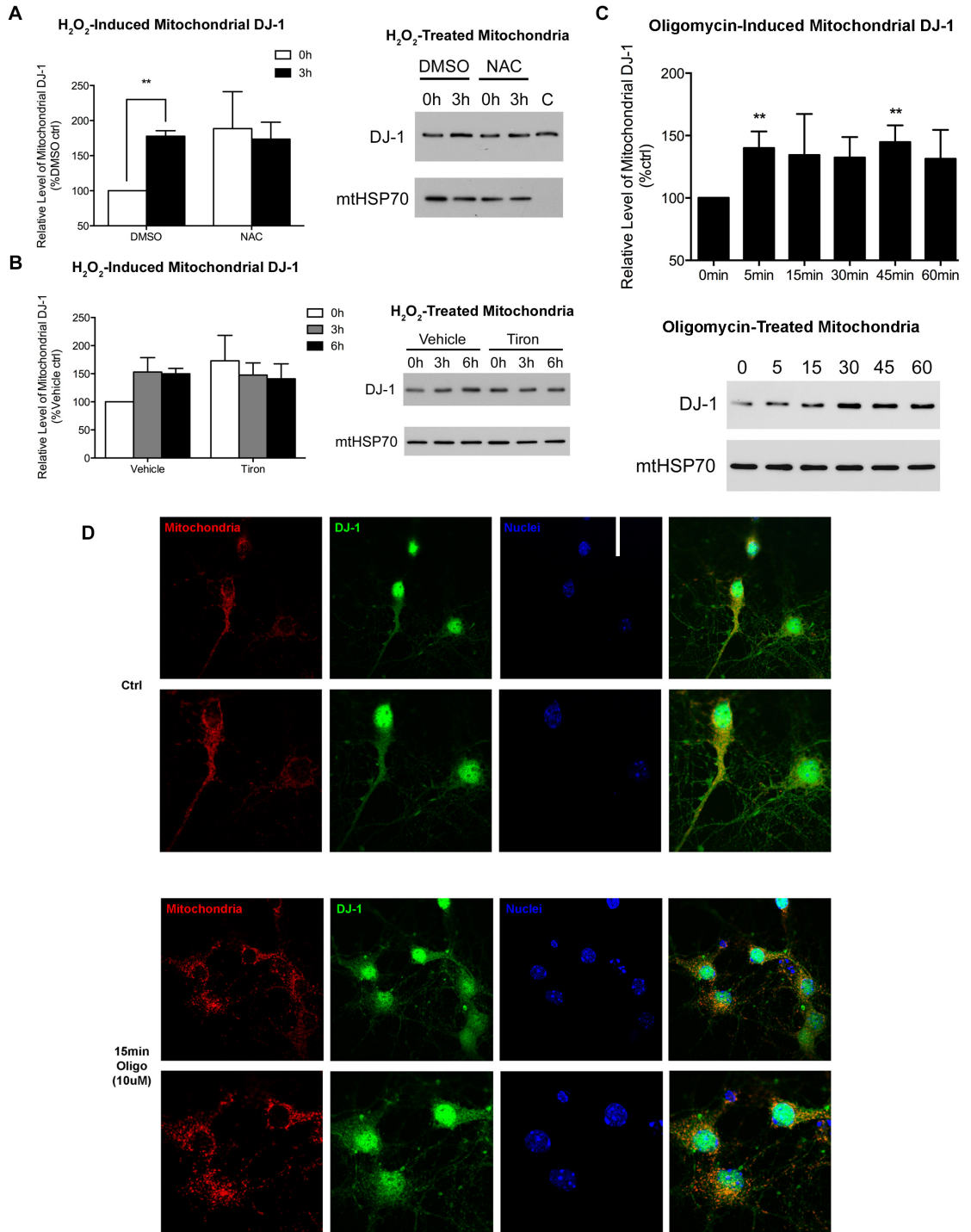
Our previous work demonstrated that various stressors could cause increased localization of DJ-1 to mitochondria (Joselin et al., 2012). We sought to determine the nature of the signal that regulates this response.

While we previously showed that oxidative stressors could increase levels of mitochondrial DJ-1 (Joselin et al., 2012), we did not determine if ROS was directly the signal causing this translocation. To investigate if ROS is indeed the signal, we used two antioxidants, N-acetyl-cysteine (NAC) and Tiron to block ROS. WT primary cortical neurons from E14.5-15.5 embryos were cultured *in vitro* for 6 days prior to treatment. First we decreased ROS by pre-treating WT primary cortical neurons with NAC for 2h prior to treatment with 30 μ M H₂O₂ for up to 3h. Mitochondrial enriched samples were obtained as mentioned above and subjected to Western blot analysis. Treatment with NAC alone increases mitochondrial DJ-1 (Figure 3.4A). However no further increase is observed following H₂O₂ treatment (Figure 3.4A). Pre-treatment of WT cortical neurons with the anti-oxidant Tiron also basally increases mitochondrial DJ-1 with no significant increase following H₂O₂ treatment (Figure 3.4B). Therefore, while blocking ROS prevents stress-induced increase in mitochondrial DJ-1, it also basally increases

mitochondrial DJ-1 levels. This indicates that mitochondrial DJ-1 regulation by ROS, similar to VDAC1, is complex.

Neurons are highly reliant on mitochondria for ATP production (Chen and Chan, 2006). Interestingly we noted decreased ATP levels in VDAC1 null cortical neurons as well as increased mitochondrial DJ-1 levels. The signal for DJ-1 translocation to mitochondria is still present in absence of VDAC1, and perhaps even heightened. We were curious as to the role of DJ-1 and ATP and therefore investigated if ATP could serve as a signal for DJ-1 translocation to mitochondria. WT primary cortical neurons from E14.5-15.5 embryos were cultured *in vitro* for 6 days prior to treatment in absence of antioxidants. WT cortical neurons were treated with 10 μ M oligomycin, an ATP synthase inhibitor, for up to 60min and subjected to subcellular fractionation and Western blot analysis (Figure 3.4C). Within 5min of ATP synthase inhibition, we observe a significant increase in mitochondrial DJ-1 that is maintained with up to 60min of treatment (Figure 3.4C). We also confirmed this localization by immunofluorescence of endogenous DJ-1 in cortical neurons (Figure 3.4D). Our results demonstrate that inhibition of ATP is a strong driver of mitochondrial localization of DJ-1.

Figure 3.4: Reduced ATP levels induce translocation of DJ-1 to mitochondria. Pre-treatment of wild-type (WT) cortical neurons harvested from E14.5-15.5 embryos with the antioxidant NAC (A) or Tiron (B) prior to 3h or 6h 30 μ M H₂O₂ treatment. Mitochondrial enriched fractions were obtained through subcellular fractionation and were analyzed by Western blot for DJ-1 and mitochondrial loading control (mtHSP70). Quantification of densitometry using Image J software (NIH). Data represent mean \pm SEM (n=2). C, cytoplasm. C) WT cortical neurons were treated with 10 μ M oligomycin for indicated time points in absence of antioxidants. Data represent mean \pm SEM (n=5-6). * P <0.01; t -test for related samples. D) Representative confocal images of oligomycin treated cortical neurons, stained for mitochondria (COXI), endogenous DJ-1 and nuclei (Hoechst); n=2.



Discussion

Previous studies by our group and others have reported a role for DJ-1 in mitochondrial health as well as stress-induced localization of DJ-1 to mitochondria to promote survival (Canet-Avilés et al., 2004; Junn et al., 2009; Irrcher et al., 2010; Krebiehl et al., 2010; Joselin et al., 2012). To better understand what regulates translocation of DJ-1 mitochondria, we investigated the potential interaction between DJ-1 and the mitochondrial protein VDAC1, as identified by an interactor screen.

In this regard, we provide evidence that overexpressed and endogenous DJ-1 interact with endogenous VDAC1. We also show that VDAC1 is important in regulating DJ-1 translocation, as stress-induced translocation of DJ-1 to mitochondria is impaired with VDAC1 deficiency in both MEFs and primary cortical neurons. Interestingly, VDAC1 KO cortical neurons have basally increased levels of mitochondrial DJ-1. As mitochondrial DJ-1 has previously been shown to have a protective effect (Junn et al., 2009), we questioned if perhaps VDAC1 deficiency has a negative impact on mitochondrial health.

Dysfunctional mitochondria produce more ROS and less ATP, two factors which can negatively impact neuronal survival (Esposito et al., 1999; Abou-Sleiman et al., 2006; Chen and Chan, 2006; Lin and Beal, 2006; Chinta and Andersen, 2008). Additionally, disruption in mitochondrial dynamics has been implicated in mitochondrial dysfunction and disease (Chen and Chan, 2006; Detmer and Chan, 2007; Archer, 2013). We demonstrate that in fact, VDAC1 deficient cortical neurons do have indices of mitochondrial stress including reduced ATP and fragmentation. We also observe decreased cell survival in the VDAC1 KO cortical neurons. We do note that MPP⁺

treatment does not cause further cell death in the VDAC1 KO cortical neurons. Most likely, these cortical neurons are able to compensate and prevent further cell death, perhaps via VDAC2 or VDAC3. Examination of cell survival following longer treatment may show additional sensitization. VDAC1 deficiency results in cortical neurons that produce more ROS with extended stress. It appears as though, again, there is some compensation mechanism with short-term stress however VDAC1 deficient cortical neurons fail to compensate with longer MPP⁺ treatment. Additionally, VDAC1 null mitochondria are more fragmented and resemble WT mitochondria that have been treated with MPP⁺. Interestingly, this shift towards a fragmented phenotype was also observed with DJ-1 KO cells (Irrcher et al., 2010). There are several commonalities between VDAC1 and DJ-1 deficiency, which suggests one factor may rely on the other for proper function. What is intriguing with our results is that there is also increased mitochondrial DJ-1 in these cortical neurons. Mitochondrial-targeted DJ-1 has been shown to be protective and to drive ATP synthesis (Junn et al., 2009; Cali et al., 2014). However we show both increased mitochondrial DJ-1 and decreased ATP production in absence of VDAC1, at least in neurons. What is the explanation for this discrepancy?

We proposed that perhaps DJ-1 localization to its appropriate mitochondrial compartment might be altered with loss of VDAC1. Various studies have claimed that DJ-1 resides at the OMM, IMM and/or matrix (Canet-Avilés et al., 2004; Li et al., 2005; Zhang et al., 2005; Hayashi et al., 2009). In our hands, in WT MEFs, we show endogenous DJ-1 to reside within mitochondria, most likely at the matrix. However, with VDAC1 deficiency the level of DJ-1 in the mitochondrial matrix is dramatically reduced following oxidative stress. Consistent with the results in MEFs we also see similar results

in neurons for matrix-specific localization of DJ-1. In primary cortical neurons, we note both OMM and matrix localization of exogenously expressed DJ-1 in a GFP complementation assay. In contrast, VDAC1 deficient cortical neurons have substantially less matrix-localized DJ-1 as observed by decreased GFP complementation. Interestingly, at least with the conditions tested in this assay in neurons, we did not observe increased mitochondrial DJ-1 as we have previously shown. This difference is likely due to the differing in conditions of stress and cell type employed as well as the expressed nature of DJ-1 required for this assay.

These findings suggest a two-step model by which DJ-1 goes to mitochondria. In the first, an unknown step regulates OMM mitochondrial localization. This signal would likely be a response to stress, and drives DJ-1 localization to the OMM. One potential signal for this step may be a reduction in ATP levels (see below). It is important to note that this step is likely not simply reliant on ROS since ROS inhibition actually induces localization of DJ-1 to mitochondria. However, ROS itself is known to be involved in critical intracellular signalling (Sena and Chandel, 2012). Thus inhibition of ROS could increase stress in the cell. In the second step, DJ-1 translocates to the matrix, a process that is dependent upon VDAC1. Taken together, we suggest that in absence of VDAC1, DJ-1 is unable to localize to the matrix. Consequently, VDAC1 deficient cortical neurons have mitochondrial defects, which may explain its reduced viability.

In our two-step model of DJ-1 translocation to mitochondria, what might be the function of matrix-localized DJ-1? Previous work has demonstrated that matrix-targeted DJ-1 promotes ATP production by mitochondria (Cali et al., 2014). This work suggests that a drop in ATP production, such as with exogenous oxidative stress or MPP^+

treatment may signal DJ-1 to enter the matrix to compensate for loss of ATP. Consistent with this, we demonstrate that inhibition of ATP production by oligomycin is a strong driver of DJ-1 translocation to mitochondria. Additionally, if matrix-DJ-1 is important in ATP production, then our observation of decreased mitochondrial-produced ATP in VDAC1 KO cortical neurons fits this model. In summary, we propose that DJ-1 must localize to the matrix of mitochondria in a VDAC1-dependent manner to regulate ATP levels and perhaps to promote survival during stress. Future work will investigate aspects of this model.

Methods and Materials

Animals

The generation and genotype of DJ-1 and VDAC1 mice has been described previously (Wu et al., 1999; Weeber et al., 2002; Kim et al., 2005a). All procedures involving animals were approved by the University of Ottawa Animal Care Committee and were maintained in strict accordance to the Guidelines for the Use and Treatment of Animals put forth by the Animal Care Council of Canada and endorsed by the Canadian Institute of Health Research.

Cell culture

Mouse embryonic fibroblasts (MEFs) were derived from E14.5-15.5 transgenic DJ-1 (C57BL/6) mice and immortalized as previously described (Aleyasin et al., 2010).

VDAC1 WT and KO MEFs were a generous gift from Dr. William Craigen and were immortalized by natural selection of cells that persist beyond typical senescence. All MEFs were maintained in Dulbecco's Modified Eagle Media (DMEM) (Sigma) supplemented with 10% fetal bovine serum (FBS) (Sigma) and antibiotic/antimycotic (Sigma). All MEFs were immortalized as previously described (Aleyasin et al., 2010).

Cortical neurons were derived from E14.5-15.5 wildtype (WT) CD1 mice or VDAC1 transgenic mice (Charles River Laboratories) of either sex and maintained in Neurobasal media (Invitrogen) supplemented with B27 with antioxidants (Gibco), N2 (Gibco), 0.5 mM L-glutamine (Sigma), and penicillin/ streptomycin (Gibco) as previously reported (Kim et al., 2005a). Neurons were plated onto poly-D-lysine coated plates as follows: 5×10^6 cells per 10cm plate for mitochondrial fractionation; 100,000 per well of 24-well plate for survival, or mitochondrial length; 200,000 per well of 24-well plate for GFP-

complementation assay; 500,000 per well of 12-well plate for ROS assay; and 2×10^6 per well of 6-well plate for ATP assay.

Mitochondrial enriched fractions

Both VDAC1 WT and KO MEFs were treated for up to 3h with $100 \mu\text{M H}_2\text{O}_2$ and then subjected to fractionation via differential centrifugation as previously described (Joselin et al., 2012). Similarly, VDAC1 KO cortical neurons harvested from E14.5-15.5 mouse embryos were grown in culture for 5 days in the presence of antioxidants. On DIV5, cultures received new media containing no antioxidants. On DIV6, cultures were treated with either $10 \mu\text{M MPP}^+$ for up to 24h or $10 \mu\text{M oligomycin}$ for up to 1h and then subjected to fractionation via differential centrifugation.

Trypsin digestion

VDAC1 WT and KO MEFs were treated with $100 \mu\text{M H}_2\text{O}_2$ for 3hr and subjected to a modified subcellular fractionation. Specifically, isolation buffer consisted of 200mM mannitol, 70mM sucrose, 10mM HEPES, and 1mM EGTA with pH 7.5 and no protease inhibitors were added. The mitochondrial-enriched fractions were digested with $25 \mu\text{g/mL}$ trypsin (Sigma) for up to 120min. To stop the digestion, $50 \mu\text{g/mL}$ of AEBSF (Fisher) was added to the reaction. This non-specific proteolysis of mitochondria will cause a progressive loss of mitochondrial proteins, starting with OMM proteins and moving in to the matrix. To ensure that our proteins of interest can be degraded by proteolysis, we subjected mitochondria to identical digestion with trypsin in the presence of Triton X-100, which allows for equal digestion regardless of location within mitochondria.

Co-immunoprecipitation

GST immunoprecipitation was performed in human embryonic kidney (HEK) 293 cell

line. GST-DJ1 or GST alone was transiently transfected using Lipofectamine 2000 (Invitrogen) and cells were lysed 24-36hr later in lysis buffer (50 mM Tris HCl pH7.5, 100 mM NaCl, 1 mM EDTA, 1 mM DTT, 0.2% NP-40 and protease inhibitor). Lysate was incubated with 40 μ L of glutathione sepharose (GE Healthcare) for 4h. Samples were washed 3 times with lysis buffer. Bound proteins were eluted by boiling samples in 2X SDS-loading buffer and analyzed by Western blot.

Endogenous immunoprecipitation of DJ-1 was performed in mitochondrial-enriched fractions from either VDAC1 WT and VDAC1 KO MEFs or DJ-1 WT and DJ-1 KO MEFs. Mitochondrial-enriched fractions were resuspended in isolation buffer and pre-cleared with TrueBlot rabbit IgG beads for 6h. Cleared lysate was incubated with 5 μ g of DJ-1 antibody (Abcam) or normal rabbit IgG (Santa Cruz) overnight. Samples were washed 5 times with isolation buffer and eluted by boiling in 2X SDS-loading buffer.

Western blot

Protein quantification was performed using Bradford (Bio-Rad) method. Samples were electrophoresed on 12% sodium dodecyl sulfate polyacrylamide gels and transferred to polyvinylidene fluoride (PVDF) membranes (Millipore). Membranes were probed with the respective primary antibodies followed by horseradish peroxidase-conjugated secondary antibodies and developed with the Immobilon Western Chemiluminescent HRP Substrate (Millipore). Densitometry analysis was carried out using ImageJ (NIH). For mitochondrial-enriched samples 10 μ g of each sample was analyzed. For mitochondrial digestion samples, equal volumes of sample were assessed. Primary antibodies included: for the OMM - Tom20 (Santa Cruz, rabbit, 1:2000); for the IMM - ATP β (Abcam, mouse, 1:1000) or NDUFA9 (Abcam, mouse, 1:2000); for the matrix and

loading control - mtHSP70 (Abcam, mouse, 1:2000); VDAC1 (Calbiochem, rabbit, 1:2000); DJ-1 (Abcam, rabbit, 1:20,000); GST (Abcam, rabbit, 1:2000).

Immunofluorescence

Following treatment, neurons were fixed in 4% formalin in growth media at room temperature for 30min. The cells were permeabilized and blocked simultaneously using 0.1% Triton X-100 and 5% normal goat serum for 1hr at room temperature. Incubation with the respective primary antibodies (DJ-1, Abcam, 1:500; Tom20, Santa Cruz, 1:500; COXI, MitoSciences, 1:300) was performed overnight at 4°C. Samples were subsequently washed in 5% normal goat serum and stained with the corresponding secondary antibodies (1:500). Following 3 washes in PBS, samples were stained with Hoechst, mounted and analyzed by confocal microscopy.

Survival assay

Following 10 μ M MPP⁺ treatment, cortical neurons were fixed in 4% formalin in growth media at room temperature for 30min. Subsequently they were stained with Hoechst and amount of apoptotic nuclei was analyzed by fluorescence microscopy.

ROS assay

The cell-permeable fluorogenic probe 5-(and-6)-chloromethyl-2', 7'-dichlorodihydrofluorescein diacetate (CM-H2DCFDA) is oxidized rapidly by ROS to a fluorescent compound. This probe is considered a general indicator for level of oxidative stress in the cell (Halliwell and Whiteman, 2004). Prior to treatment, cortical neurons were loaded with 10 μ M CM-H2DCFDA (Invitrogen) for 10min. Cortical neurons were subsequently washed with PBS and then placed in unsupplemented, dye-free Neurobasal media (Invitrogen). Following 10 μ M MPP⁺ treatment, fluorescence was determined using

a plate reader (excitation 485; emission 530) over 15min. Data is averaged and presented as % treatment versus control.

Mitochondrial length

Mitochondrial length was assessed using ImageJ (NIH) as previously described (Irrcher et al., 2010). Briefly, length of mitochondria stained for Tom20 was measured in VDAC1 WT and KO cortical neurons for control and 10 μ M MPP⁺ treated conditions. Lengths were either averaged or binned accordingly. A minimum of 500 mitochondria were counted per sample size (n).

ATP assay

The CellTiter Glo Luminescent (Promega) assay relies on level of ATP in the cell to produce luminescence and has been previously described to assess cellular ATP levels (Khacho et al., 2014). Following 10 μ M MPP⁺ treatment, cortical neurons were harvested by gentle trypsinization using TrypLE reagent (Invitrogen). Each sample was divided into 6 wells of an opaque 96-well plate, of which 3 wells were incubated with 10 μ M oligomycin for 1h to inhibit mitochondrial-produced ATP. An aliquot of each sample was used to determine cell number using a hemocytometer. Luminescence was recorded using a plate reader. A range of standard ATP concentrations was used to determine ATP concentrations in samples. Data is presented as μ M of ATP, corrected for cell number.

GFP complementation system

A bi-fluorescent complementation system has been developed to examine sub-mitochondrial localization of DJ-1 (Cali et al., 2014). Specifically, one part of GFP is fused with DJ-1 and the complementing part of GFP is targeted to either the OMM or matrix. As such, GFP fluorescence occurs only when both parts of GFP are in the same

area, that is, if DJ-1 localizes to the OMM in the presence of OMM-GFP. At DIV4, we transfected primary cortical neurons with WT-DJ1-S11 and OMM-GFP1-10 (targeted to outer mitochondrial membrane) or mt-GFP1-10 (targeted to matrix) using Lipofectamine 3000 (Invitrogen). Following 24hr, media was changed to NB without AO and neurons were treated with 10 μ M MPP⁺ for 3h and then fixed. Samples were stained with COXI to label mitochondria. We analyzed the relative level of GFP to mitochondrial fluorescence.

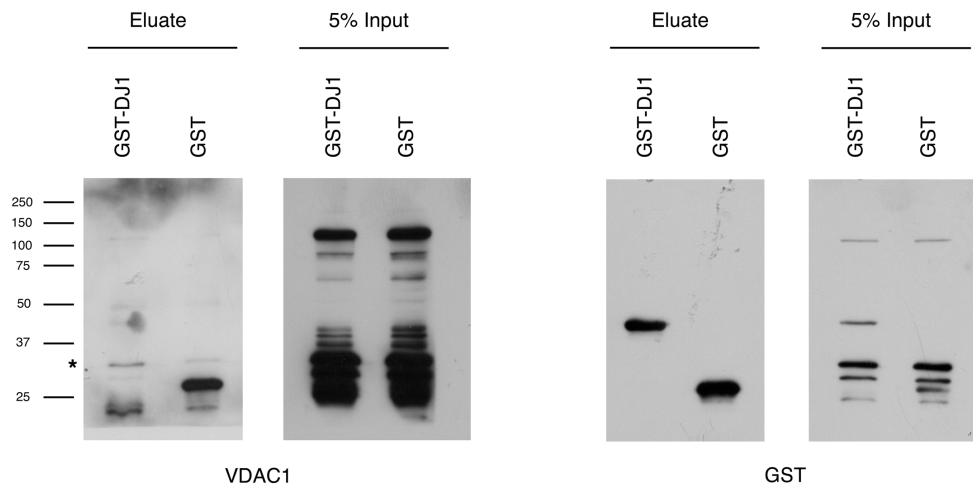
Statistical analysis

Statistical significance was determined using two-tailed Student's *t*-test for related samples or two-way ANOVA (with either Tukey's or Bonferroni post-hoc analysis) when comparing WT versus KO conditions. All data are presented as mean \pm standard error of the mean (SEM). Significance at $P < 0.05$ (*), $P < 0.01$ (**), $P < 0.001$ (***) and $P < 0.0001$ (****).

Supplementary Information

Figure 3.S1. DJ-1 interaction with VDAC1. A) GST-DJ1 but not GST alone interacts with endogenous VDAC1 in HEK293 cells, as observed by GST co-immunoprecipitation studies. Samples were analyzed by Western blot and probed for DJ-1 and GST. This is representative of two experiments. * denotes VDAC1 specific band. B) Endogenous DJ-1 interacts with endogenous VDAC1 in mitochondrial enriched fractions from VDAC1 WT MEFs. VDAC1 KO MEFs are used as a negative control. Samples were analyzed by Western blot and probed for DJ-1 and VDAC1. This is representative of three experiments.

A



B

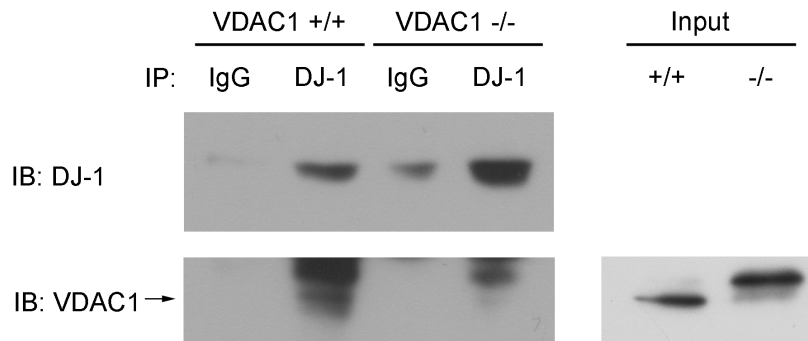


Figure 3.S2. Mitochondria in VDAC1 KO cortical neurons are basally fragmented compared to WT mitochondria. Cortical neurons harvested from WT and VDAC1 KO E14.5-15.5 embryos were cultured for 6 days *in vitro* prior to 10 μ M MPP⁺ for 3h or 6h, in absence of antioxidants. Mitochondrial length was calculated using Image J (NIH). Length was binned accordingly. Data represent mean \pm SEM (n=4-5), minimum 500 mitochondria/n. ** P <0.01, *** P <0.001 and **** P <0.0001; two-way ANOVA with Bonferroni post-doc analysis.

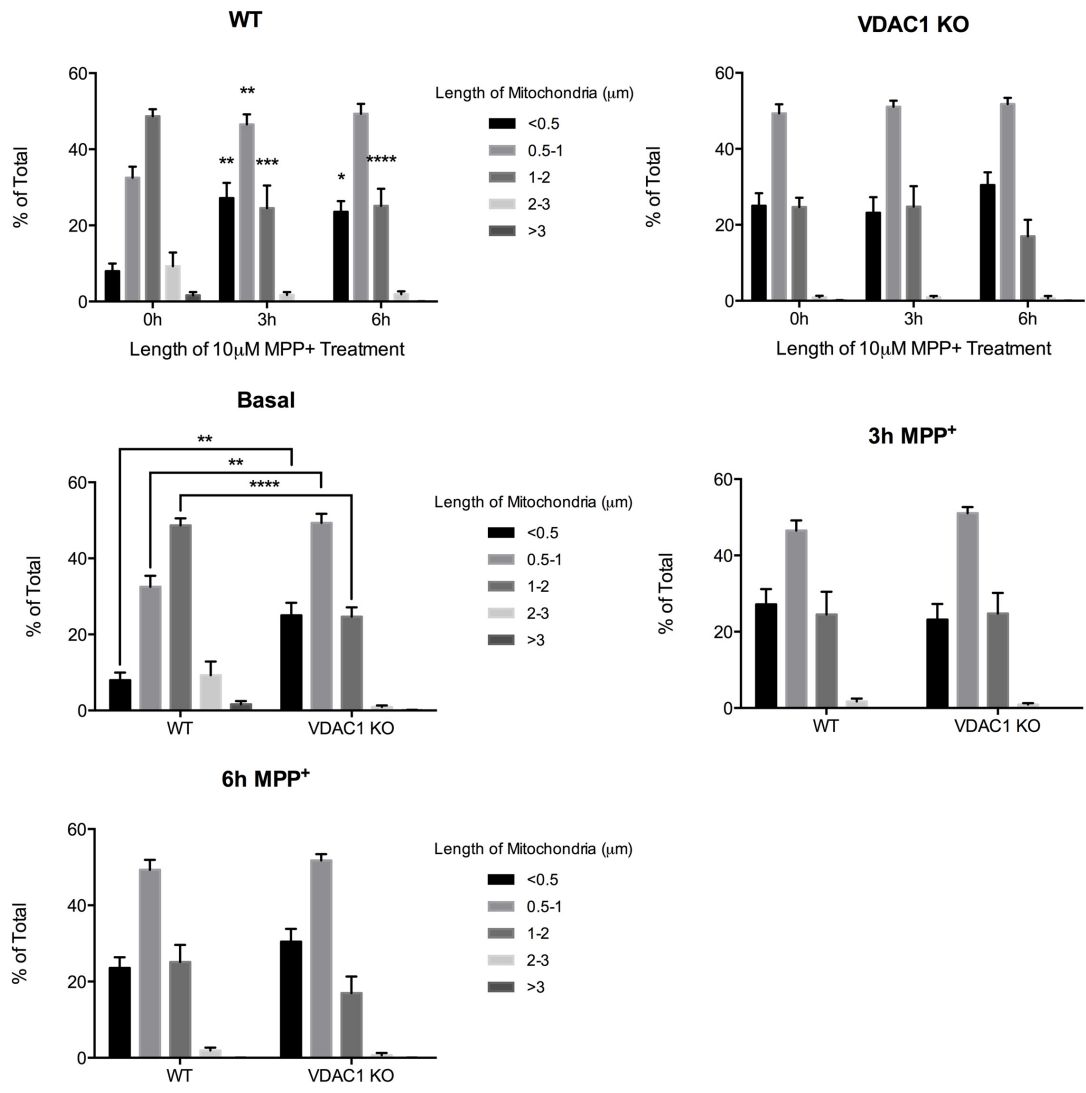
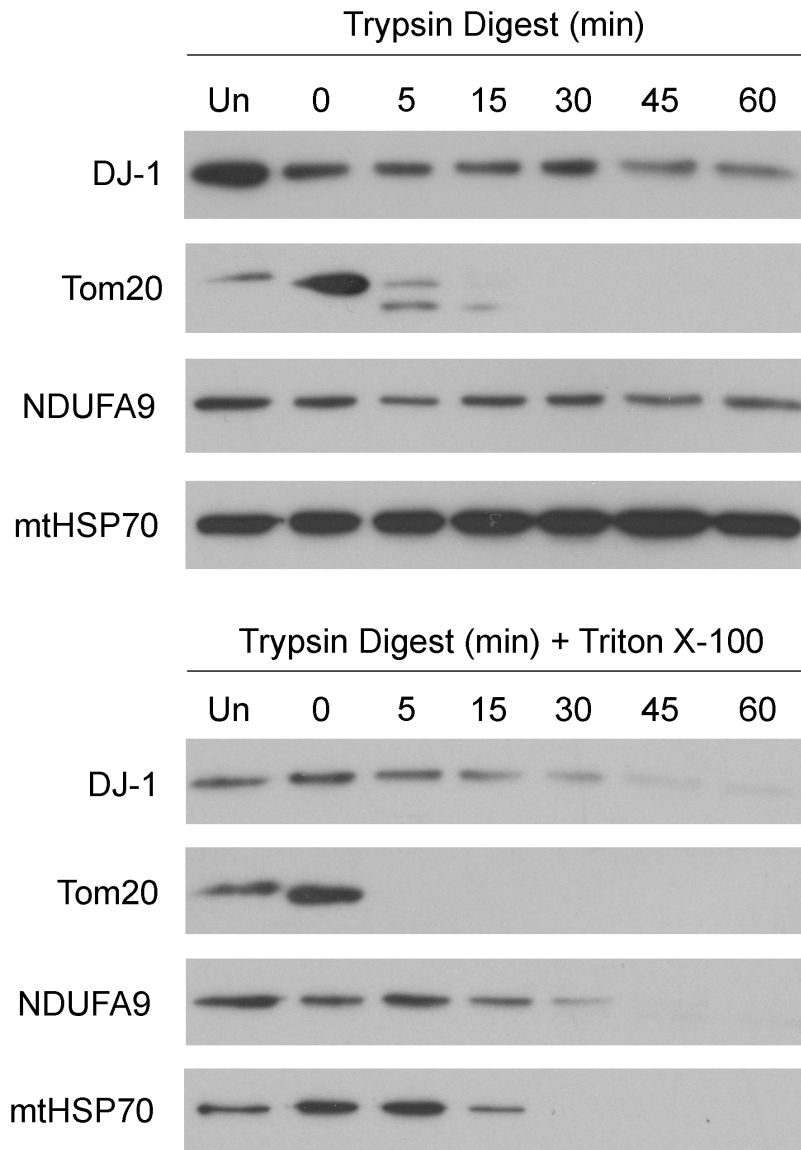


Figure 3.S3. DJ-1 is localized to matrix and is not resistant to proteolytic digestion.

WT MEFs were subjected to trypsin digestion for up to 60min and subsequently analyzed by Western blot to assess degradation of mitochondrial components (top). Addition of Triton X-100 to samples prior to digestion allows for equal digestion to all proteins, regardless of localization (bottom). Tom20 was used to identify outer mitochondrial membrane (OMM), NDUFA9 was used to identify inner mitochondrial membrane (IMM) and mtHSP70 was used to identify matrix. This is representative of three experiments.



CHAPTER 4

General Discussion

Parkinson's disease (PD) is the most common movement disorder and second most common neurodegenerative disease. With 90% of cases having unknown origin, it is difficult to discern the mechanism by which the degeneration occurs. There are numerous studies that suggest protein aggregation, inflammation, oxidative stress and mitochondrial dysfunction being involved in PD pathogenesis (Okazaki et al., 1961; Davis et al., 1979; McGeer et al., 1988; Dexter et al., 1989; Schapira et al., 1989; Hoozemans et al., 2007; Lira et al., 2011). Unfortunately many of the findings come from post-mortem analysis, in which cause versus consequence of the disease process cannot be determined.

With the discovery of genetic causes to PD, we can much more readily explore possible pathways involved in the pathogenesis of the disease. Loss-of-function mutations of one such gene, *DJ-1*, cause early-onset PD (Abou-Sleiman et al., 2003; Bonifati et al., 2003; Clark et al., 2004; Hering et al., 2004; Annesi et al., 2005). We and others have previously shown the pro-survival role of DJ-1 during stress and its involvement in mitochondrial health (Canet-Avilés et al., 2004; Kim et al., 2005a; Andres-Mateos et al., 2007; Junn et al., 2009; Irrcher et al., 2010; Krebiehl et al., 2010). Further understanding of the regulation of mitochondrial-localized DJ-1 is the subject of this dissertation.

Endogenous DJ-1 translocation to mitochondria

Numerous studies have examined mitochondrial localization of DJ-1 following induction of stress (Canet-Avilés et al., 2004; Blackinton et al., 2005; Junn et al., 2009). However, none of these studies have been conducted in primary neurons. Additionally,

some groups have examined the effects/consequences of exogenously expressed DJ-1, which may not be representative of endogenous mechanisms. Here we show for the first time that endogenous DJ-1 translocates to mitochondria in primary cortical neurons, using various stressors such as H₂O₂, MPP⁺ and CCCP. We also investigated the importance of the PD genes *Parkin* and *Pink1* in translocation of DJ-1 to mitochondria. We demonstrate that in both *Parkin* KO MEFs and cortical neurons, this translocation does not occur. Interestingly, in absence of DJ-1, *Parkin* translocation to mitochondria is enhanced. It is also interesting to note that the mitochondria membrane uncoupler, CCCP, which induces *Parkin* translocation to mitochondria, also induces DJ-1 translocation to mitochondria. Further investigation into the role of *Parkin* in DJ-1 translocation to mitochondria would provide additional insight into the regulation of mitochondrial DJ-1. As *Parkin* is an E3 ubiquitin ligase (Imai et al., 2000), the impact of this function on mitochondrial DJ-1 could be determined as well as whether it is cytosolic or mitochondrial localized *Parkin* that is important. We also found that no stress-induced increase in mitochondrial DJ-1 was observed with *Pink1* deficiency in MEFs or cortical neurons. Notably, basal level of mitochondrial DJ-1 was increased in both cell types. While this could indicate that the amount of DJ-1 at mitochondria is saturated, it could also suggest that *Pink1* is important in the stress-induced localization of DJ-1. Further inquiry into the importance of *Pink1* and its kinase activity into DJ-1 translocation to mitochondria will give further insights into this pathway. Intriguingly, loss of either *Parkin* or *Pink1* causes mitochondrial defects (Palacino et al., 2004; Wood-Kaczmar et al., 2008). *Parkin* null mice have decreased ETC complexes, decreased respiratory capacity and increased oxidative stress (Palacino et al., 2004). *Pink1* deficiency decreases

survival, alters mitochondrial morphology and increases ROS production in a human dopaminergic neuron model (Wood-Kaczmar et al., 2008). As stress-induced DJ-1 translocation is absent with loss of either Parkin or Pink1, it would be interesting to investigate the importance of mitochondrial DJ-1 in regards to these noted defects. Additionally both Parkin and Pink1 are involved in mitochondrial quality control (MQC) (Narendra et al., 2008; Geisler et al., 2010). While not directly involved in this process itself, DJ-1 appears to require both Parkin/Pink1 for proper mitochondrial localization during oxidative stress. The interplay between these PD genes gives us better insight into the complexity in familial PD and the importance of mitochondrial health. We suggest that mitochondrial health is regulated by at least two pathways that act in parallel. First, there is the classic mechanism by which Parkin is recruited to damaged mitochondria that are then cleared by mitophagy. Second, there is a pathway by which Parkin and Pink1 regulate stress-induced increase in mitochondrial DJ-1. These two pathways, involving DJ-1, Parkin and Pink1, help maintain mitochondrial integrity. However, the actual signal and mechanism for translocation of DJ-1 to mitochondria remain unclear. Accordingly, we further explored the mechanisms of DJ-1 localization to mitochondria in Chapter 3.

Interaction of DJ-1 and VDAC1

An unbiased interactor screen suggests that DJ-1 interacts with the outer mitochondrial membrane (OMM) protein VDAC1. We investigated this interaction in hopes of better understanding the regulation of mitochondrial DJ-1. We were able to confirm the interaction between DJ-1 and VDAC1. We next explored the effect of

VDAC1 deficiency on mitochondrial localization of DJ-1. Specifically we queried whether VDAC1 signals for DJ-1 translocation to mitochondria.

Both VDAC1 null MEFs and cortical neurons show no stress-induced increase in mitochondrial DJ-1. VDAC1 is required for stress-induced increase of mitochondrial DJ-1. However, as DJ-1 is able to localize to VDAC1 deficient mitochondria, we do not believe that VDAC1 is the central signal for translocation to the OMM. Instead, we propose that VDAC1 is critical for sub-compartmentalization of DJ-1 to inner compartments such as the matrix (see below). Interestingly, similar to Pink1 KO conditions, VDAC1 KO cortical neurons exhibit basally increased level of mitochondrial DJ-1. Why would basal level of mitochondrial DJ-1 be increased in cortical neurons, but not MEFs that lack VDAC1? Without knowing the role of DJ-1 at mitochondria, it is difficult to identify why this difference is observed. However, comparing the two cell models may give us some insight. MEFs are actively dividing cells that are maintained in high glucose media. This media gears cells towards higher levels of glycolysis, therefore relying minimally on mitochondria for ATP production (Ibsen, 1961). Primary cortical neurons are terminally differentiated and rely much more heavily on mitochondria for ATP production (Bolaños et al., 2010). This reliance on mitochondria may add additional stress to the cell, specifically to the mitochondria themselves. If there is a mitochondrial defect, it could be exacerbated by oxidative phosphorylation, which is at a much higher level in cortical neurons versus MEFs. As such, we investigated the affect of VDAC1 deficiency on mitochondrial health in neurons.

Role of VDAC1 on mitochondrial health

VDAC1 deficiency has been characterized in numerous mouse cell types. Muscle from VDAC1 KO mice has altered mitochondrial morphology (Anflous et al., 2001). Isolated mitochondria from VDAC1 KO mouse liver undergo normal permeability transition following induction of apoptosis (Krauskopf et al., 2006). VDAC1 KO mouse embryonic stem cells have decreased oxygen consumption and decreased activity of complex IV of the ETC (Wu et al., 1999). MEFs lacking VDAC1 have altered mitochondrial morphology, but normal permeability transition and no altered sensitivity to stress (Baines et al., 2007).

Given the noted mitochondrial dysfunction with VDAC1 deficiency, it is surprising at the lack of studies in neural populations. We therefore investigated the consequences of VDAC1 KO on primary cortical neurons. Common indications of mitochondrial health include cell survival, level of cellular ROS, mitochondrial length and level of mitochondrial ATP production (Esposito et al., 1999; Abou-Sleiman et al., 2003; Chen and Chan, 2006; Lin and Beal, 2006; Detmer and Chan, 2007; Chinta and Andersen, 2008; Archer, 2013). We clearly demonstrate that VDAC1 KO cortical neurons have mitochondrial impairment. Specifically, there is reduced cell survival basally, increased ROS production following extended stress, basally fragmented mitochondria and decreased basal ATP production by mitochondria with VDAC1 deficiency. Interestingly, there is significant overlap between VDAC1 KO and DJ-1 KO cortical neuron phenotype (Kim et al., 2005a; Irrcher et al., 2010). DJ-1 null cortical neurons show hypersensitivity to oxidative stress (Kim et al., 2005a). With VDAC1 deficiency, cortical neurons have basally increased cell death. DJ-1 null cortical neurons

have fragmented mitochondria (Irrcher et al., 2010) similar to what we observed with VDAC1 deficiency. Isolated mitochondria from DJ-1 KO mouse whole brain lysates produced more ROS (Irrcher et al., 2010). We also show increased ROS production with VDAC1 KO cortical neurons following extended stress. Other groups have demonstrated reduced ATP production in DJ-1 KO MEFs and in a DJ-1 null dopaminergic cell line (Giaime et al., 2012; Heo et al., 2012), coinciding with our findings of decreased ATP production with VDAC1 deficiency.

Sub-mitochondrial localization of DJ-1

The sub-mitochondrial localization of DJ-1 has been studied, however OMM, inner mitochondrial membrane (IMM), and/or matrix localization have all been suggested (Canet-Avilés et al., 2004; Li et al., 2005; Zhang et al., 2005; Hayashi et al., 2009). It is important to note the variation in methods utilized in these studies – some rely purely on interaction with proteins in known mitochondrial compartments (Li et al., 2005; Hayashi et al., 2009). Recently a bi-fluorescent complementation system, which uses a split-GFP methodology, was employed to demonstrate DJ-1 localization to both the OMM and matrix (Calì et al., 2014). In conditions of stress, the matrix pool, but not the OMM pool, of DJ-1 increases (Calì et al., 2014). We investigated the sub-mitochondrial localization of DJ-1 in our hands. We found that in WT MEFs, mitochondrial DJ-1 is highly resistant to proteolytic digestion, suggesting it resides within the mitochondria, most likely at the matrix. While we noted a similar sub-mitochondrial localization of DJ-1 in untreated VDAC1 KO MEFs, but with H₂O₂ treatment, DJ-1 is much more readily digested. This

suggests that during times of stress, DJ-1 exists more externally within VDAC1 null mitochondria, perhaps at the OMM.

Using the above-mentioned GFP complementation system, we demonstrate a similar finding in cortical neurons. VDAC1 KO cortical neurons exhibit highly reduced matrix, but not OMM, localized DJ-1 that is further decreased following stress induction. We suggest that in absence of VDAC1, sub-mitochondrial localization of DJ-1 is altered in neurons. This finding coincides with the finding that more DJ-1 is localized to mitochondria in VDAC1 deficient cortical neurons. We suggest that the signal exists for DJ-1 to translocate to mitochondria however DJ-1 fails to enter mitochondria and remains at the OMM. As the signal persists in the VDAC1 null cells, more DJ-1 is recruited to the outside of mitochondria and total mitochondrial DJ-1 level is increased. Interestingly, we did not observe an increase in matrix DJ-1 in treated WT cortical neurons using expressed DJ-1. This observation may be due to the use of expressed DJ-1. We can conclude, however, that VDAC1 is required for proper sub-mitochondrial localization of DJ-1, especially during times of stress. With VDAC1 deficiency, DJ-1 cannot localize to the matrix and this specific sub-mitochondrial localization may be important in its pro-survival function.

Future work will investigate if we can rescue the observed mitochondrial defects in VDAC1 KO cortical neurons by expressing DJ-1 that is specifically targeted to mitochondria. We expect that matrix-targeted, but not OMM-targeted DJ-1 will rescue the observed defects. DJ-1 targeted to the matrix would bypass the VDAC1-dependent facilitated import of DJ-1 into mitochondria. While matrix localization of DJ-1 appears to be important, we still do not know the functional consequence of this localization.

Regulation and function of mitochondrial DJ-1

There have been numerous studies suggesting potential roles of DJ-1 at mitochondria. Earlier work suggested that DJ-1 could act as an atypical peroxiredoxin-like peroxidase to locally quench ROS (Taira et al., 2004; Andres-Mateos et al., 2007). The degree to which DJ-1 can quench ROS is debated, as is the role that this potential peroxidase activity has in promoting survival (Shendelman et al., 2004; Yang et al., 2005; Andres-Mateos et al., 2007). The oxidation of DJ-1, specifically at C106, has been implicated in localization of DJ-1 to mitochondria (Canet-Avilés et al., 2004). However another study reported that while C106 can be oxidized, this oxidation is not necessary for mitochondrial localization of DJ-1 (Maita et al., 2013). Given this ROS link, we questioned if ROS could perhaps be the signal for DJ-1 to translocate to mitochondria. Interestingly, pre-treatment of cells with an antioxidant in cortical neurons increases basal level of mitochondrial DJ-1. While no stress-induced increase is observed, the involvement of ROS as a signal for DJ-1 translocation to mitochondria appears complex. We have shown that ROS can induce translocation of DJ-1 to mitochondria, however it is most likely an indirect effect.

Neurons have higher energetic demands and rely significantly on mitochondria for ATP production (Chen and Chan, 2006). We noted decreased ATP levels in VDAC1 null cortical neurons as well as increased mitochondrial DJ-1 levels. These findings suggest that the signal for translocation of DJ-1 to the outside of mitochondria still exists and is potentially even higher with VDAC1 deficiency in cortical neurons. We were curious about the connection between ATP and DJ-1 and therefore investigated if decreased ATP could serve as a signal for DJ-1 translocation to mitochondria. A direct

mechanism to inhibit mitochondrial ATP production is to inhibit ATP synthase using the compound oligomycin (Bertina et al., 1974; Penefsky, 1985). Indeed, inhibition of ATP synthase induces DJ-1 translocation to mitochondria. The robust nature of the response of DJ-1 to oligomycin treatment is encouraging to the idea that cellular ATP level could in fact be a signal for translocation. As such, we propose a two-step model in which DJ-1 translocates to mitochondria. The first step relies on a signal, such as decreased ATP levels, for translocation of DJ-1 to the outside of mitochondria. The second step allows for DJ-1 to localize to the matrix in a VDAC1-dependent manner.

In this two-step model, what may be the role of matrix-localized DJ-1? We noted a decrease in ATP production by mitochondria in VDAC1 KO cortical neurons. Previous work has shown that DJ-1 specifically targeted to mitochondria is protective, more so than untargeted DJ-1 (Junn et al., 2009). More importantly, DJ-1 targeted to the matrix increases ATP production (Cali et al., 2014). Given that DJ-1 is localized to the matrix and responds to decreased ATP levels, we propose that DJ-1 is somehow involved in modulating ATP production.

In summary, understanding the role of DJ-1 at mitochondria during oxidative stress is important in understanding which pathways are important in promoting survival. Here we show that DJ-1 translocates to the matrix of mitochondria following induction of stress in a two-step process. We suggest that DJ-1 is involved in sensing ATP levels during times of oxidative stress. We also show that VDAC1 is important in the proper sub-mitochondrial localization of DJ-1, and this lack of proper localization appears to negatively impact the health of mitochondria. We demonstrate the complex interaction between DJ-1 and two other PD genes, Parkin and Pink1. Loss of one PD gene can

clearly negatively affect the function of another PD gene, which sheds some light on the complicated nature of this disease. Elucidating the mechanisms of action of the various PD genes is important in progressing our understanding of the disease. Our findings contribute to a growing pool of knowledge that will assist in discerning the mechanisms by which neurons degenerate in PD. We cannot hope to truly prevent or cure the disease without understanding how and why this degeneration occurs.

APPENDIX I

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APPENDIX III

Additional Publications

DJ-1 protects the nigrostriatal axis from the neurotoxin MPTP by modulation of the AKT pathway

Hossein Aleyasin^{a,1}, Maxime W. C. Rousseaux^{a,1}, Paul C. Marcogliese^a, Sarah J. Hewitt^a, Isabella Irrcher^a, Alvin P. Joselin^a, Mohammad Parsanejad^a, Raymond H. Kim^b, Patrizia Rizzu^c, Steve M. Callaghan^a, Ruth S. Slack^a, Tak W. Mak^{b,2}, and David S. Park^{a,d,2}

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Contributed by Tak Wah Mak, December 24, 2009 (sent for review December 15, 2009)

Loss-of-function DJ-1 (PARK7) mutations have been linked with a familial form of early onset Parkinson disease. Numerous studies have supported the role of DJ-1 in neuronal survival and function. Our initial studies using DJ-1-deficient neurons indicated that DJ-1 specifically protects the neurons against the damage induced by oxidative injury in multiple neuronal types and degenerative experimental paradigms, both in vitro and in vivo. However, the manner by which oxidative stress-induced death is ameliorated by DJ-1 is not completely clear. We now present data that show the involvement of DJ-1 in modulation of AKT, a major neuronal pro-survival pathway induced upon oxidative stress. We provide evidence that DJ-1 promotes AKT phosphorylation in response to oxidative stress induced by H₂O₂ in vitro and in vivo following 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) treatment. Moreover, we show that DJ-1 is necessary for normal AKT-mediated protective effects, which can be bypassed by expression of a constitutively active form of AKT. Taken together, these data suggest that DJ-1 is crucial for full activation of AKT upon oxidative injury, which serves as one explanation for the protective effects of DJ-1.

neurodegeneration | Parkinson disease | reactive oxygen species

Individuals with homozygous loss-of-function mutations of DJ-1 (PARK7) have been clinically characterized with familial early onset Parkinson disease (PD) (1, 2). Although the physiological role of DJ-1 is not completely understood, several lines of evidence indicate a protective role for DJ-1 in multiple models of neuronal and nonneuronal oxidative stress-induced cell death (3–7). For example, we have previously shown that genetic ablation of DJ-1 in mice hyper-sensitizes dopamine neurons to the toxic effects induced by the mitochondrial toxin, 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP). This sensitivity was reversed by the induction of virally delivered human DJ-1 (8). These observations are in line with data by other groups showing sensitivity of dopaminergic neurons in DJ-1-deficient *Drosophila* models, as well as increased susceptibility to oxidative stress in vitro (9–11). To further support the importance of DJ-1 in managing oxidative stress, we provided evidence showing that DJ-1 protects the brain against ischemic injury that models clinical stroke. Moreover, our data indicated a direct correlation between DJ-1 neuroprotective activity and the reduced levels of oxidized DNA nucleotide species, 8-oxo guanine, a marker of oxidative damage (12).

Despite the fact that the neuroprotective role of DJ-1 has been consistently shown in multiple models of neurodegeneration, the exact mechanism of the neuroprotective function has not been fully elucidated. A direct antioxidant property of DJ-1 as a reactive oxygen species (ROS) scavenger has been proposed as a mechanism to overcome oxidative stress (7, 13). In fact, recombinant human DJ-1 confers some ROS scavenging activity; however, this activity is much weaker than any known peroxidase, thus not fully explaining its neuroprotective function (10, 13). Several alternative mechanisms to account for the neuroprotective function of DJ-1 have been suggested. For example, via its putative role in transcription regu-

lation (14), DJ-1 up-regulates the expression of other antioxidant genes, such as glutathione synthase, during oxidative stress (15). Interestingly, it has also been reported that DJ-1 enhances the activity of the transcription factor Nrf2, a master regulator of antioxidant genes (16, 17). Alternatively, DJ-1 has also been shown to modulate key signaling pathways (3, 10). One signaling pathway implicated with DJ-1 function and relevant to the present work is AKT (10, 18).

AKT is a member of a larger class of serine/threonine kinases called AGC [protein kinase A (AMP protein kinase), PKG (GMP protein kinase), and PKC]. AKT has an N-terminus pleckstrin homology domain that mediates the interaction of AKT with a plasma membrane phospholipid, phosphatidylinositol 3,4,5-triphosphate (PIP3). Extensive studies have shown that recruitment of AKT to the plasma membrane, and its association with PIP3, is crucial for its activation (19, 20). Phosphatase and tensin homolog deleted on chromosome 10 (PTEN) is particularly known for its action to convert PIP3 to phosphatidylinositol-4,5-bisphosphate (PIP2). This function of PTEN directly antagonizes PI3K to eventually down-regulate AKT (21, 22). Several lines of evidence indicated that the AKT signaling pathway responds to oxidative stress (23) and exerts a neuroprotective function (24, 25). Moreover, a large number of studies in vitro have illustrated that pharmacological compounds that protect cells against oxidative stress exert their neuroprotective effects through activation of the AKT pathway (26–30).

Early studies described DJ-1 as a negative regulator of PTEN using a *Drosophila* genetic screen (31). Evidence to confirm this negative regulation was demonstrated via down-regulation of DJ-1 using small interfering RNA, which resulted in the inhibition of endogenous AKT phosphorylation in cancer cell lines as well as in the *Drosophila* brain (10, 31, 32). Furthermore, loss of DJ-1 has been shown to reduce AKT activation in response to hypoxia in murine embryonic fibroblasts (MEFs) (33). However, the relevance of this pathway has yet to be shown in the context of neurons either in vitro or in vivo. Evidence to support a role for DJ-1 in the regulation of the AKT pathway would be particularly important when one considers the genetic linkage of DJ-1 to familial PD. Presently, we provide direct evidence, both in vitro and in vivo, that DJ-1 exerts an important role in the regulation of the AKT pathway in response to oxidative stress and neuronal protection. In

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addition, based on our results, we propose a mechanism suggesting that DJ-1 acts as an upstream regulator of AKT through membrane recruitment to confer neuroprotection.

Results

Phosphorylation of AKT in Response to Oxidative Stress Is Reduced in the Absence of DJ-1 in Vitro and in Vivo. To examine the role of DJ-1 on AKT signaling, we first determined whether lack of DJ-1 affects AKT phosphorylation following hydrogen peroxide (H₂O₂) treatment. To test this, neurons harvested from DJ-1^{-/-} or DJ-1^{+/+} embryos were treated with 100-μM H₂O₂ for indicated time points. As demonstrated in Fig. 1A, phosphorylation of AKT peaked in wild-type neurons at 15 min, whereas in the knockout there was a reduction in AKT phosphorylation. Quantification of three independent experiments revealed a significant reduction in p-AKT 15 min following treatment (3.67 ± 0.17 in DJ-1^{+/+} vs. 1.49 ± 0.76 in DJ-1^{-/-}), as demonstrated in Fig. 1B. To further support this observation and to examine this response in a more clinically relevant model of PD, we examined AKT phosphorylation in dopaminergic neurons of the *substantia nigra* (SNc) in response to MPTP treatment. As indicated in Fig. 1C, and quantified in Fig. 1D, AKT phosphorylation in response to MPTP was reduced in the SNc cells of DJ-1^{-/-} compared to wild-type controls (1.19 ± 0.10 vs. 1.52 ± 0.14, respectively). There was no significant increase in AKT phosphorylation when comparing saline and MPTP treated DJ-1^{-/-} animals (1.00 ± 0.2 vs. 1.19 ± 0.10, respectively). To further confirm these results, we also examined AKT phosphorylation in response to H₂O₂ in human lymphoblasts from human PD patients harboring DJ-1 mutations. As demonstrated in Fig. 1E, AKT response was significantly attenuated in L166P mutated cells compared to the controls.

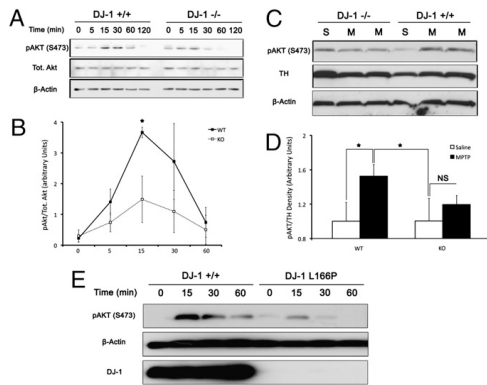


Fig. 1. AKT activation is suppressed in the absence of DJ-1. (A) Cortical neurons from DJ-1^{+/+} and DJ-1^{-/-} embryos were harvested, plated, and treated with H₂O₂ (100 μM) in a time-dependent fashion. Extracts were probed for pAKT (S473), total AKT, and β-actin by Western blot. (B) Quantification of A from three independent experiments. Values are presented as mean optical density relative to total AKT. (C) Eight- to 10-week-old C57Bl6 mice of WT and DJ-1 knockout genotype were treated with two 30-mg/kg doses of MPTP (M), or saline (S), given 24 h apart. Three hours following the second injection, mice brains were quickly dissected for SNc and samples were processed for Western blot analysis. (D) Quantification of C. n = 3–6 per group. (E) Immortalized lymphoblasts derived from patients with the DJ-1 L166P mutation or healthy control lymphoblasts were treated with H₂O₂ in a time dependant manner. Analysis of cell lysates was carried out by Western blot. Blot presented is representative of two independent experiments. Data are presented as mean ± SEM.

DJ-1 Is Necessary for AKT-Mediated Neuroprotective Function in Vitro and in Vivo. We next evaluated the functional role of DJ-1 in the protective effects of AKT following oxidative stress. First, we examined the role of AKT in protecting neurons against oxidative stress induced by H₂O₂ in vitro. Neurons, transfected with HA-tagged wild-type AKT along with GFP expression vectors as a marker of transfection (or GFP/empty vector transfection as control) were treated with H₂O₂, 24 h after transfection, and survival was assessed as described in *Materials and Methods* (Fig. 2A). As shown in Fig. 2B, induction of exogenous wild-type AKT confers protection in DJ-1^{+/+} neuronal cells in response to H₂O₂. Next, DJ-1^{-/-} cortical neurons were tested to examine whether induction of wild-type AKT could provide similar protection in DJ-1-deficient cells. Surprisingly, induction of exogenous AKT failed to protect DJ-1^{-/-} neurons against H₂O₂-induced death (Fig. 2C). To confirm these observations, we cultured neurons harvested from DJ-1^{-/-} and DJ-1^{+/+} litters at the same time. Three days after plating, the cells were transiently transfected with wild-type AKT together with or without a DJ-1

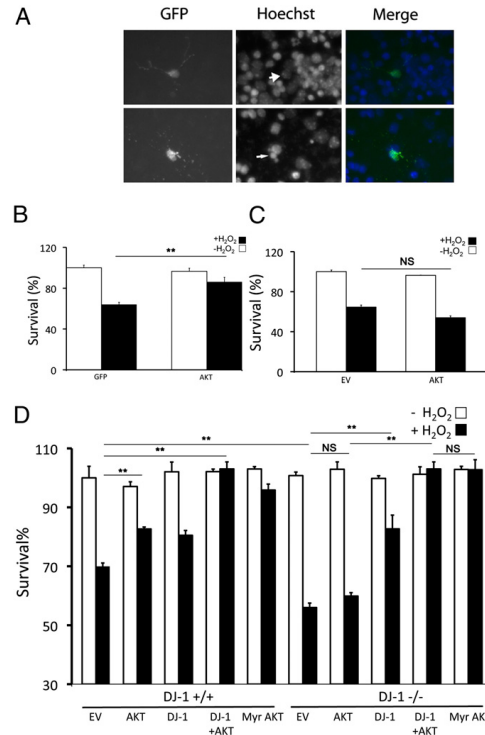


Fig. 2. AKT requires DJ-1 to exert its neuroprotective function in vitro. (A) Representative pictures of alive (Upper, large arrowhead) and dead (Lower, thin arrowhead) neurons. Neuronal survival was measured by identifying GFP-positive cells and determining their nuclear integrity by Hoechst stain. (B–D) Cortical neurons from either DJ-1^{+/+} or DJ-1^{-/-} embryos were harvested, plated, and transfected with empty vector (EV), AKT, DJ-1, or Myr AKT. Cells were treated with H₂O₂ (30 μM) or vehicle control (–H₂O₂) for 3 h. Quantification was assessed as in A. Data are presented as mean ± SEM. **, P < 0.01; NS, no significant difference.

expression vector, DJ-1 only, or myristoylated AKT, a membrane-anchored constitutively active form of AKT (34). After treatment with H_2O_2 , cell survival was assessed. The results of this experiment clearly verified our findings in Fig. 2C, indicating the protective role of wildtype AKT expressed in DJ-1^{+/+} neurons but not in DJ-1^{-/-} cells ($82.65 \pm 0.65\%$ DJ-1^{+/+} vs. $59.88 \pm 1.18\%$ DJ-1^{-/-}) (Fig. 2D). Interestingly, myristoylated AKT significantly protects neurons against oxidative damage induced by H_2O_2 regardless of DJ-1 genotype ($95.85 \pm 2.02\%$ DJ-1^{+/+} vs. $102.77 \pm 3.38\%$ DJ-1^{-/-}).

Suppression of AKT Abolishes the Neuroprotective Function of DJ-1 In Vitro and In Vivo. The observations that DJ-1 deficiency reduces AKT activation and that wild-type AKT requires DJ-1 to effectively protect neurons against oxidative stress suggests DJ-1 acts as an upstream activator of AKT. We next determined whether DJ-1 exerts its neuroprotective effects, at least partially, through the AKT pathway. To examine this, we first used a conventional pharmacological inhibitor of AKT, LY294002 (LY) (35). Because the basal activity of AKT is essential for the long-term health of cultured neurons, we determined the optimal dose of inhibitor that suppressed AKT with minimal toxicity to the cultured neurons (Fig. 3A). We next infected cultured cortical neurons with adenoviral vectors expressing GFP only or DJ-1 and GFP on separate promoters at the time of plating. Thirty-six hours after plating, we pretreated the cells with $10\text{-}\mu\text{M}$ LY or vehicle for 30 min before application of H_2O_2 or vehicle for 3 h. Cells were then assessed for survival. As shown in Fig. 3B, the neuroprotective activity of DJ-1 is significantly reduced upon suppression of AKT phosphorylation by LY ($52.78 \pm 0.20\%$ vs. $40.55 \pm 0.55\%$, respectively). We also used

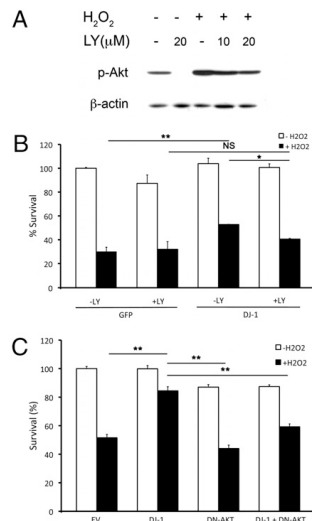


Fig. 3. DJ-1 requires AKT activation to promote cellular survival in vitro. (A) Cortical neurons were treated for either 10 or $20\text{-}\mu\text{M}$ of LY with and without H_2O_2 ($100\text{-}\mu\text{M}$, 15 min) to determine the effective dose of LY. (B) Cortical neurons were infected with either GFP or DJ-1 with GFP. Cells were then pretreated with LY followed by H_2O_2 treatment for survival assessment. (C) Cortical neurons were cotransfected with GFP and empty vector (EV), DJ-1, DN-AKT, or a DJ-1/DN-AKT combination followed by H_2O_2 treatment. Survival was assessed as in B. Data are presented as mean \pm SEM. *, $P < 0.05$; **, $P < 0.01$; NS, no significant difference.

a more specific molecular strategy to validate our results by transiently transfecting a phosphorylation mutant, dominant-negative form (DN-AKT) of AKT (AAA-AKT) into cortical neurons. In this mutant, all phosphorylation sites of AKT have been mutated to alanine; therefore, this artificial mutant of AKT is incapable of being phosphorylated and displays dominant-negative properties toward endogenous AKT (21). As shown in Fig. 3C, the results of this experiment confirmed that suppression of AKT diminished the neuroprotective function of DJ-1 ($84.46 \pm 2.90\%$ without DN-AKT vs. $59.26 \pm 2.01\%$ with DN-AKT).

DJ-1 Is Necessary for AKT-Mediated Neuroprotection In Vivo Following MPTP Treatment. In vitro experiments indicated that DJ-1 is necessary for AKT activation and is neuroprotective in response to H_2O_2 . To confirm these results and to test this hypothesis in a more clinically relevant paradigm, we examined whether induction of wild-type AKT can protect nigrostriatal neurons against the dopaminergic specific neurotoxin MPTP in vivo. To achieve this, we injected adenoviral vectors harboring HA-tagged wild-type AKT or myristoylated AKT into the striatum of DJ-1^{+/+} and DJ-1^{-/-} age-matched mice. β -gal expressing adenoviruses

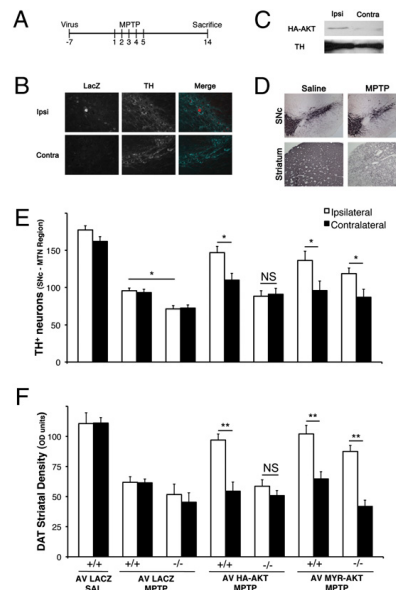


Fig. 4. AKT requires DJ-1 to exert its neuroprotective function in an in vivo model of PD. (A) Schematic representation of treatment course. Mice were injected ipsilaterally in the striatum with adenovirus (LacZ, HA-AKT, Myr-AKT) 7 d before commencement of MPTP injections. MPTP was injected for 5 consecutive days and brains were collected 14 days following the first MPTP injection. (B) Confirmation of virus expression was performed by immunohistochemistry. Dual labeling of both TH and protein of interest in the SNc. (C) HA expression was tested in the SNc by Western blot analysis. (D) Representative pictures of both striatum and SNc of mice treated with MPTP or saline. SNc and striatum were stained for TH and DAT, respectively. (E) Quantification of TH-immunoreactive neurons was performed at the MTN region of the SNc where virus expression was highest. "Ipsi" denotes the side of the brain ipsilateral to the virus injection, whereas "contra" denotes the contralateral side. (F) Quantification of DAT-positive fibers normalized to cortex (DAT-negative). Data are presented as mean \pm SEM. *, $P < 0.05$; **, $P < 0.01$; NS, no significant difference.

In light of our findings above, together with the knowledge that AKT is considered to be part of the survival pathway, we sought to further investigate the nature of the DJ-1/AKT relationship. We first demonstrated that overexpression of AKT alone protects cultured neurons exposed to oxidative stress *in vitro* as well as dopamine neurons exposed to MPTP *in vivo*. Furthermore, inhibition of the PI3K/Akt pathway significantly reduces the protection that is conferred by DJ-1. Importantly, we also demonstrated that wild-type AKT required DJ-1 to exert its protective effect as DJ-1 deficiency abrogated the effect of AKT on cell survival. Interestingly, the protective effects of AKT in a DJ-1-deficient background can be bypassed using myristoylated AKT, its membrane-anchored constitutively active form. This latter observation is consistent with reports that membrane-bound AKT is sufficient to provide protection following MPP⁺ treatment both *in vitro* (49) as well as 6-OHDA treatment *in vivo* (50). Because AKT recruitment to the membrane is a prior event to its phosphorylation and activation (51, 52), these results, in addition to the cell fractionation experiments presented in our study, suggested that DJ-1 permits AKT translocation to the membrane fractions.

Our study therefore proposes a working model in which DJ-1 acts upstream of AKT, thereby facilitating its activation following neuronal injury via oxidative stress. We propose that DJ-1 may be involved in fine-tuning the response of neurons to ROS and modulation of signaling pathways that mediate survival. In this regard, it will be critical in future studies to address the possible mechanisms underlying the ROS-mediated, DJ-1-dependent activation of AKT. One might consider the possibility that DJ-1 regulates AKT by modulating its recruitment to the membrane in a ROS-dependent manner. It is noteworthy that the AKT response to H₂O₂ can be altered depending on antioxidant protein activity within the cell (53–55). Thus, further studies in models that permit well-controlled ROS levels are needed to address these questions. However, other possibilities exist. For example, a recent study has suggested that DJ-1 interacts with PTEN to permit AKT activation, although this needs to be further investigated in more physiologically relevant models (56). Additionally, DJ-1 may interact with other PI3K pathway kinases, such as mTOR and PDK, to permit AKT phosphorylation. Finally, while DJ-1 plays a significant role in facilitating AKT phosphorylation, other factors may also each play a role (21, 57, 58). Thus, additional studies should be performed to investigate the nature of the DJ-1/AKT interdependence.

Finally, it is interesting to note that even though it is clear that DJ-1 is linked to familial PD, there is a report of an epidemiological association with certain haplotype of AKT1 and a reduced risk of PD (59). This observation provides further strength to the notion that the DJ-1/AKT signaling axis may be important in regulating dopaminergic function or death. Elucidation of these mechanisms may provide an eventual basis for neuroprotective therapies.

Materials and Methods

Cell culture, Western blot analysis, and *in vivo* stereotaxic injections and MPTP administration were performed as previously described (60). All procedures involving animals were approved by the University of Ottawa Animal Care Committee and were maintained in strict accordance with the Guidelines for the Use and Treatment of Animals put forth by the Animal Care Council of Canada and endorsed by the Canadian Institutes of Health Research. For additional *in vivo* and *in vitro* procedures, see *SI Materials and Methods*.

Subcellular Fractionation. Membrane fractions were obtained similarly for MEFs and DIV 6 cortical neurons using differential centrifugation. Briefly, cells were harvested in cold PBS and centrifuged at 1,200 × *g* for 3 min. The cell pellet was resuspended in 200 μL of hypo-osmolar buffer [50 mM Tris-HCl, pH 7.4; 50 mM NaCl; protease inhibitor complex (Roche)] and homogenized for 30 s. Samples were centrifuged at 20,000 × *g*, at 4 °C for 20 min. Supernatants (cellular debris) were transferred to 1.5-mL ultracentrifuge tubes (Beckman) and centrifuged at 100,000 × *g*, at 4 °C for 3 h. The pellets (microsomal enriched) were resuspended in RIPA buffer (150 mM NaCl; 1% Nonidet P-40; 0.5% deoxycholic acid; 0.1% SDS; 50 mM Tris-HCl, pH 8.0) and sonicated briefly for subsequent Western blot analysis. Supernatants from final spin were used as a cytoplasmic control.

Statistical Analysis. Statistical significance was either determined by Student's *t*-test or one-way ANOVA followed by Tukey's post hoc test. All data are presented as mean ± SEM. Significance at *P* < 0.05 (*) and *P* < 0.01 (**), and NS denotes no significant difference.

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Loss of the Parkinson's disease-linked gene DJ-1 perturbs mitochondrial dynamics

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Growing evidence highlights a role for mitochondrial dysfunction and oxidative stress as underlying contributors to Parkinson's disease (PD) pathogenesis. DJ-1 (PARK7) is a recently identified recessive familial PD gene. Its loss leads to increased susceptibility of neurons to oxidative stress and death. However, its mechanism of action is not fully understood. Presently, we report that DJ-1 deficiency in cell lines, cultured neurons, mouse brain and lymphoblast cells derived from DJ-1 patients display aberrant mitochondrial morphology. We also show that these DJ-1-dependent mitochondrial defects contribute to oxidative stress-induced sensitivity to cell death since reversal of this fragmented mitochondrial phenotype abrogates neuronal cell death. Reactive oxygen species (ROS) appear to play a critical role in the observed defects, as ROS scavengers rescue the phenotype and mitochondria isolated from DJ-1 deficient animals produce more ROS compared with control. Importantly, the aberrant mitochondrial phenotype can be rescued by the expression of Pink1 and Parkin, two PD-linked genes involved in regulating mitochondrial dynamics and quality control. Finally, we show that DJ-1 deficiency leads to altered autophagy in murine and human cells. Our findings define a mechanism by which the DJ-1-dependent mitochondrial defects contribute to the increased sensitivity to oxidative stress-induced cell death that has been previously reported.

INTRODUCTION

Parkinson's disease (PD), the second most common neurodegenerative disorder, is characterized by the progressive loss of neurons within the substantia nigra *pars compacta* (1,2). Though the pathogenic mechanisms underlying PD are not well understood, growing evidence supports a role for mitochondrial dysfunction, oxidative stress and more recently autophagy.

Mitochondrial dysfunction was initially tied to PD in studies demonstrating the presence of aberrant mitochondrial function in idiopathic PD patients (3,4). Moreover, several dopamin-

ergic toxins acted as mitochondrial toxins by inhibiting the electron transport chain, producing toxic-free radicals in the process (5,6). Since this time, several familial PD genes, including, Parkin (PARK2), Pink1 (PARK6) and DJ-1 (PARK7), have been linked to mitochondria. Their loss results in abnormal mitochondrial morphology (7,8). Interestingly, the interplay of Pink1 and Parkin dynamically regulates mitochondrial morphology via mitochondrial fission/fusion and also affects mitochondrial quality control (9–11). As the function of Pink1 and Parkin in these contexts continues to be elucidated, the role(s) of DJ-1 is less understood.

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Homozygous loss-of-function mutations in DJ-1 (PARK7) result in early onset PD (12). Several lines of evidence, including our own, indicate that DJ-1 protects neurons against oxidative stress-induced cell death (13,14). It has been postulated that DJ-1 exerts its protective function by regulating mitochondrial homeostasis or participating in the oxidative stress response either serving as an antioxidant scavenger or a redox sensor (14–17). More recently, DJ-1 was found to affect mitochondrial quality control (18,19). Given the importance of reactive oxygen species (ROS) in regulating mitochondrial dynamics and the observations that loss of Pink1 and Parkin has also been linked to mitochondrial dysfunction, we wanted to address whether DJ-1 also affects mitochondrial dynamics and function.

Here we examined mitochondrial morphology and function in DJ-1 deficient tissues and hypothesized that loss of DJ-1 would produce a fragmented mitochondrial phenotype, accounting increased sensitivity to cell death of DJ-1 deficient neurons previously reported (14). We demonstrate that DJ-1 deficiency leads to a fragmented mitochondrial phenotype in multiple contexts including neurons and human DJ-1 patient cells. Second, we provide evidence that ROS plays a critical role in this fragmentation phenotype and that DJ-1 deficiency results in elevated ROS levels. Third, we show that this mitochondrial phenotype is an important contributor to the sensitivity to oxidative stress caused by the loss of DJ-1. Fourth, we show that Pink1 and Parkin can rescue the mitochondrial fragmentation induced by the loss of DJ-1. Finally, we also show that the loss of DJ-1 results in increased autophagic activity.

RESULTS

Loss of DJ-1 alters mitochondrial morphology and dynamics

Based upon the growing evidence for mitochondrial morphology and dynamics as underlying contributors to PD, we first investigated a role for DJ-1 in mitochondrial remodeling. Primary cortical neurons and mouse embryonic fibroblasts (MEFs) from DJ-1^{+/+} or DJ-1^{-/-} embryos (E15.5) were cultured. Mitochondria were quantified and binned according to length, as done previously (20). As shown in Figure 1A and quantified in Figure 1B, mitochondrial lengths in DJ-1^{+/+} primary cortical neurons at 3 days *in vitro* were significantly longer and less fragmented than in DJ-1^{-/-} neurons. This fragmented mitochondrial phenotype was also evident in MEFs (Fig. 1C and D) and *in vivo* in the striatum of DJ-1^{+/+} and DJ-1^{-/-} mice (Fig. 1E and F). Thus, the fragmented morphology appears to be a more generalized phenomenon rather than restricted to a specific cell type, occurring both *in vitro* and *in vivo*. These data demonstrate that mitochondrial morphology is altered with the loss of DJ-1.

To address whether the DJ-1-dependent mitochondrial fragmentation was related to alterations in mitochondrial fusion rates, DJ-1^{+/+} or DJ-1^{-/-} MEFs were transduced with a matrix-targeted photoactivatable GFP lentivirus (PA-GFP). PA-GFP was activated in ~10% of the cell using a 405 nm laser line at 75% intensity (21). Upon photoactivation, the spread of the GFP signal throughout the mitochondrial reticu-

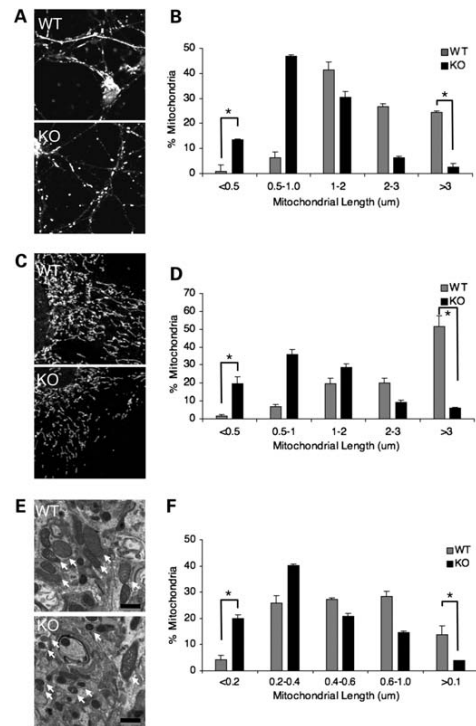


Figure 1. DJ-1 deficiency results in altered mitochondrial morphology *in vitro* and *in vivo*. (A) Primary cortical neurons (3 DIV) and (C) MEFs from wild-type (WT) and knockout (KO) DJ-1 embryos were harvested and fixed as described under Materials and Methods and immunostained with antibodies to Tom20 to visualize mitochondria. Quantification of mitochondrial lengths in (B) primary cortical neurons and (D) MEFs was done as described previously [Jahani-Asl *et al.* (20); $n = 4$ independent experiments with a minimum of 500 mitochondria/experiment counted]. Scale Bar = 2 μm . * $P < 0.05$ versus respective $+/+$ control. (E) Electron microscopic images of WT and KO DJ-1 striatum prepared as described in Materials and Methods. (F) Quantification of mitochondrial diameters in the striatum of WT and KO DJ-1 mice from three mice/genotype. Scale bar = 500 nm. * $P < 0.05$ versus respective WT DJ-1 control. DIV, days *in vitro*. White arrows in (E) depict mitochondria.

lum was assessed immediately post-activation and following 20 min (Fig. 2A). The data in Figure 2B demonstrate that mitochondrial fusion in MEFs is decreased by 30% DJ-1^{-/-} when compared with DJ-1^{+/+}. Steady-state levels of the mitochondrial fission and fusion proteins, Dynamin Related Protein-1 (Drp1) and mitofusin 1 (MFN1) were also measured to determine whether the loss of DJ-1 would result in altered expression. As shown in Figure 2C, Drp1 levels were not altered, while decreases in the levels of MFN1 were observed.

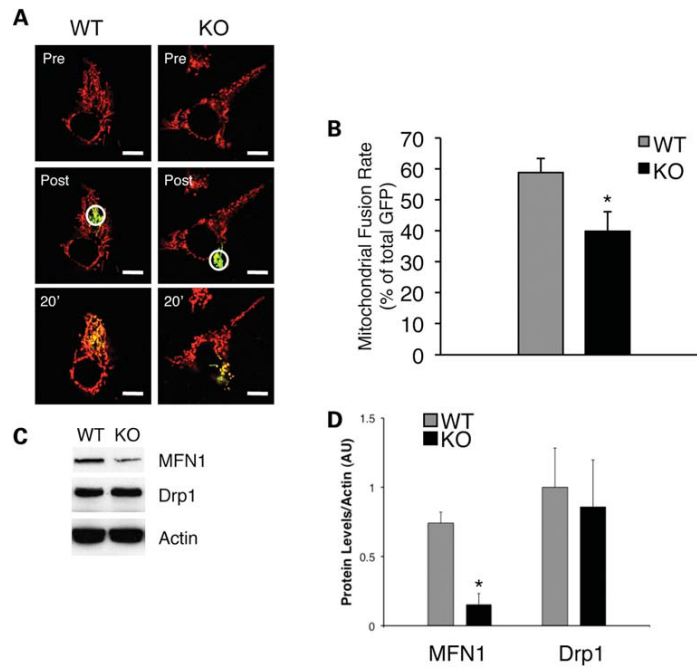


Figure 2. Mitochondrial fusion is decreased with DJ-1 deficiency. (A) Confocal images of mitochondria from DJ-1^{+/+} (WT) and DJ-1^{-/-} (KO) MEFs transfected with mitochondrial matrix-targeted DS-red and PA-GFP lentiviruses as described in the Supplementary Information. Images shown are from pre-activation (Pre), immediately following activation (Post) in a small region of interest (indicated by open white circles) as well as following 20 min (20') of activation. (B) Quantification of mitochondrial fusion 20 min post-activation from DJ-1^{+/+} ($n = 14$ cells) and DJ-1^{-/-} ($n = 12$ cells) MEFs. (C) Protein extracts were made from DJ-1^{+/+} and DJ-1^{-/-} MEFs and subjected to western blotting for Drp-1, Mfn1 and actin (for loading control). Data shown are representative of at least three independent experiments. (D) Quantification of Drp1 and MFN1 protein levels, corrected with actin for loading in DJ-1 WT and KO MEFs. * $P < 0.05$.

Rescue of mitochondrial length in DJ-1^{-/-} neurons abrogates neuronal cell death

Our previous work has shown that overexpression of DJ-1 protects primary cortical neurons from oxidative stress (14). Here we report that DJ-1 deficiency promotes mitochondrial fragmentation. To determine whether these phenomena are linked, primary cortical neurons from DJ-1^{+/+} and DJ-1^{-/-} embryos were infected with dominant-negative dynamin-related protein 1 (DRP1K38E), a mutant form of the mitochondrial fission factor that promotes an elongated mitochondrial reticulum when expressed in cells. Expression levels of Drp1 K38E are shown in Figure 3A and were previously described (21). When primary cortical neurons were subjected to oxidative stress in the form of MPP⁺ (10 μ M), a metabolite of the parkinsonism-inducing drug MPTP (22) for 48 h, the hypersensitive DJ-1^{-/-} neurons showed an increase in cell death. However, DJ-1^{-/-} cortical neurons infected with DRP1K38E were completely protected from the toxic effects of MPP⁺ suggesting that mitochondrial fragmentation contributes to oxidative stress-induced sensitivity to cell death (Fig. 3B).

NAC treatment rescues the mitochondrial phenotype in DJ-1^{-/-} neurons

ROS can significantly influence mitochondrial morphology, producing a fragmented phenotype (23). Thus, to assess whether the DJ-1-dependent mitochondrial morphology is related to ROS, we determined whether quenching with N-acetyl-L-cysteine (NAC) might affect mitochondrial fragmentation observed in DJ-1 deficient cells. DJ-1^{+/+} and DJ-1^{-/-} primary cortical neurons were incubated with the ROS scavenger NAC (1 mM) for 48 h (Fig. 4A). Quantification of mitochondrial lengths in vehicle-treated (VEH) DJ-1^{+/+} and DJ-1^{-/-} neurons revealed a similar pattern of mitochondrial morphology deficits as described in Figure 1. While treatment with NAC did not significantly alter mitochondrial length in the DJ-1^{+/+} neurons, treatment of DJ-1^{-/-} neurons with NAC completely reversed the mitochondrial fragmentation where the percentage of mitochondria exhibiting lengths greater than 3 μ m increased (i.e. $1.14 \pm 0.305\%$ in KO-VEH to $32.144 \pm 3.141\%$ in KO-NAC; Fig. 2B) and the percentage of fragmented mitochondria decreased (i.e.

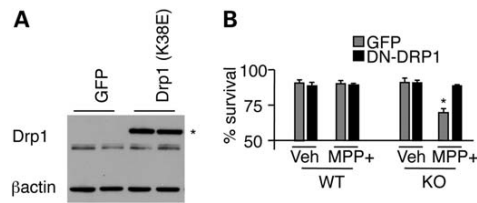


Figure 3. Mitochondrial length is critical for neuronal cell survival. (A) Primary cortical neurons infected with either GFP or DN-Drp1 were treated with vehicle (Veh) or MPP+ (10 μ M) for 24 h. (B) Cell survival was assessed by counting infected cells with intact or dead nuclei plotting the ratio of live:dead cells in treated and untreated DJ-1^{+/+} and DJ-1^{-/-} ($n = 3$ independent experiments, each experiment was performed in triplicate).

<0.5 μ m; $15.928 \pm 3.03\%$ in KO-VEH versus $0.198 \pm 0.038\%$ in KO-NAC; Fig. 4B), suggesting that elevated levels of ROS can cause mitochondrial fragmentation, which can be reversed if ROS levels are reduced.

Wild-type DJ-1 but not the DJ-1 C106A mutant rescue mitochondrial morphology defects

It has been previously reported that DJ-1 exerts its effect on oxidative stress via an isoelectric pH shift resulting in a more acidic molecule (24). Importantly, the residue that appears to be sensitive to oxidative modification, in particular hydrogen peroxide-induced oxidation, is a cysteine residue in position 106 (25,26). Thus, to provide additional relevance for the role of ROS and the importance of DJ-1 and oxidative stress in the regulation of mitochondrial morphology, we investigated whether DJ-1 itself actively regulates mitochondrial morphology and to further ascertain whether the DJ-1 mutant that is defective in handling ROS would fail to rescue the DJ-1 deficient phenotype. DJ-1^{+/+} and DJ-1^{-/-} cortical neurons were infected with adenoviruses encoding GFP (as a control), wild-type DJ-1 (DJ-1) or an oxidant mutant form of DJ-1 (C106A). This DJ-1 mutant harbors a cysteine to alanine point mutation at amino acid 106 rendering the oxidative capacity of DJ-1 non-functional. Expression levels of viruses are shown in Supplementary Material, Fig. S1. As shown in Figure 5A and quantified in Figure 5B, DJ-1^{+/+} or DJ-1^{-/-} cortical neurons infected with GFP virus alone display the wild-type mitochondrial phenotype as shown in Figure 1, demonstrating that viral expression of GFP alone does not significantly alter mitochondrial length. Next, while overexpression of DJ-1 had no effect on mitochondrial morphology in DJ-1^{+/+} neurons, DJ-1 expression in DJ-1^{-/-} neurons increased the percentage of mitochondria exhibiting lengths greater than 3 μ m ($5.15 \pm 0.826\%$ in KO-GFP versus $47.97 \pm 12.51\%$ in KO DJ-1) and decreased the percentage of fragmented mitochondria ($42.00 \pm 2.56\%$ in KO-GFP versus $1.403 \pm 1.4\%$ in KO DJ-1) supporting the idea that wild-type DJ-1 plays a role in regulating mitochondrial morphology. On the other hand, the oxidant mutant C106A cannot recapitulate the full rescue displayed by WT DJ-1 indicating that the redox function of DJ-1 is critical in promoting a fused mitochondrial reticulum.

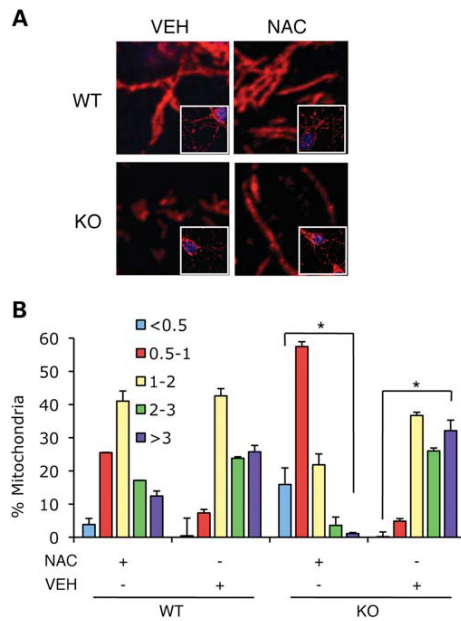


Figure 4. NAC rescues the mitochondrial morphology in DJ-1-deficient primary cortical neurons. (A) Confocal images of neurons taken from vehicle- (VEH) and NAC-treated (NAC) WT and KO neurons. Neurons were harvested and fixed 48 h post-treatment and immunostained with antibodies to Tom20 (red) to visualize mitochondria. Scale bar = 2 μ m. Inset: lower magnification images. (B) Quantification of mitochondrial lengths as described previously [Jahani-Asl *et al.* (20)]; $n = 3$ independent experiments with a minimum of 500 mitochondria/experiment were counted. Scale bar = 2 μ m. * $P < 0.05$ versus respective controls.

DJ-1 deficiency alters ROS production

If ROS were indeed important in promoting the fragmented mitochondrial phenotype induced by DJ-1 deficiency, we would expect that ROS production would be elevated in mitochondria isolated from DJ-1^{-/-} mice when compared with DJ-1^{+/+} controls. Accordingly, we isolated mitochondrial fractions from brain and skeletal muscle; tissues typically associated with high metabolic requirements and mitochondria and are therefore significant sources of ROS. As predicted, we observed that H₂O₂ production in mitochondria isolated from DJ-1^{-/-} mice is increased 1.4-fold ($P < 0.05$) compared with DJ-1^{+/+} controls in both brain (Fig. 6) and skeletal muscle (Supplementary Material, Fig. S2A), respectively. In either tissue, H₂O₂ production in the DJ-1^{-/-} animals was not further increased with the addition of the mitochondrial Complex I inhibitor rotenone, suggesting that ROS production in DJ-1 deficient mitochondria is generated primarily via Complex I. Despite the increased H₂O₂ production, we did not observe gross differences in mitochondrial function

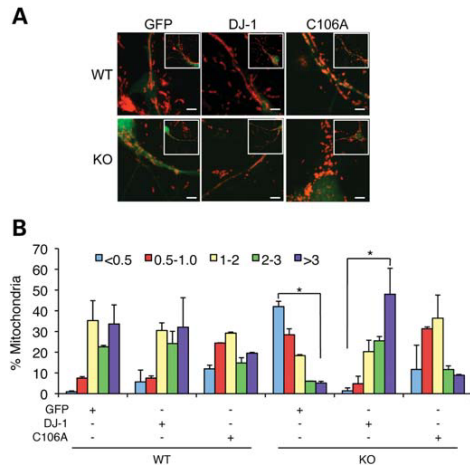


Figure 5. Restoration of wild-type mitochondrial phenotype upon re-expression of DJ-1 *in vitro*. (A) Confocal images from WT and KO DJ-1 primary cortical neurons infected with GFP, GFP-DJ-1 and GFP-DJ-1 C106A adenoviruses as described in Materials and Methods. Neurons were harvested and fixed 48 h post-infection and immunostained with antibodies to Tom20 (red) to visualize mitochondria. Inset: lower magnification images. (B) Quantification of mitochondrial lengths as described previously [Jahani-Asl *et al.* (20); $n = 3$ independent experiments with a minimum of 500 mitochondria/experiment that were counted per condition]. * $P < 0.05$ versus respective controls.

measurements that were performed such as mitochondrial respiration and citrate synthase activity in DJ-1^{-/-} mice, at least in the brain (Supplementary Material, Fig. S2B and S2C). However, it should be noted that both mitochondrial respiration and citrate synthase activity were decreased in skeletal muscle (Supplementary Material, Fig. S2D and S2E).

Pink1 and Parkin rescue mitochondrial length in DJ-1^{-/-} primary cortical neurons

Previous work conducted in *Drosophila* has demonstrated that Pink1 and Parkin participate in mitochondrial remodeling and are part of the same genetic pathway where Pink1 is upstream of Parkin (9–11,27–29). More recent evidence in mammalian cells is supportive of this notion and also implicates Parkin and Pink1 in the regulation of autophagy, a lysosomal degradation pathway responsible for the degradation of damaged proteins and organelles, including mitochondria (29–31). Thus, we determined whether Pink1 and Parkin could rescue the mitochondrial phenotype in DJ-1^{-/-} primary cortical neurons. Accordingly, we infected DJ-1^{+/+} and DJ-1^{-/-} primary cortical neurons with Pink1 and Parkin viruses, and quantified mitochondrial length as before. Viral expression of Parkin was confirmed in Supplementary Material, Fig. S3.

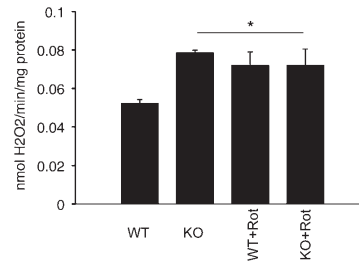


Figure 6. Brain mitochondria isolated from DJ-1 deficient animals produce more ROS. H₂O₂ production was measured in mitochondria isolated from WT and KO DJ-1 brains. * $P < 0.05$ versus WT DJ-1 (P/M, pyruvate/malate; Rot, rotenone).

Viral expression of Pink1 was previously described (32). As shown in Figure 7A and C and quantified in Figure 7B and D, overexpression of either Pink1 or Parkin in DJ-1^{-/-} primary cortical neurons promoted an increase in the percentage of mitochondria that were greater than 3 μm in length ($5.151 \pm 0.826\%$ in KO-GFP versus $44.08 \pm 1.646\%$ in KO-Pink1; Fig. 7B and $1.686 \pm 0.133\%$ in KO-GFP versus $30.126 \pm 8.068\%$ in KO-Parkin; Fig. 7D) and decreased the percentage of fragmented mitochondrial (i.e. $<0.5 \mu\text{m}$; $42.00 \pm 2.562\%$; Fig. 7B in KO-GFP versus $0.948 \pm .271\%$ in KO-Pink1 and $34.108 \pm 5.50\%$ in KO-GFP versus $4.888 \pm 2.924\%$ in KO-Parkin; Fig. 7D) respectively, suggesting that both Pink1 and Parkin can rescue the fragmentation phenotype observed with the loss of DJ-1.

To further confirm these findings, we also quantified the percentage of cells that contained fragmented mitochondria a dopaminergic cell line (SH-5Y5Y) in which DJ-1 was transiently knocked down and subsequently overexpressed with Parkin or Pink1. Confirmation of DJ-1, Pink1 and Parkin overexpression is shown in Supplementary Material, Fig. S4A, S4B and S4C, respectively. As seen in DJ-1^{-/-} primary cortical neurons, transient knockdown of DJ-1 produced a significant increase in cells exhibiting fragmented mitochondria and this phenotype could be prevented with overexpression of DJ-1, Pink1 or Parkin (Fig. 7E and F).

DJ-1 deficiency results in enhanced autophagic flux

As mentioned above, Pink1 and Parkin have both been implicated in the regulation of autophagy in response to mitochondrial damage (9–11,30,31). Our present data show that the loss of DJ-1 leads to increased mitochondrial ROS production and fragmentation. Since both of these parameters are linked with autophagy, we evaluated whether a downstream autophagic response might also be altered with DJ-1 deficiency. To this end, we employed conventional autophagy assays including the evaluation of steady-state microtubule-associated protein light chain 3-II (LC3-II) and the LC3-associated protein p62, under basal conditions as well as GFP-LC3 puncta formation (33). As shown in Figure 8A, the markers

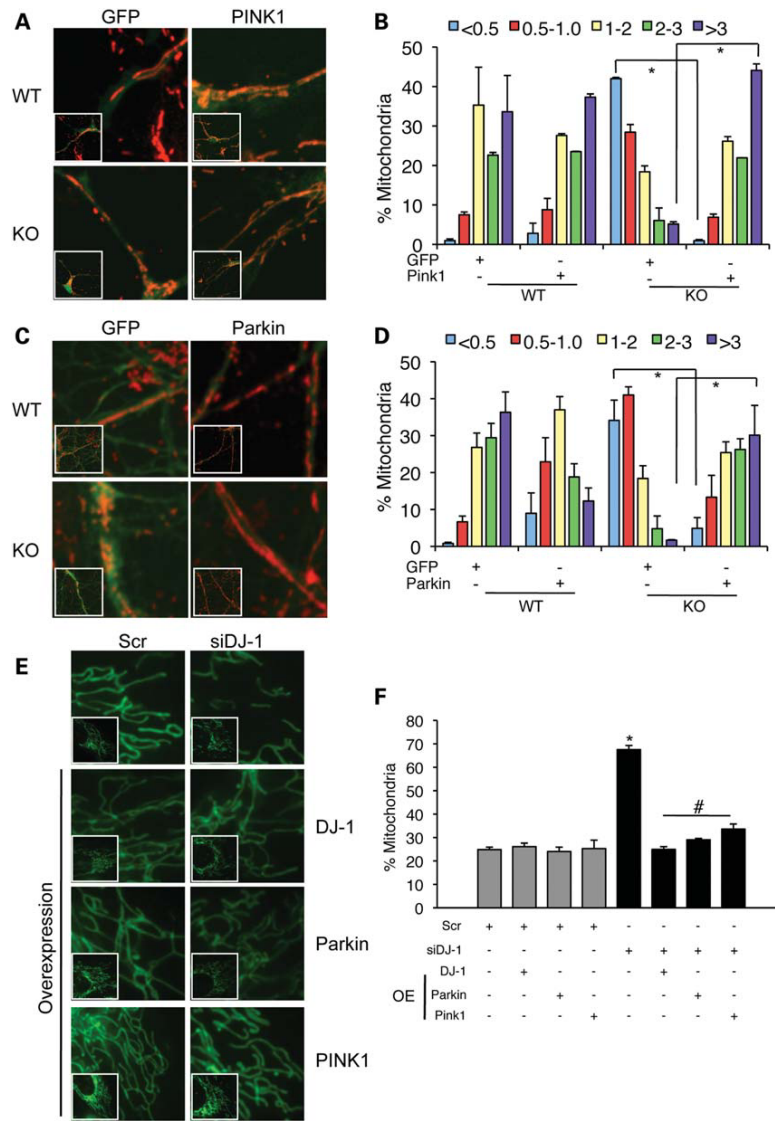


Figure 7. Rescue of mitochondrial morphology with Pink1 and Parkin in a DJ-1-deficient background. (A) Confocal images from WT and KO DJ-1 primary cortical neurons infected with GFP or GFP-PINK1 adenoviruses as described in Materials and Methods. Neurons were harvested and fixed 48 h post-infection and immunostained with antibodies to Tom20 (red) to visualize mitochondria. Inset: lower magnification images. (B) Quantification of mitochondrial lengths as described previously [Jahani-Asl *et al.* (20); $n = 3$ independent experiments with a minimum of 500 mitochondria/experiment that were counted per condition]. Scale bar = 5 μm . * $P < 0.05$ versus respective controls. (C) Confocal images from WT and KO DJ-1 primary cortical neurons infected with eGFP or eGFP-Parkin adeno-associated viruses as described in Materials and Methods. Neurons were harvested and fixed 4 days post-infection and immunostained with

of autophagy p62 and LC3-II levels in DJ-1^{-/-} mouse embryonic fibroblasts (MEFs) are decreased compared with DJ-1^{+/+} controls, indicating that the loss of DJ-1 results in a reduction in autophagosomes since levels of LC3-II correlate with autophagosome number (34,35). This reduction can either be attributed to the downregulation of autophagosome formation or enhanced autophagic degradation (34). The use of bafilomycin A1, a late inhibitor of autophagy (34), restores steady-state p62 as well as LC3-II protein levels suggesting that the loss of DJ-1 enhances autophagic degradation, in other words autophagic activity is overactive. Next, we made use of the H1299 cell line in which GFP-LC3 is stably expressed and transiently reduced DJ-1 protein levels via siRNA to confirm the DJ-1-dependent perturbations in the autophagic pathway. As shown in Figure 8B, at 48 h post-transfection, the level of DJ-1 was significantly reduced upon transfection of a siRNA specifically targeted to DJ-1. The effect of DJ-1 knockdown was accompanied by a significant decrease in p62 levels, and an increased accumulation of cleaved GFP demonstrating that autophagic activity is enhanced by transient knockdown of DJ-1 (Fig. 8B). This was further observed with immunofluorescence where GFP puncta formation was increased by 1.5-fold ($P < 0.05$) with transient knockdown of DJ-1 (Fig. 8C and D). Given the recent involvement of Parkin and PINK1 in the regulation of mitochondria specific autophagy (mitophagy), we also assessed the steady-state levels of mitochondrial markers to determine whether DJ-1 may also play a role. As shown in Figure 8E, loss of DJ-1 does not induce significantly altering the expression of *cytochrome c* oxidase (COX) subunits of complex I or complex V. Furthermore, expression of the outer mitochondrial membrane marker Tom20 was also unchanged. This suggests that mitophagy, at least at a gross level, is not affected by the loss of DJ-1. This theory is supported by initial observations that Parkin is not significantly recruited to mitochondria in DJ-1 KO cells under basal conditions (Joselin *et al.*, unpublished data).

Mitochondrial morphology and autophagy are also perturbed in human DJ-1-linked Parkinson's disease

Finally, to provide evidence that the DJ-1-dependent perturbations in mitochondrial homeostasis also extend to a human model of DJ-1-linked PD, we obtained human lymphoblasts isolated from control and PD patients. The PD lymphoblasts were obtained from an Italian and Dutch family, respectively (12). The previously described L166P pathogenic mutation found in the Italian family consists of a leucine to proline substitution at amino acid 166, while the Deletion (Del) mutation, found in a Dutch family, results from a complete loss of exons 1–5 (12). As shown in Figure 9A, similar to the pattern of

mitochondrial morphology observed in DJ-1^{+/+} and DJ-1^{-/-} murine tissues, electron microscopic analysis of lymphoblasts isolated from human PD patients (L166P, DEL) contained a greater percentage of fragmented mitochondria compared with control lymphoblasts (i.e. $< 0.5 \mu\text{m}$; $41.578 \pm 2.41\%$ and $48.316 \pm 6.02\%$ in PD versus $12.62 \pm 3.03\%$ and $9.755 \pm 2.23\%$ in controls) and a smaller percentage of mitochondria that were longer than $> 1.0 \mu\text{m}$ ($23.019 \pm 0.84\%$ and $23.997 \pm 0.94\%$ in PD versus $41.578 \pm 2.41\%$ and $48.316 \pm 6.02\%$ in controls; Fig. 9B). We also evaluated whether autophagy was similarly affected in human DJ-1-linked PD and observed that p62 was decreased in both PD patient cell lines when compared with CTRL lymphoblasts (Fig. 9C). These data confirm that the mitochondrial morphology as well as changes in autophagic markers observed in DJ-1^{+/+} and DJ-1^{-/-} are also present in human DJ-1-linked PD.

DISCUSSION

Mitochondrial dysfunction appears to contribute to the progression of sporadic PD and it has been postulated that excess ROS produced as the result of mitochondrial dysfunction may be an important reason for which neurons exhibit increased sensitivity to oxidative stress-induced neuronal cell death (36,37). Emerging evidence points to underlying defects in mitochondrial morphology and dynamics as a potential mechanism to explain this increased sensitivity (38). In PD, this relationship is significant since several PD-linked genes (DJ-1, Parkin, PINK1) have been found to reside or translocate to the mitochondrial compartments (7,8,29,39–42), participate in mitochondrial remodeling (7,9–11) and actively regulate mitochondrial quality control (18,19,41–43). Of the three PD-linked genes that have been associated with mitochondria, the least is known regarding the role of DJ-1.

Mitochondrial morphology, dynamics and ROS production are altered by the loss of DJ-1

We first began our investigation by characterizing the impact of DJ-1 deficiency on mitochondrial morphology and function under steady-state conditions in a variety of experimental systems. We demonstrated both *in vitro* and *in vivo* neuronal and non-neuronal cells, as well as in brain tissue that mitochondria are significantly more fragmented with the loss of DJ-1. Importantly, we also extended these findings to human DJ-1-linked PD to convincingly implicate that an aberrant DJ-1-dependent mitochondrial phenotype in a more disease relevant model. We also demonstrated that the mitochondrial phenotype produced by the loss of DJ-1 contributes to the

antibodies to Tom20 (red) to visualize mitochondria. Inset: lower magnification images. (D) Quantification of mitochondrial lengths as described previously [Jahani-Asl *et al.* (20); $n = 3$ independent experiments with a minimum of 500 mitochondria/experiment that were counted per condition]. Scale bar = $5 \mu\text{m}$. * $P < 0.05$ versus respective controls. (E) Confocal images from SH-5Y5Y cells in which DJ-1 has been knocked down via siRNA, and transfected with DJ-1, Parkin or PINK1 as described in the Materials and Methods. Inset: lower magnification images. (F) Quantification of at least 300 cells/condition was performed as described in the Materials and Methods. Data are representative of at least three independent experiments where each condition was done in triplicate. OE, overexpression. Scale bar = $5 \mu\text{m}$. * $P < 0.05$ versus siDJ-1- and [#] $P < 0.05$ versus siDJ-1.

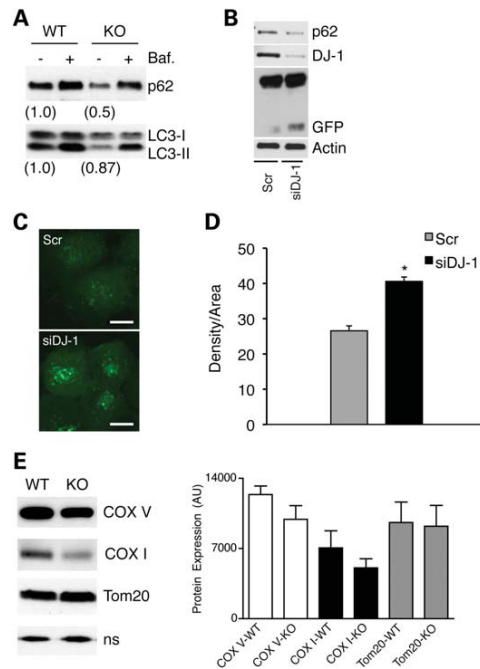


Figure 8. Cells deficient for DJ-1 undergo enhanced autophagic activity. (A) Proteins were extracted from WT and KO DJ-1 MEFs treated with (+) or without (-) Bafilomycin (10 μ g/ml, 3 h) and subjected to western blotting for p62 and LC3-I and LC3-II levels. Numbers below representative images refer to fold changes versus WT (-Baf) after correction for actin. Data are representative of three independent experiments. (B) Total cell lysates from H1299 cells stably expressing GFP-LC3 and transfected with either scrambled (Scr) or a siRNA against DJ-1 (siDJ-1) were analyzed by western blotting for DJ-1, p62 and free GFP. Data are representative of at least three independent experiments. (C) Confocal images of H1299 cells stably expressing GFP-LC3 cells transfected with either scrambled (Scr) or a siRNA against DJ-1 (siDJ-1). (D) The density of GFP puncta in Scr versus siDJ-1 conditions was analyzed in at least 150 cells/condition. Data are representative of three independent experiments. * $P < 0.05$, siDJ-1 versus Scr. control. Scale bar = 2 μ m. (E) Total cell lysates from DJ-1 WT and KO MEFs were subjected to western blotting for COX V, COX I and Tom20 levels (n.s., non-specific band was used as a loading control). Data are representative of five to seven independent experiments.

oxidative stress-induced sensitivity to cell death since reversal of the mitochondrial phenotype by overexpression of DN-Drp1 to rescue mitochondrial fragmentation abrogated neuronal cell death induced by MPP+. Is the fragmented phenotype a result of increased fission or decreased fusion? Since mitochondrial fusion rates and the steady state levels of the mitochondrial fusion protein MFN1 are decreased in DJ-1 deficient cells, we would be tempted to speculate that mitochondrial fusion is decreased. However, our results also do not rule out that an increase in mitochon-

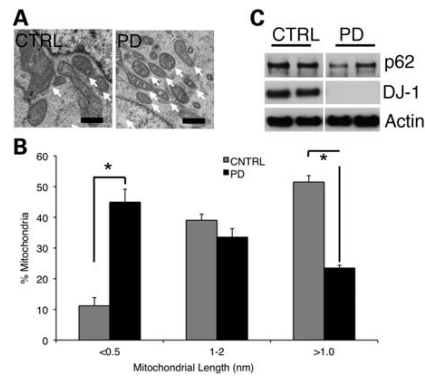


Figure 9. Mitochondrial morphology and autophagy are also perturbed in human DJ-1-linked PD. (A) EM images of mitochondria from human lymphoblasts isolated from healthy control (C48 and GEPa) and PD (L166P and Del) patients. (B) Quantification of mitochondrial diameters in human lymphoblasts ($n = 4$; at least 200 mitochondria/experiment were counted). Scale bar = 500 nm. * $P < 0.05$, PD versus control. (C) Total protein was extracted from human control (CTRL), and PD (L166P and Del) lymphoblasts were subjected to western blotting for DJ-1, p62 and actin. Data are quantified as the relative changes in steady state protein levels corrected for loading using actin. Five independent experiments are represented. * $P < 0.05$, PD versus control. White arrows in (A) depict mitochondria.

drial fission is also a possibility. Indeed, during the preparation of this manuscript, Krebseh *et al.* (44) demonstrated that altered mitochondrial morphology induced by the loss of DJ-1 could be attributed to changes in mitochondrial fission. The implications of decreased or increased mitochondrial fusion or fission that occurs with DJ-1 deficiency could readily explain the increased sensitivity of these cells to oxidative stress (14), as it is known that fragmented mitochondria precedes apoptosis, or alternatively renders mitochondria more susceptible to death-inducing stimuli (20,45–48).

ROS is important in establishing the DJ-1-dependent phenotype

Based on the known impact of excess ROS on mitochondrial morphology (23), we suspected that the increased ROS produced by mitochondria from DJ-1^{-/-} animals could be responsible for the fragmented phenotype. Indeed, we confirmed this hypothesis by first demonstrating that scavenging ROS with the use of NAC or WT DJ-1 (itself a suspected free radical scavenger), but not an oxidant mutant of DJ-1 (C106A), was able to rescue the fragmented phenotype observed in DJ-1 deficient primary cortical neurons. Our data also show that while the excess H₂O₂ produced within mitochondria by the loss of DJ-1 is sufficient to alter mitochondrial morphology, they are not produced in sufficient concentrations to cause overt changes in mitochondrial oxygen consumption and citrate synthase activity, at least in the

brain. In all likelihood, these factors contribute to the lack of any gross neuronal abnormalities including dopaminergic neuron numbers in the substantia nigra, fiber densities and dopamine levels in the striatum and the absence of any behavioral deficits in untreated DJ-1 deficient mice (14). It is therefore more likely that DJ-1 deficiency compromises the sub-cellular milieu rendering them more vulnerable to additional stress. Indeed, the observation that DJ-1 deficiency does not seem to grossly affect mitophagy leading to the accumulation, instead of the removal of fragmented mitochondria further adds to this possibility. This theory is also supported by initial observations that Parkin is not significantly recruited to mitochondria in DJ-1 KO cells under basal conditions (Joselin *et al.*, unpublished data).

Indeed, as we have previously demonstrated, DJ-1 deficient animals/cells are hypersensitive to MPTP or hydrogen peroxide treatment and this hypersensitization results in the previously described dopaminergic cell death and behavioral deficits, effectively recapitulating some pathological and clinical features of human PD (14).

Pink1 and Parkin can rescue DJ-1 deficient mitochondrial fragmentation

We also assessed the relationship of DJ-1 with Parkin and Pink1, two recessively linked PD genes, as they have all been implicated in regulating aspects of mitochondrial morphology and/or dynamics. Previous studies using the *Drosophila melanogaster* model have shown that the loss of Pink1 and Parkin independently compromise mitochondrial integrity (9,11,28,49). Since double mutants produce an identical phenotype to each mutant alone, and overexpression of Parkin rescues Pink1 deficits but not *vice versa*, it was postulated that they function in the same pathway with Pink1 positioned upstream of Parkin (9,11,28,49). More recently, it has been shown that Pink1 and Parkin actively participate in mitochondrial quality control (18,19,41–43). Given that DJ-1 deficiency induces oxidative stress and mitochondrial defects, we hypothesized that overexpression of these mitochondrial quality control factors would rescue the DJ-1 deficient mitochondrial phenotype. We confirmed this hypothesis using two different models. First, Pink1 and Parkin were overexpressed in DJ-1 deficient primary cortical neurons. In this model, overexpression of either Pink1 or Parkin rescued the fragmented mitochondrial phenotype in DJ-1 deficient cells. Second, we used a dopaminergic cell line to overexpress Pink1 and Parkin in cells where DJ-1 levels were reduced down by siRNA. Similar to our findings in primary cortical neurons, the DJ-1-induced fragmentation phenotype produced by knockdown of DJ-1 was reversed with overexpression of either Pink1 or Parkin. It is important to stress that the exact mechanistic link between DJ-1 and Pink/Parkin is not clear. However, we would propose that DJ-1 somehow modulates the actions or activity of Pink1 and/or Parkin, possibly via its effect on the ROS environment. Given the effects of Parkin and PINK1 deficiency on antioxidant capacity and ROS production (50–52), it is also tempting to speculate that overexpression of either gene could potentially ameliorate that ROS milieu of the DJ-1 deficient cells, thereby reversing

the fragmented phenotype. Alternatively, a more direct regulation is also possible.

DJ-1 deficiency increases autophagic activity

Increasing evidence has implicated several PD-linked genes including Pink and Parkin in the process of autophagy (18,19,41–43). Two recently published studies have now implicated DJ-1 (19,44). We also pursued this phenomenon in the present manuscript and suggest that the loss of DJ-1 promotes enhanced autophagy resulting in increased turnover. According to Mizushima and Yoshimori (34) and Rubinsztein *et al.* (35), a loss in the levels of the autophagy markers LC3-II and p62 at a given time is either attributed to a downregulation of autophagosome formation or enhanced degradation. If the level of LC3-II or p62 rises following incubation with autophagy inhibitors such as Bafilomycin A1, as was seen in the present study, it is considered that during the course of the experimental time frame that the number of molecules degraded exceeds the number being produced. We further assessed the effect of transient DJ-1 knockdown on autophagic activity and found that within 48 h of DJ-1 knockdown, the autophagy was increased, as measured by the decrease in p62 levels and the increase in LC3 puncta formation. It has previously been shown that following acute starvation, autophagy is increased and that prolonged starvation leads to excessive activity and turnover (35). Acute starvation led to decreased p62 levels and LC3 puncta formation, whereas a complete loss of LC3-II levels was observed during prolonged starvation. By analogy, one could interpret that acute DJ-1 knockdown results increase autophagic activity, while germline deletion is associated with excessive autophagic activity resulting in increased turnover. In either condition, autophagic activity is enhanced with DJ-1 deficiency. Future studies will more carefully evaluate the nature of this phenomenon. Additionally, whether DJ-1 more directly regulates the autophagic response or merely influences the ROS environment leading to increased flux is unknown and warrants further study. The evidence suggesting that ROS triggers autophagy would be in keeping with the latter suggestion (53–55). Furthermore, the idea that DJ-1 participates in the Pink1/Parkin pathway tentatively suggests the possibility that DJ-1 could modulate Pink1/Parkin activity and thereby regulate autophagic activity. Alternatively, DJ-1 may more directly regulate additional upstream activators of autophagy, including mTOR and AMPK, which has been suggested previously (19). More careful analyses will be required to validate these possibilities.

In conclusion, this study demonstrates that DJ-1 plays an active role in the remodeling of mitochondria and regulation of autophagy. Cells lacking DJ-1 display a fragmented mitochondrial morphology that can be rescued with ROS scavengers, wild-type DJ-1, Parkin and Pink1. This DJ-1-dependent mitochondrial morphology contributes to oxidative stress-induced sensitivity to cell death since reversal of this mitochondrial phenotype abrogates neuronal cell death. Finally, we also show that DJ deficiency leads to altered autophagy in DJ-1-deficient murine and human cells. We propose that under conditions of oxidative stress, these derangements may account for the reported increased sensitivity to cell death of DJ-1 deficient neurons.

MATERIALS AND METHODS

Antibodies

The following antibodies were used in this study: mouse anti-Drp-1 (BD Transduction), chicken anti-MFN1 (Novus Biological), rabbit anti-MFN2 (Santa Cruz), mouse anti-COX V (Mitosciences), mouse anti-COX I (Mitosciences), rabbit anti-Tom20 (Santa Cruz), rabbit anti-LC3 (Novus Biologicals), guinea pig anti-p62 (ARP), mouse anti-p62 (Santa Cruz), mouse anti DJ-1 (Stressgen), mouse anti-parkin mouse PRK8 (Santa Cruz), anti-PINK1 polyclonal antibody (Novus Biologicals), anti-DJ1 polyclonal antibody (Abcam), mouse anti- β -cactin (Sigma), horseradish peroxidase-conjugated secondary antibodies (Bio-Rad).

Cell lines, transfections, viral infections and plasmids

MEFs and primary cortical neurons were derived from E14.5–15.5 transgenic DJ-1 animals as previously described (14). Immortalized human lymphoblasts obtained from DJ-1-linked PD (Del or L166P) or healthy controls were cultured as described previously (56). H1299 cell line stably expressing GFP-LC3 cultured as previously described (57). SH-5Y5Y cells were cultivated as previously described (58). For RNA interference, SH-5Y5Y or H1299 cells were reverse-transfected with Stealth siRNA (Invitrogen) using Lipofectamine RNAiMAX (Invitrogen) or siRNA (Santa Cruz) using siLentFect (Bio-Rad), respectively, according to the manufacturer's instructions. *DNA Constructs (SH-5Y5Y cells)*: Human wild-type (wt) parkin and human wild-type PINK1 were described earlier (49,59). Human wild-type DJ was amplified from a human brain cDNA library and inserted into the pcDNA3.1 vector (Invitrogen). *Viral plasmids and infections (primary cortical neurons)*: for rescue studies, cortical neurons were harvested from DJ-1^{+/+} or DJ-1^{-/-} littermate embryos (produced by a heterozygote cross) at E15.5 and plated at a density of 150 000 cells per well (24-well dish) on glass cover slips coated with 1XPoly-D-Lysine. Viral particles expressing GFP, DJ-1, DJ-1 C106A, Pink1 or Parkin were administered at a multiplicity of infection (MOI) of 30 at the time of plating. Cortical neurons infected with DJ-1, DJ-1C106A and Pink1 were harvested 48 h following infection. Cortical neurons infected with Parkin were harvested 4 days post-infection and plating. For cell survival studies, cortical neurons harvested as described above were infected with either control (EGFP) adenovirus or dominant-negative Drp-1 (ECFP-C1 DLVP K38E) adenoviruses at MOI of 40 and then immediately seeded into 24-well plates at an approximate density of 350 000 neurons/well. Neurons were cultured for 3 days and then treated with 10 μ M MPP⁺ for 24 h.

Cell survival

Neuronal survival was evaluated by assessing nuclear integrity of GFP/CFP-positive neurons as done previously (14).

Citrate synthase activity

Maximal activity of citrate synthase (EC 4.1.3.7) was measured at 25°C in previously frozen homogenate and mitochondria from brain and skeletal as previously described (60).

Confocal microscopy/immunofluorescence/mitochondrial fusion rates

Confocal images were acquired with a 63 \times objective (1.4) by an inverted Laser Scanning Microscope (LSM510 META, Zeiss). Mitochondrial fusion rates were calculated as previously described (21).

Generation and genotyping of DJ-1 mice

The generation and genotype of the DJ-1 deficient mice has previously been described in detail (61).

H₂O₂ generation

Mitochondrial H₂O₂ production rate was determined in freshly isolated mitochondria from skeletal muscle and brain using the *p*-hydroxyphenylacetate (PHPA) fluorometric assay (62). Mitochondria (0.1 mg/ml) were incubated in standard incubation medium (IM: 120 mM KCl, 1 mM EGTA, 5 mM KH₂PO₄, 2 mM MgCl₂ and 3 mM HEPES; pH 7.4) supplemented with 0.3% defatted BSA. H₂O₂ production was monitored for up to 25 min using a temperature-controlled fluorimeter (BioTek, FLx800) at 37°C. Fluorescence readings were converted to H₂O₂ production rates by use of a standard curve.

Immunofluorescence (primary cortical neurons and MEFs)

Cortical neurons or MEFs were fixed with 4% PFA diluted in cell culture medium for 15 min at 37°C. Cells were then washed 3 \times with 1XPBS. Immediately following this, cells were permeabilized and blocked with 10% normal goat serum-0.1% Triton X/PBS for 1 h at room temperature. Cells were then stained with Tom-20 (1:100, a kind gift from Dr Gordon Shore or from Santa Cruz) or *cytochrome c* (1:100, BD Biosciences, in 5% normal goat serum overnight at 4°C) for the visualization of mitochondria. The following day, cells were washed 3 \times with 5% normal goat serum/PBS and then incubated for 1 h with the appropriate Alexa conjugated fluorophores in 5% normal goat serum/PBS. Cells were then washed 3 \times with 1XPBS, rinsed in sterile H₂O and mounted onto microscope slides using Gel Mount (Sigma).

Fluorescent staining of mitochondria and western blot analysis (SH-5Y5Y cells)

SH-5Y5Y cells were grown on 15 mm glass cover slips. Cells were fluorescently labeled with 0.1 μ M DiOC₆ (3) in cell culture medium for 15 min. After washing the cover slips with medium, living cells were analyzed for mitochondrial morphology by fluorescence microscopy using a Leica DMRB microscope (Leica, Wetzlar, Germany). Cells were categorized in two classes according to their mitochondrial morphology: tubular or fragmented. Cells displaying an intact network of tubular mitochondria were classified as tubular. When this network was disrupted and mitochondria appeared predominantly spherical or rod-like, they were classified as fragmented. The mitochondrial morphology of at least 300 cells per plate was determined in a blinded manner, i.e. the researcher was blind to the transfection status.

Quantifications were based on triplicates of at least three independent experiments. Proteins were analyzed by SDS-PAGE and western blotting using polyvinylidene difluoride membranes (Millipore, Schwalbach, Germany). The membranes were blocked with 5% non-fat dry milk in TBS containing 0.1% Tween 20 (TBS-T) for 1 h at room temperature and then incubated with the primary antibody in blocking solution for 16 h at 4°C. After extensive washing with TBS-T, the membranes were incubated with HRP-conjugated secondary antibody for 60 min at room temperature. Following washing with TBS-T, the antigen was detected with the enhanced chemiluminescence (ECL) detection system or ECL plus detection system (Amersham Biosciences, Freiburg, Germany).

Immunoblotting

Cell lysis was carried out identically for both MEFs and neurons. Cells were washed twice with PBS, scraped in lysis buffer containing 50 mM Tris-HCl pH 7.5, 100 mM NaCl, 0.4% Triton X-100, 1 mM DTT and 1× protease inhibitor cocktail (Roche). Samples were kept on ice for 20 min and then spun with maximal speed at 20 000g at 4°C for 5 min. Protein quantification was carried out using both Bradford (Bio-Rad) and BCA (Pierce) methods. Fifteen micrograms of each lysate was electrophoresed on 12% SDS-polyacrylamide gels, or 4–20% gradient gels (Invitrogen) and transferred to polyvinylidene fluoride (PVDF) or nitrocellulose membranes (Millipore). For tissue lysates, 15 µg of each tissue lysate was electrophoresed on 12% SDS-PAGE gels and transferred to polyvinylidene fluoride (PVDF) or nitrocellulose membranes (Millipore).

Isolation of mitochondria

DJ-1^{+/+} or DJ-1^{-/-} mice (4–6 months old) were euthanized by decapitation for isolation of skeletal muscle and brain mitochondria. Isolation of skeletal muscle mitochondria was performed using a modified method of Chappell and Perry (63), as previously described in detail (64). Brain mitochondria were isolated as described (50).

Lentivirus production and transduction

Lentiviral vectors were generated by transient transfection in 293T cells using PEI. The constructs for manufacturing the lentiviruses were obtained from Addgene.org. Protocols used to manufacture and purify lentiviruses were done according to Tronolab's protocols (www.tronolab.com).

Oxygen consumption

Oxygen consumption was measured in isolated brain mitochondria (0.3 mg/ml) at 37°C using a Clark-type oxygen electrode (Hansatech, Norfolk, UK), incubated in standard incubation medium (IM: 120 mM KCl, 1 mM EGTA, 5 mM KH₂PO₄, 2 mM MgCl₂ and 3 mM HEPES; pH 7.4) containing 0.3% defatted BSA and assumed to contain 406 nmol O/ml at 37°C (65). State 3 (maximum phosphorylating) respiration was determined using 5 mM glutamate/5 mM malate as substrate, and 500 µM ADP. State 4 (non-phosphorylating or

maximal leak-dependent respiration) was determined following addition of oligomycin (8 µg/ml). All measurements were performed in duplicate.

Statistical analyses

Unless otherwise described, data analysis was carried out using independent two-tailed *t*-tests. Significance was marked by * when *P* < 0.05. All data are presented as means ± SEM.

SUPPLEMENTARY MATERIAL

Supplementary Material is available at *HMG* online.

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Conflict of Interest statement. None declared.

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Progressive dopaminergic cell loss with unilateral-to-bilateral progression in a genetic model of Parkinson disease

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DJ-1 mutations cause autosomal recessive early-onset Parkinson disease (PD). We report a model of PD pathology: the DJ1-C57 mouse. A subset of DJ-1-nullizygous mice, when fully backcrossed to a C57BL/6J background, display dramatic early-onset unilateral loss of dopaminergic (DA) neurons in their *substantia nigra pars compacta*, progressing to bilateral degeneration of the nigrostriatal axis with aging. In addition, these mice exhibit age-dependent bilateral degeneration at the *locus ceruleus* nucleus and display mild motor behavior deficits at aged time points. These findings effectively recapitulate the early stages of PD. Therefore, the DJ1-C57 mouse provides a tool to study the preclinical aspects of neurodegeneration. Importantly, by exome sequencing, we identify candidate modifying genes that segregate with the phenotype, providing potentially critical clues into how certain genes may influence the penetrance of DJ-1-related degeneration in mice.

animal model | PARK7 | neuritic beading | neuronal death | neuroinflammation

Parkinson disease (PD) is a progressive neurodegenerative disorder with complex symptomatology and etiology affecting an ever-increasing number of individuals. Although multifactorial in nature, increasing insight has been gained with regard to the pathogenesis of PD through investigation of genes linked to the disease. Because monogenic forms of PD can be modeled in a laboratory, numerous animal models have been created to recapitulate the disease. For instance, loss-of-function mutations in the *DJ-1* (*PARK7*) gene cause early-onset autosomal recessive PD (1, 2). Patients harboring *DJ-1* mutations exhibit certain key characteristics principally in early-onset PD and may lack certain neuropathological attributes present in sporadic PD cases such as Lewy bodies (LBs) (3). However, generation of DJ-1-nullizygous mice (*DJ-1*^{-/-}) on mixed background by various laboratories, including our own, failed to detect any basal levels of neurodegeneration even in aged mice (4–11) (see Table S1). Similarly, a number of PD-related, genetically manipulated mice have been created in attempts to recapitulate the disease process, whereas little or none has shown clear or robust neurodegeneration specific to the *substantia nigra pars compacta* (SNc) (reviewed in ref. 12). Therefore, the creation of murine PD models that demonstrate significant dopaminergic (DA) loss remains an acute need in the field. The need for an early-onset model of PD is made more pressing given that no postmortem analyses of human DJ-1 mutant-carrying patients have been reported. This is particularly critical if we are to understand how specific signaling pathways govern DA loss in monogenic forms of early-onset human PD. Presently, most mechanistic studies of DA loss rely on acute toxin models of Parkinsonism. However, the relevance of such studies to the human condition remains uncertain, because acute neurotoxins are rarely the culprit in the majority of PD cases. This potential discrepancy is highlighted by

a number of failed clinical trials that have heavily relied on toxin models as preclinical evidence for efficacy (13–16). A more representative model of DA loss that uses known factors in human PD is likely vital to develop better therapeutic outcomes.

Results

In the course of our studies examining the effects of environmental perturbations in *DJ-1*^{-/-} mice, we continued to examine the long-term effects of DJ-1 deficiency on DA neuron loss. Importantly, this was accomplished in animals completely backcrossed onto a C57BL/6J background (14× backcrossed, *DJ-1*^{-/-}; herein, referred to as DJ1-C57). Intriguingly, unilateral SNc degeneration in a subset of these DJ1-C57 knockout mice is observed as early as 2 mo of age (Fig. 1A, Fig. S1, and Table S2). This phenotype is not observed in animals younger than 2 mo ($n = 8$; Fig. S1), thus indicating that this defect is unlikely to be developmental in origin. Moreover, this phenotype is not observed in any of the wild-type (WT) mice examined ($n = 71$). In addition, the ventral tegmental area (VTA) of these mice is mostly spared (Fig. 1D). This latter finding is particularly interesting given the observation that in postmortem brains from PD patients, VTA neurons remain relatively protected compared with their nigral counterparts (17).

To objectively assess this phenotype, mice in this study are classified as either “affected” (unilateral phenotype: having a greater than 40% unilateral reduction of DA cells in the SNc compared with the other side) or “unaffected” (no unilateral phenotype: having similar bilateral DA cell numbers). No clear side or sex specificity is observed (right, 53%; female, 67%, respectively). Thus, to maintain consistency, “side A” is the term given for the side of the brain with the least number of neurons, regardless of the genotype (side B being the side with more DA neurons). When quantified, affected DJ1-C57 mice exhibit a dramatic reduction of neurons in their SNc, as visualized by tyrosine hydroxylase (TH) and cresyl violet (CV) staining (Fig. 1B and C and see Fig. 3A). Upon closer magnification of the SNc, the affected DJ1-C57 mice exhibit TH-positive fiber

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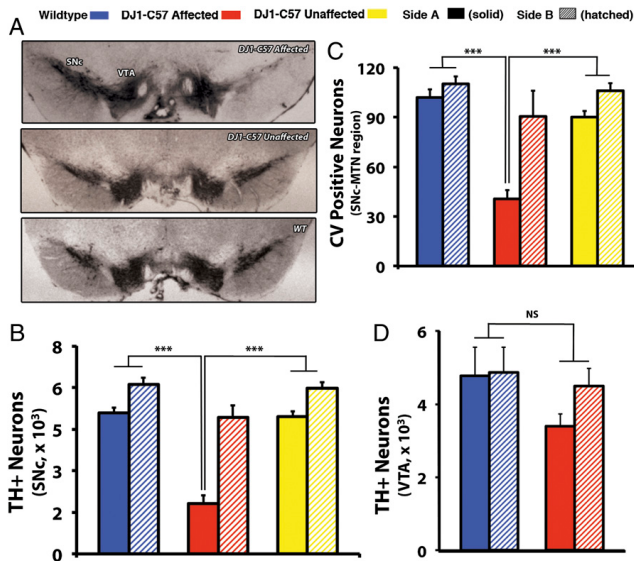


Fig. 1. Young affected DJ1-C57 mice exhibit selective unilateral degeneration in their SNc. (A) Representative midbrain sections of DJ1-C57 affected (Top), DJ1-C57 Unaffected (Middle), and WT (Bottom) mice depicting TH staining in the SNc and VTA. (B and C) Quantification of A by stereology of total number of TH-positive cells in the SNc (B) and of CV-stained cells at the level of the MTN in the SNc (C). (D) Quantification of TH-positive neurons in the VTA of WT and DJ1-C57 affected mice. Note that WT, DJ1-C57 affected and DJ1-C57 unaffected are represented by blue, red, and yellow bars, respectively. Side A is depicted as solid shading and side B as hatched shading. NS, not significant ($P > 0.05$); *** $P < 0.001$; ANOVA, followed by Tukey's LSD post hoc tests. Data are represented as means ($n = 7-80$ per group) \pm SEM.

staining but with clear neuronal process disruption. When quantified, the remaining fibers at the level of the SNc in the affected DJ1-C57 mice display an elevated number of shortened processes with obvious neuritic beading (Fig. 2A) compared with unaffected DJ1-C57 or control mice. Consistent with this finding, an increase in CD11b-positive microglia is noted in young, affected animals (Fig. 3B), whereas no clear increase in astrogliosis on the affected side is observed (Fig. S2).

To assess whether this histopathological phenotype corresponds with a functional outcome, we subjected animals to behavioral testing. However, DJ1-C57 affected mice do not exhibit a clear decrease in gross motor function at 2, 6, or 12 mo of age (Fig. S3 A-C) or any differences in drug-induced rotational behavior (Fig. S3D). The lack of behavioral differences may be accounted for by two observations. First, examination of the striatal DA terminals revealed no clear loss in striatal fibers in young animals (Fig. 2B). This finding raised the possibility that sprouting of neurites within the nigrostriatal pathway may be compensatory in young mice. This is of marked interest because we note significant sprouting of dysmorphic neurites (as seen in Fig. 2A) in the SNc, which may be compensating for the loss of cell bodies as reported previously (18, 19). Second, an increase in the striatal postsynaptic marker Δ FBJ murine osteosarcoma viral oncogene homolog B (Δ FosB) is observed in affected DJ1-C57 mice (Fig. 2C). PD patients have been shown to have up-regulated Δ FosB in their caudate/putamen (20). Moreover, Δ FosB has been shown previously to be up-regulated in toxin models of neurodegeneration such as 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) and 6-hydroxydopamine (6-OHDA) as a compensatory response to a loss of DA innervation (21, 22).

With aging of DJ1-deficient animals, an increase in the prevalence of the DJ1-C57 affected unilateral phenotype was observed over time, peaking at 12 mo of age (42.9% penetrance, Fig. 4A and Table S2). When only affected unilateral DJ1-C57 animals are considered, there was a clear loss in total number of SNc DA neurons even at early time points (Fig. S4). However, if all (affected and unaffected) DJ1-deficient animals were

evaluated together, the total number of DA neurons was not significantly reduced until later aging stages (15 mo). At this time, the unilateral phenotype dissipated and a more bilateral phenotype of nerve cell loss was observed (Fig. 4A and B and Table S2). Interestingly, these aged mice, unlike at the earlier times, exhibited a decrease in DA-synthesizing TH-positive striatal terminals (Fig. 4C). Upon evaluation of any neuritic beading in these aged animals, we noted that although process length itself did not further change between young and aged DJ1-C57 mice (Fig. S5 A and B), aged DJ1-C57 mice exhibited a decreased number of sprouting processes in the SNc region (Fig. S5C). Moreover, long-term behavior testing revealed a mild motor defect in the aged (14-16 mo) DJ1-C57 mice when examined by both the grid test (Fig. 4E) and the pole test (males; Fig. 4F).

The neuropathology of PD encompasses degeneration not only of the SNc but also of other nuclei in the brainstem including the *locus ceruleus* (LC) (23). Therefore, LC of DJ1-C57 mice were examined for TH-immunoreactive cell bodies. A significant reduction in TH-positive cells of the LC was observed in aged DJ1-C57 mice compared with WT controls (Fig. 4D). Furthermore, because α -synuclein aberrant processing is a hallmark of idiopathic PD, we examined whether our DJ1-C57 mice exhibited altered expression or localization of the protein. No visible changes were noted in the expression of endogenous α -synuclein between DJ1-C57 mice and littermate controls (Fig. S6 A and B). In addition, upon examination of leucine-rich repeat kinase 2 (LRRK2) expression (another autosomal dominant PD-linked protein), we did not note any significant changes in expression or localization of the protein (Fig. S6B).

Finally, to elucidate potential mechanism(s) through which this selective neurodegeneration occurs in a subset of these DJ1-C57 mice, we performed whole-exome sequencing on affected ($n = 3$) and unaffected ($n = 3$) DJ1-C57 mice as an approach to identify candidate modifiers (Fig. 5A). After filtering for coding regions and for variants found in all three affected but none of the three unaffected mice, only five candidates in coding regions were

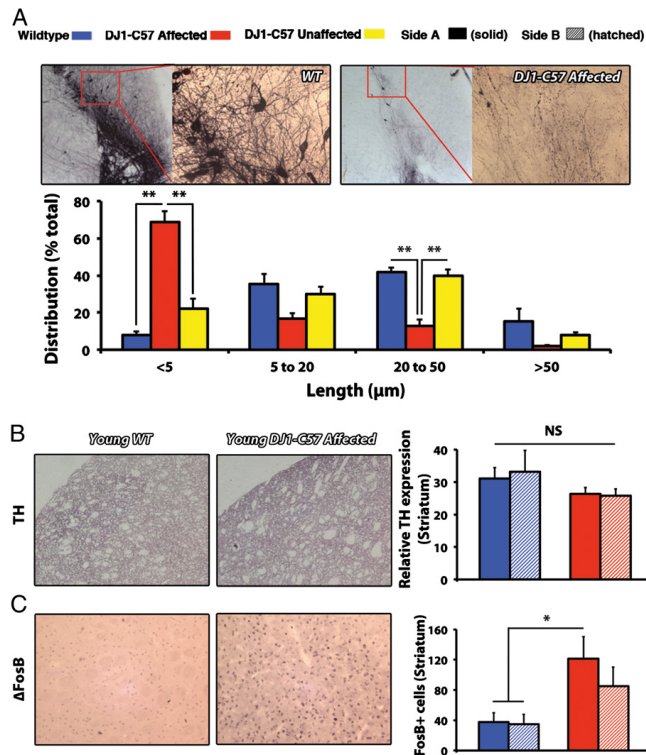


Fig. 2. Widespread process disruption and aberrant striatal innervation in young affected DJ1-C57 mice. (A) Fiber sprouting in WT (Upper Left) and DJ1-C57 affected animals (Upper Right). Distribution of quantified uninterrupted process (TH⁺) length in a single vision plain (in microns) is presented (Lower). (B) Representative sections of striatum stained for ΔFosB in young WT (Left) and DJ1-C57 affected (Center) mice. (Right) Quantification of ΔFosB-positive puncta in the striatum. (C) Representative sections of the striatum stained for TH as in B. Quantification of striatal TH density is shown (Right). WT, DJ1-C57 affected, and DJ1-C57 unaffected are represented by blue, red, and yellow bars, respectively. Side A is depicted as solid shading and side B as hatched shading. NS, not significant ($P > 0.05$); * $P < 0.05$; ** $P < 0.01$; ANOVA, followed by Tukey's LSD post hoc tests. Data are represented as means ($n = 3-11$ per group) \pm SEM.

identified as potential modifiers of the phenotype [signal regulatory protein β (Sirpb)1A, 2610203C20Rik, zinc finger, SWIM domain containing 6 (Zswim6), kinesin family member (Kif) C5b, and SWI5-dependent recombination repair 1 (Sfr1); Fig. 5B]. Moreover, because exome sequencing also covers flanking intronic sequences, an additional 23 candidates were identified in non-coding regions (Table S3), although none of these were in known intron-exon splice sites. Together, these results suggest the segregation of several genomic loci with the phenotype.

Discussion

In our DJ1-C57 mice, we have uncovered an early PD-type phenotype that progressed with age and showed incomplete penetrance. In backcrossing and extensively interbreeding DJ1-null mice, we obtained a subset of DJ1-C57 mice that exhibited robust unilateral nigral degeneration as early as 8 wk of age: a finding potentially consistent with the early-onset pathogenicity of DJ1 loss in human carriers of DJ1 mutations (1). This cell loss was accompanied with compensatory sprouting and the appearance of dysmorphic and beading neurites, as well as microgliosis, a result congruent with the notion that microglia may induce neuritic

beading during neuronal dysfunction (24). Furthermore, findings of compensatory sprouting upon cell loss, dysmorphic neurites, and an increase in proinflammatory responses are all present in postmortem samples from PD patients (25-30). Therefore, given the early age of onset of degeneration in these mice, our findings are of particular significance and may correlate with features of autosomal recessive PD. This loss-of-function phenotype has not yet been modeled successfully in rodents, with the possible exception of a partial reduction in LC neurons in one *parkin*^{-/-} mouse model (31).

We also noted that although DJ1 loss-mediated neurodegeneration will invariably lead to PD in humans, this might not be as dramatic in mice with a relatively short lifespan of ~24 mo. However, early pathological changes associated with this genetic form of PD are nonetheless observed. Thus, much like preclinical PD, where no clear clinicopathological correlate may be apparent until over 80% of the nigral cell population has been lost, a compensatory mechanism such as neuritic sprouting or postsynaptic sensitization may account for the lack of motor defects in these young animals. Furthermore, the relevance of this model is made even more apparent as the DJ1-C57 mice

A

Genomic DNA isolation from affected/unaffected DJ1-C57 → Targeted Exome Capture (Agilent SureSelect⁺) → Illumina HiSeq2000 Paired end sequencing (2x100bp) → Alignment (C57BL/6J genome) → Variant Calling (Genome Analysis Toolkit) → Identify Putative Mutations: Segregation by Group

B

Gene name	Gene description	Position	Chromosome	Mutation type	Codon	Effect	Amino Acid	Function	Presence	
									Affected (/3)	Unaffected (/3)
<i>Sirpb1a</i>	signal-regulatory protein beta 1A	15,417,016	3	SNP	tCc/ATc	Missense Mutation	S84F	Phagocytosis	3	0
<i>Sirpb1a</i>	signal-regulatory protein beta 1A	15,417,020	3	SNP	CaT/Tat	Missense Mutation	H83Y	Phagocytosis	3	0
2610203C20Rik	RIKEN cDNA 2610203C20 gene	41,389,287	9	SNP	Acc/Ccc	Missense Mutation	T59P	Unknown	3	0
2610203C20Rik	RIKEN cDNA 2610203C20 gene	41,389,294	9	SNP	cAc/cCc	Missense Mutation	H61P	Unknown	3	0
<i>Zswim6</i>	zinc finger, SWIM domain containing 6	108,679,774	13	SNP	gCg/gGg	Missense Mutation	A157G	Unknown	3	0
<i>Kifc5b</i>	kinesin family member CSB	27,061,155	17	SNP	Gtc/Atc	Missense Mutation	V319I	Chromosomal segregation	3	0
<i>Sfr1</i>	SWI5 dependent recombination repair 1	47,807,383	19	SNP	Ccc/Acc	Missense Mutation	P93T	DNA recombination	3	0

Fig. 5. List of exonic variants unique to affected DJ1-C57 mice. (A) Schematic workflow of exome sequencing to determine candidate mutations in affected DJ1-C57 mice (vs. unaffected littermate controls). (B) Table of variants present in all three examined affected animals and no unaffected littermates. See *Experimental Procedures* for selection criteria.

exons. In this regard, we observed that 23 intronic modifiers segregated with the phenotype. The specific role of these polymorphisms/indels remains unclear, because they do not correspond to splice donor/acceptor sites. Finally, it is possible that a combination of all of these factors may contribute to the phenotype. Therefore, more careful analyses must be performed to examine among these possibilities. What is important, however, is that our studies demonstrate that a defined group of polymorphisms can segregate with our phenotype. How these factors regulate DA loss in DJ1-deficient mice will require further analyses.

Collectively, we present a murine model that reproduces a clinically detectable phenotype owing to the modification of a PD-related gene. Affected DJ1-C57 mice display: (i) unilateral DA cell loss with a predilection for the SNc versus VTA as early as 2 mo of age; (ii) development of aberrant neuritic processes with ensuing microgliosis in the SNc and increased Δ FosB staining in the striatum at a young age; and (iii) progression to bilateral degeneration of the nigrostriatal axis and of the LC at an older age (model; Fig. 6), which are associated with mild motoric changes. This progression to a bilateral phenotype is of particular interest to us given the typical unilateral-to-bilateral progression of the disease in humans (33). Interestingly, no significant changes were noted in α -synuclein or LRRK2 expression, suggesting a disease process independent of Lewy body generation. These results strongly suggest that this murine model of early parkinsonism mimics autosomal recessive early-onset PD pathology, rather than that of sporadic PD (3). It, thus, provides a tool to elucidate the cascade of pathogenic changes that occurs in autosomal recessive, early-onset PD, as well as a platform to explore neuroprotective interventions in the future.

Experimental Procedures

DJ1-C57 Mouse Creation. DJ1^{-/-} mice were generated as described previously (9). Mice were subsequently backcrossed 14 times onto a pure C57BL/6J background (Charles River) to obtain DJ1-C57 mice. Animals were then interbred extensively for colony maintenance and experimentation. Animals were kept at 25 °C on a light (12 h)/dark (12 h) cycle with ad libitum access to standard rodent laboratory chow and water. Animal care was carried out in accordance with the guidelines of the Canadian Council and Care of Animals in Research and the Canadian Institutes of Health Research and was approved by the University of Ottawa Animal Care Veterinary Services.

Histology. After being perfused transcardially, mouse brains were fixed in 4% paraformaldehyde and cryoprotected as described elsewhere (34). Midbrain sections containing the SNc (40 μ m), pontine sections containing LC (40 μ m), and striatal (14 μ m) sections were immunostained via avidin-biotin complex staining as described previously (26).

DA Cell Survival Quantification. DA neuron survival in the SNc was blindly assessed by stereology using Stereo Investigator as described previously (26). Striatal TH quantification was performed at 200 \times . For each picture, five samples of striatum and one sample of corpus callosum were used for densitometric analysis. Relative intensity of immunodetection was calculated using ImageJ v.1.41o (National Institutes of Health). For each sample, three slices of striatum were used to calculate the mean striatal density.

Neuritic Beading Measurement. Neuritic beading was measured using ImageJ. Briefly, average length of uninterrupted process in a visually focused plane

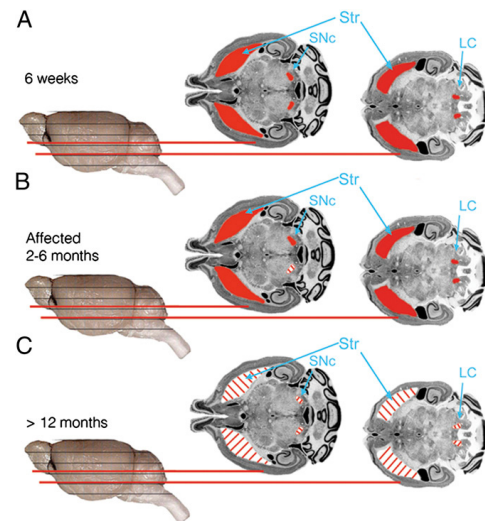


Fig. 6. DJ1-C57 preclinical model of DA neurodegeneration. (A) Altered representative micrographs reproduced with permission from the Mouse Brain Library [www.mbl.org; Rosen et al. (36)] depicting healthy (red) SNc, striatum, and LC in 6-wk-old DJ1-C57 mice or all WT groups examined. (B) Affected DJ1-C57 mice demonstrate unilateral DA cell loss in the SNc but not in the LC. (C) Aged DJ1-C57 mice exhibit widespread degeneration in their nigrostriatal tract, as well as their LC.

was measured as 20 measurements/section and measuring three sections per animal. Raw data were then binned into five categories of length and represented as percentage distribution.

ΔFosB and CD11b Measurement. Striatal (ΔFosB) and midbrain [cluster of differentiation (CD)11b] sections were stained, and three pictures were taken per animal, per side. Puncta in a given visual field were assessed blindly using ImageJ v1.41o.

Locus Coeruleus Neuron Quantification. Noradrenergic cell survival in the LC was measured by counting four representative sections and projecting their counts to a total value as described previously (35).

CV Quantification. CV staining and quantification were performed as described previously (26). Briefly, cell viability in the medial terminal nucleus (MTN) region of the midbrain was assessed as per the nuclear integrity of the cells present.

Antibodies Used. CD11b (1:200; AbD Serotec), FosB (1:250; Santa Cruz Biotechnologies), glial fibrillary acidic protein (GFAP) (1:1,000; Cell Signaling), DJ-1 (1:50,000; Abcam), α-synuclein (1:1,000; BD Transduction), LRRK2 (1:50,000; Epitomics), and TH (1:10,000; Immunostar or 1:2,000; Chemicon) were used for either avidin-biotin complex (ABC) visualization by 3,3'-diaminobenzidine (DAB) or via fluorophore-conjugated secondary antibody.

Motor Behavior Testing. The grid test was carried out by placing DJ1-C57 affected, unaffected, and WT mice on a metal grid (0.5-cm spacing between metal wires) and then turning the grid over for 60 s. If a mouse could hold on for the entire 60 s, it was scored as "success," whereas if it fell before the set time, it was scored as a "fail." The pole test was used to measure the latency to descent an 18-inch pole wrapped in gauze.

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Exome Sequencing. Genomic DNA (6 μg) was isolated from ear samples of affected/unaffected mice using the DNeasy Blood and Tissue kit (Qiagen). Samples underwent targeted exome capture using the Agilent SureSelectXT Mouse All Exon kit and subsequently underwent next-generation sequencing via an Illumina HiSeq 2000 sequencer. Raw data were aligned to the mouse genome, and variants were called using the Broad Institute GATK (Genome Analysis Toolkit).

Statistical Analysis. Data throughout the paper are expressed as averages ± SEM for a given sample size (n). Statistical analysis for histological and behavioral data were performed by means of either a paired t test or one-way ANOVA, followed by Tukey's least significant difference (LSD) post hoc test, as indicated in *SI Text* and the figure legends.

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