### Kinase-Based Regulation of Fast Axonal Transport in Health and Disease

ΒY

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### THESIS

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I dedicate this thesis to my mother, Sunja Oh, who sacrificed everything to support me in every possible way and without whom it would have never been accomplished.

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MK

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### **Contribution of Authors**

Parts of the work presented in **Chapter I** and **Chapter II** have been adapted from a previously published manuscript featuring the author of this thesis as its first author. The contributions of each author are described below.

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## LIST OF ABBREVIATIONS

AD	Alzheimer's disease
Akt	Protein kinase B
ALS	Amyotrophic lateral sclerosis
AMPA	$\alpha$ -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid
ANOVA	Analysis of variance
aPKC	Atypical protein kinase C
ARPP-16	cAMP-regulated phosphoprotein 16
ARPP-21	cAMP-regulated phosphoprotein 21
ASO	Antisense oligonucleotide
ATC	Axon terminal compartment
ATP	Adenosine triphosphate
Ax	Axonal compartment
BCA	Bicinchoninic acid
BDNF	Brain-derived neurotrophic factor
BICD1/2	Bicaudal 1/2
Ca2⁺	Calcium ion
CAMK	Ca <sup>2+</sup> /calmodulin- dependent protein kinase
CCD	Charge-coupled device
CDyn	Cytoplasmic dynein
CI	Confidence interval
CIPN	Chemotherapy-induced peripheral neuropathy

CK2	Casein kinase 2
CNTF	Ciliary neurotrophic factor
CO <sub>2</sub>	Carbon dioxide
cPKC	Conventional kinesin
CRIB	Cdc42- and Rac-interactive binding
CSK	C-terminal Src kinase
DAG	Diacylglycerol
DARPP-32	Dopamine- and cAMP-regulated phosphoprotein 32kDa
DHC	Dynein heavy chain
DIC	Dynein intermediate chain
DIV	Days in vitro
DLC	Dynein light chain
DLIC	Dynein light intermediate chain
DMEM	Dulbecco's modified eagle medium
Drp1	Dynamin-related protein 1
DTI	Diffusion tensor imaging
DTT	Dithiothreitol
EDTA	Etyhlendiaminetetraacetic acid
EGF	Epithelial growth factor
ERK	Extraceullar signal-regulated kinase
FANTOM5	Functional Annotation of the Mammalian Genome 5 project
FAT	Fast axonal transport

FBS	Fetal bovine serum
FGF	Fibroblast growth factor
Fis1	Mitochondrial fission 1
FRET	Förster resonance energy transfer
GABA	gamma-Aminobutyric acid
GAPDH	Glyceraldehyde 3-phosphate dehydrogenase
GDNF	Glial cell-derived neurotrophic factor
GDP	Guanosine diphosphate
GEF	Guanine nucleotide exchange factor
GPe	External globus pallidus
GPi	Internal globus pallidus
Grb2	Growth factor receptor-bound protein 2
GSK3β	Glycogen synthase kinase 3 beta
GST	Glutathione S-transferase
GTEx	Genotype-Tissue Expression project
GTP	Guanosine triphosphate
HCI	Hydrochloric acid
HD	Huntington's disease
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
HIP1	Huntingtin-interacting protein 1
HIV	Human immunodeficiency virus
HPA	Human Protein Atlas project

Htt	Huntingtin
IL-11	Interleukin 11
IL-6	Interleukin 6
IP3	Inositol triophosphate
JNK1/2/3	c-Jun N-terminal kinase 1/2/3
K•Aspartate	Potassium aspartate
КНС	Kinesin heavy chain
KLC	Kinesin light chain
L-Z	Leucine zipper
Lis1	Lissencephaly 1
Μ	Mean
MAPK	Mitogen-activated protein kinase
MAPKK	Mitogen-activated protein kinase kinase
MAPKKK	Mitogen-activated protein kinase kinase kinase
МВО	Membrane-bound organelle
MEK	Extracellular signal-regulated kinase kinase
МеОН	Methanol
MFC	Microfluidic chamber
Mfn1/2	Mitofusin 1/2
MgCl <sub>2</sub>	Magnesium chloride
mHtt	Mutant huntingtin
MKK7	Mitogen-activated protein kinase kinase 7

MLK	Mixed-lineage kinase
MOPS	3-(N-morpholino)propanesulfonic acid
MPP+	1-methyl-4-phenylpyridinium
MSN	Medium spiny neuron
МТ	Microtubule
n.a.	Numerical aperture
Na₃VO₄	Sodium orthovanadate
NaCl	Sodium chloride
NaF	Sodium floride
Ndel1	Nuclear distribution protein nudE-like 1
NGF	Nerve growth factor
NIR	Near-infrared imaging
NMDA	N-methyl-D-aspartate
nPKC	Novel protein kinase C
NT-3	Neurotrophin 3
NT-4/5	Neurotrophin 4/5
р75 <sup>NTR</sup>	Neurotrophin receptor p75
PAGE	Polyacrylamide gel electrophoresis
PD	Parkinson's disease
PDK1	Phosphoinositide-dependent kinase
Phos-Tag	Phosphate-binding tag
PI3K	Phosphoinositide 3 kinsae

PIS	Post-immunoprecipitation supernatant
PKC	Protein kinase C
PKD1	Protein kinase D1
ΡLCγ	Phospholipase C gamma
PMA	Phorbol 12-myistate 13-acetate
polyQ	Polyglutamine
PRD	Proline-rich domain
PSD-95	Postsynaptic density 95
PVDF	Polyvinylidene difluoride
QD	Quantum-dot
rpm	Rotation per minute
RTK	Receptor tyrosine kinase
SD	Standard deviation
SDC	Somatodendritic compartment
SDS	Sodium dodecyl sulfate
SFK	Src family kinase
SH2	Src homology 2
SH3	Src homology 3
SN	Substantia nigra
SOD1	Superoxide dismutase 1
Sos	Son of sevenless
TBS	Tris-buffered saline

TBS-T	Tris-buffered saline with tween-20
TEMED	Tetramethylethylenediamine
TGF-β	Transforming growth factor beta
тн	Tyrosine hydroxylase
TrkA/B/C	Tropomyosin A/B/C
UIC	University of Illinois at Chicago
VEC-DIC	Video-enhanced contrast differential interference contrast
VEGF	Vascular endothelial growth factor
YFP	Yellow fluorescent protein
Zn <sup>2+</sup>	Zinc ion

#### SUMMARY

Neurons have unique morphologies with distinct intracellular compartments responsible for particular functions. The most essential function of neurons is to receive information from and deliver to other cells by electrochemical connections at the synapses. Synthesis and post-translational processing of proteins required for proper activity and maintenance of neuronal connections occur in the neuronal soma, and synthesized proteins must be transported to the site of utilization by microtubule-based molecular motor proteins conventional kinesin and cytoplasmic dynein, a process referred to as fast axonal transport. Defective fast axonal transport lead to neurodegeneration, and impairments fast axonal transport have been found in several neurodegenerative diseases such as Alzheimer's disease, Huntington's disease, and amyotrophic lateral sclerosis. Phosphorylation of motor proteins represents a major regulatory mechanism of fast axonal transport, and a body of evidence accumulated from decades of research in our lab demonstrated that aberrant kinase signaling in neurodegenerative diseases lead to abnormal phosphorylation of motor proteins and impairments in fast axonal transport. This work extends our understanding of kinase signaling-based regulation of axonal transport in both pathological and non-pathological conditions.

**Chapter I** provides an overview of axonal transport machineries, previous work describing the regulation of axonal transport, and examples of neurodegenerative disease featuring impaired axonal transport. **Chapter II** describes amelioration of Huntington's disease pathology by genetic deletion of c-Jun N-terminal kinase 3 (JNK3), a kinase our lab previously identified to be mediating the axonal transport defects in Huntington's disease, in R6/2 mouse model of Huntington's disease, which highlights therapeutic

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potentials of maintaining intact fast axonal transport by correcting aberrant kinase signaling. Work presented in **Chapter III** demonstrates identification of a novel signaling cascade involving tropomyosin receptor kinase B (TrkB), Src family kinases (SFKs), and protein kinase D1 (PKD1) that activates retrograde axonal transport upon neurotrophin signaling by phosphorylation of intermediate chain subunit of cytoplasmic dynein. Finally, **Chapter IV** discusses the conclusions that can be drawn from this work and their implications for future research.

#### **CHAPTER I**

#### I. Introduction

Parts of this chapter were adapted from previously published work with the permission from the publisher. The citation for the published manuscript is as follows:

Minsu Kang, Lisa Baker, Yuyu Song, Scott T. Brady, Gerardo Morfini. Biochemical analysis of axon-specific phosphorylation events using isolated squid axoplasms. Methods in Cell Biology. 2016;131:199-216. doi: 10.1016/bs.mcb.2015.06.003 Epub 2015 Sep 2.

#### 1.1 Background

#### 1.1.1 <u>Neuronal morphology</u>

Neurons are highly polarized cells with distinct compartments. The neuronal soma contains the nucleus, endoplasmic reticulum and Golgi apparatus that carry out basic cell functions such as transcription and translation. Specialized cytoplasmic compartments projecting from the soma called dendrites and axons receive and propagate electrochemical information from and to other neurons, respectively, by forming synaptic connections. The lack of axonal protein synthesis and long distances between the cell body and discrete axonal and synaptic compartments, which can be thousands-fold times the length of their cell body, impose a unique challenge on neurons. Therefore, appropriate functions and survival of neurons rely on adequate delivery of membrane-bound organelles in both anterograde and retrograde direction by motor proteins,

conventional kinesin and cytoplasmic dynein respectively, in a process referred to as fast axonal transport (FAT).

#### 1.1.2 Axonal transport of intracellular cargoes by molecular motors

Axons comprise the bulk of the total cell volume for most neurons, yet the vast majority of components needed for the generation and maintenance of this compartment, including lipids and membrane proteins, are synthesized in the neuronal cell body. Within the neuronal soma, these components are sorted and packaged into specific membrane-bound organelles (MBOs), which are later delivered to their final sites of utilization in axons by a cellular process collectively known as fast axonal transport (FAT) (Morfini et al. 2012). Anterograde FAT of MBOs from the cell body to axons and dendrites is largely executed by microtubule (MT)-based motor proteins of the kinesin superfamily, whereas MBOs moved in retrograde FAT are transported by cytoplasmic dynein (Hirokawa and Takemura 2005).

#### 1.1.2.1 Conventional kinesin

Conventional kinesin represents the best characterized and most abundant member of the kinesin superfamily in mature neurons (Wagner et al. 1991) and is responsible for anterograde FAT of a wide variety of MBOs including mitochondria, plasmalemmal proteins, and synaptic vesicle precursors (Leopold et al. 1992). This multisubunit motor protein is a heterotetramer consisting of two kinesin heavy chain (kinesin-1, KHC) and two kinesin light chain (KLC) homodimer subunits and is responsible for specific functional activities of the holoenzyme (DeBoer et al. 2008). Kinesin-1 activities involve adenosine triphosphate (ATP) hydrolysis and MT-binding, which are essential for processive movement of conventional kinesin along axonal MTs (Wagner et al. 1991). KLCs contain tandem repeat domains that play a major role in the binding of conventional kinesin to MBOs (Stenoien and Brady 1997). Three kinesin-1 and two KLC genes are expressed in mammalian nerve tissue, and isoform-specific sequences located at the carboxy terminus of each subunit appear to mediate the sorting of biochemically heterogeneous forms of conventional kinesin to specific MBOs (DeBoer et al. 2008). The critical role of conventional kinesin and cytoplasmic dynein on neuronal function and the maintenance of axonal connectivity is illustrated by the identification of mutations in specific subunits of these motor proteins, which cause neurodegenerative diseases featuring axonal degeneration as a major pathological hallmark (Morfini et al. 2009; Roy et al. 2005).

#### 1.1.2.2. Cytoplasmic dynein

Cytoplasmic dynein (CDyn) is a large protein complex comprising two heavy chains (DHCs) and multiple other subunits such as intermediate chains (DICs), light intermediate chains (DLICs), and a variety of light chains (DLCs) (Hirokawa et al. 2010). Several accessory proteins have been reported to interact with one or more of the dynein subunits such as lissencephaly1 (Lis1) (Maday et al. 2014), nuclear distribution protein nudE-like 1 (Ndel1) (Kardon and Vale 2009), Bicaudal 1/2 (BICD1/2) (McKenney et al. 2014), and dynactin complex (Kardon and Vale 2009). The compositions of CDyn complex and accessary proteins are thought to take part in various CDyn functions.

The roles of individual subunits and interacting proteins are not well known except for DHCs, which have ATPase activity and MT-binding domains (Carter 2013), and DICs, which appear to mediate the interaction between CDyn and its cargoes (Vaughan et al. 2001; Pfister 2015). Potential roles of other subunits have been studied but are not as well established as those of DHCs and DICs.

#### 1.1.3 <u>Regulation of axonal transport</u>

The restricted distribution of different kinesin-1 MBO cargoes at specific axonal subcompartments (i.e., sodium channels at nodes of Ranvier, or synaptic vesicle precursors to presynaptic terminals) long implied the existence of regulatory mechanisms that allow for localized unloading of protein cargoes (Morfini et al. 2001). A hint on such mechanisms first came from studies showing that both kinesin-1 and KLC subunits are phosphorylated in vivo (Hollenbeck 1993; Elluru et al. 1995). More recently, a number of specific protein kinases were identified, which regulate functional activities of conventional kinesin by phosphorylating specific subunits. For example, both c-Jun amino-terminal kinase 3 (JNK3), p38a MAP kinase, and casein kinase 2 (CK2) phosphorylate kinesin-1 subunits at residues located in close proximity to MT-binding domains. Consistent with the enzymatic activities of kinesin-1, these phosphorylation events were found to inhibit processive movement of this subunit along axonal MTs (Morfini et al. 2013; Morfini et al. 2009). On the other hand, both glycogen synthase kinase 3 (GSK3 $\beta$ ) and CK2 were shown to phosphorylate KLCs instead, and these events were associated with detachment of conventional kinesin from MBOs (Morfini 2002; Morfini et al. 2001). Other proteins were found to regulate this motor protein indirectly, by modulating the activity of these kinases above (Morfini et al. 2004; Ratner et al. 1998).

#### 1.1.4 Dying-back neuropathy

Dying-back neuropathy is a pattern of neurodegeneration where distal portion of neurons progressively degenerate towards the cell body *prior* to the neuronal cell death. This type of neurodegeneration has been shown in chemotherapy-induced peripheral neuropathy (CIPN) caused by anti-tumor chemical agents such as vincristine, paclitaxel, eribulin, and ixabepilone, which exert their anti-tumor properties by disrupting microtubule dynamics to inhibit mitosis (Legha 1986; Lobert et al. 1996; Jordan 2012; Boyette-Davis et al. 2015). Dying-back neuropathy is also well characterized in axonal injury where the onset of neuronal cell death is delayed for several days after the injury (Goshgarian et al. 1983; Berkelaar et al. 1994; Dale et al. 1995; Fishman and Parks 1998). In addition, neurons affected in several adult-onset neurodegenerative diseases such as Alzheimer's disease (Kowall and Kosik 1987; Ihara et al. 2010; Bell and Claudio Cuello 2006; Shankar and Walsh 2009; Kanaan et al. 2013), Parkinson's disease (Dauer and Przedborski 2003), amyotrophic lateral sclerosis (Fischer et al. 2004), and Huntington's disease (Morfini et al. 2009; Gatto et al. 2015) follow dying-back pattern of degeneration.

The etiologies of CIPN, axonal injury, and adult-onset neurodegenerative diseases vary significantly from one another, yet they somehow converge onto dying-back neuropathy. One common pathology found in all of them is disruption of microtubulebased fast axonal transport where there is a failure to deliver membrane-bound cargoes to appropriate locations within specific domains within a neuron such as nodes of Ranvier and synapses. Axonal injuries such as axotomy evidently cause disruption of FAT (Delcroix et al. 1997; Goshgarian et al. 1983), and microtubule-targeting drugs that causes CIPN have been shown to inhibit axonal transport as well (LaPointe et al. 2013). Various adult-onset neurodegenerative diseases also feature axonal transport deficits (Morfini et al. 2006; Morfini et al. 2009; LaPointe et al. 2009; Pigino et al. 2009; Bosco et al. 2010; Kanaan et al. 2011). These findings indicate that inhibition of FAT can lead to dying-back neuropathy.

Studies of genetic mutations in microtubule-based molecular motor proteins conventional kinesin and cytoplasmic dynein (CDyn) further confirmed that FAT impairments suffice to cause dying-back neurodegeneration. For instance, loss-offunction mutations in kinesin heavy chain KIF5A cause axonal degeneration in hereditary spastic paraplegia type 10 and Charcot-Marie-Tooth disease type 2 (Reid et al. 2002; Crimella et al. 2012; Karle et al. 2012; López et al. 2015). Similarly, mutations in CDyn accessory protein p150glued lead to degeneration of motor neurons in several diseases such as spinal-bulbar muscular atrophy (Puls et al. 2005; Hafezparast 2003) and Perry syndrome (Farrer et al. 2009; Konno et al. 2017). Impaired FAT, as evidenced by neuropathological conditions described above, causes synaptic, and axonal dysfunctions eventually leading to dying-back neurodegeneration. The link between FAT defects and dying-back pattern of degeneration is further supported by the differential vulnerability of neurons to such pathology where neurons with long axons (i.e. projection neurons) and extensive axonal arborization are particularly susceptible to dying-back neuropathy compared to those with short axons (i.e. interneurons). However, many of the adult-onset neurodegenerative diseases that feature dying-back neuropathy are not caused by mutations in motor proteins or physical injury to the axons while still involving FAT impairments. As described above, motor proteins exist as phosphoproteins and phosphorylation of motor proteins by different kinases regulate their functions. This suggests that abnormal activation of protein kinases involved in regulation of motor proteins may underlie FAT defects in neurodegenerative diseases that are not caused by mutations in motor proteins or axonal injury.

# 1.1.5 <u>Disruption of fast axonal transport in neurodegenerative diseases via</u> <u>aberrant kinase signaling</u>

Several neuropathogenic proteins in these diseases were shown to activate protein kinases involved in motor protein phosphorylation (Morfini et al. 2009). For example, pathogenic forms of huntingtin protein that cause Huntington's disease (HD) were found to inhibit kinesin-1-based FAT through a mechanism involving JNK3 activation (Morfini et al. 2009). Also, both mutant and misfolded forms of superoxide dismutase 1 (SOD1) associated with familial and sporadic forms of amyotrophic lateral sclerosis (ALS) similarly inhibited kinesin-1-based motility. Further study revealed that inhibitory effect of pathogenic forms of SOD1 on axonal transport was mediated by p38 kinase (Bosco et al. 2010; Morfini et al. 2013). Inhibitory effects of the Alzheimer's disease-related proteins tau and beta-amyloid on kinesin-1 function were also identified, which were mediated by GSK3 and CK2, respectively (LaPointe et al. 2009; Pigino et al. 2009; Kanaan et al. 2011). Many neurodegenerative diseases feature dying-back neurodegeneration, and *in vitro* and *in vivo* experimental models demonstrate that neuropathogenic proteins implicated in those diseases inhibit FAT through dysregulation of kinase signaling. Therefore, the

identification of specific kinases that alter phosphorylation of kinesin and CDyn within axonal compartment has important implications for the elucidation of specific pathogenic mechanisms, and the identification of therapeutic targets.

#### 1.2 Specific aims and overall hypothesis

Over decades, our lab and others have identified dozens of kinases that regulate fast axonal transport through phosphorylation of motor proteins. Some kinases inhibit axonal transport of molecular cargoes while others activate it, indicating that phosphoregulation of axonal transport does not *only* represents pathogenic conditions unless there are disturbances in activities of kinases and phosphatases. The work described in the following chapters embodies the overall hypothesis that phosphorylation of motor proteins represents a major regulatory mechanism of FAT. Here, this hypothesis is examined in two different contexts: Huntington's disease in which an aberrant kinase signaling impairs axonal transport, and neurotrophin signaling in which activation of specific kinases promotes retrograde FAT of signaling endosomes.

# 1.2.1 <u>To address role of c-Jun N-terminal kinase 3 in Huntington's disease</u> <u>pathology</u>

Published work from our lab (Morfini et al., 2006; Morfini et al., 2009) has identified c-Jun N-terminal kinase 3 (JNK3) as the kinase mediating the toxic effect of mutant huntingtin on FAT via phosphorylation of kinesin-1. Impaired axonal transport leads to dying-back pattern of neurodegeneration, which has been shown in Huntington's disease (HD) patients as well as animal models (Gatto et al. 2015). To investigate the role of JNK3 in mutant huntingtin-mediated neurodegeneration *in vivo*, we combined a mouse model of HD (R6/2 mice, as reviewed in Ehrnhoefer et al. 2014) with genetic deletion of JNK3 (R6/2-JNK3<sup>-/-</sup>). Based on our previous finding that JNK3 inhibits fast axonal transport, we hypothesized that HD neuropathology which is recapitulated by R6/2 mice will be ameliorated by genetic deletion of JNK3.

# 1.2.2 <u>To identify protein kinases that regulate retrograde fast axonal transport of</u> <u>neurotrophin-containing signaling endosomes</u>

Neurotrophins are essential for neuronal survival and functions (Kaplan and Miller 2000). They are released from postsynaptic cells and bind to neurotrophin receptors at the presynaptic terminal. Neurotrophin signaling triggers various local signaling cascades as well as modulating transcriptional activation of multiple genes that play critical roles in neuronal survival and synaptic plasticity (Kaplan and Miller 2000; Reichardt 2006; Park and Poo 2013). In order to produce their transcriptional activation effect, neurotrophins that bind to their receptors must be transported to the neuronal cell body by cytoplasmic dynein (CDyn) in a membrane-bound organelle called signaling endosome (Wu and Mobley 2010; Marlin and Li 2015). While multiple signaling cascades are activated upon ligand binding and subsequent activation of neurotrophin receptors, mechanisms underlying the activation of CDyn-based retrograde FAT of signaling endosomes that contain activated neurotrophin receptors remain elusive. Experiments under this aim were designed to identify protein kinase pathways that trigger retrograde FAT of signaling endosomes in the context of brain-derived neurotrophic factor (BDNF).

### CHAPTER II.

# II. ROLE OF JNK3 IN MUTANT HUNTINGTIN-MEDIATED AXONAL TRANSPORT DEFECTS

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### 2.1 Background

### 2.1.1 <u>Huntington's disease</u>

Huntington's disease (HD) is a fatal hereditary neurodegenerative disease featuring motor dysfunctions such as chorea (Reilmann et al. 2001) as well as cognitive (Paulsen 2011) and psychiatric impairments such as depression (Paulsen et al. 2005; Julien et al. 2007). The world-wide prevalence of HD is approximately 3 in 10,000 and it is more common among European and North American populations (Pringsheim et al. 2012). HD is a monogenic disease caused by polyglutamine (polyQ) expansion mutation in the huntingtin (htt) protein (CAG repeat expansion in htt gene) where healthy individuals have between 8 and 36 glutamine repeats while HD patients have 37 or more repeats. Interestingly, the typical age of onset is around 35-50 years (Harper 1996), but the length of the polyQ repeats correlate with earlier onset of the disease with. Patients

with 70 or more repeats often have a juvenile form of HD in which symptoms begin to develop in teenage years (Vonsattel and DiFiglia 1998).

A neuroanatomical hallmark of HD is the massive degeneration of medium spiny neurons (MSNs) in the striatum (Reiner et al. 1988; Deng et al. 2004) as well as the cerebral cortex (Mann et al. 1993). MSNs, which comprise up to 95% of total neurons in the striatum, are GABAergic projection neurons with characteristic medium-sized cell bodies, spiny dendrites and a long axon that projects to external (GPe) or internal (GPi) segments of the globus pallidus and substantia nigra (SN) depending on the subtypes: dopamine receptor D1 -expressing "direct" and D2-expressing "indirect" pathway neurons (Han et al. 2010; Smith et al. 1998; I. J. Mitchell et al. 1999). These MSNs with a long axon are particularly susceptible to degeneration in HD while striatal interneurons, which have short axons and are involved in local circuitry rather than connecting different areas of the brain, are largely spared in HD (Ferrante et al. 1985; Ferrante et al. 1986; Ferrante et al. 1987; Dawbarn et al. 1985; Massouh et al. 2008). Similar to the striatum, there is differential loss of neuronal populations in the cerebral cortex where a subset of pyramidal projection neurons in layers V, VI, and III are lost (Cudkowicz and Kowall 1990; Macdonald and Halliday 2002; Hedreen et al. 1991) while the cortical interneurons are spared in HD (Cudkowicz and Kowall 1990; Sotrel et al. 1991), indicating that longer axons contribute to neuronal vulnerability in HD.

#### 2.1.2 Animal models of HD

Following the discovery of the huntingtin gene as the causative gene and the nature of the mutation that leads to HD in 1993, several animal models of HD have been

generated by introducing either full-length or a fragment of huntingtin gene with varying CAG repeat lengths (Mangiarini et al. 1996; Hemachandra Reddy et al. 1998, 1999; Hodgson et al. 1999; Schilling et al. 1999; Menalled and Chesselet 2002; Slow et al. 2003; Heng et al. 2008; Pouladi et al. 2013). One of the earliest and best-characterized mouse models of HD is the R6/2 mouse, which expresses the exon 1 fragment of the human huntingtin gene with around 150 CAG repeats (Mangiarini et al. 1996). The transgene expression in R6/2 mice is driven by the human huntingtin promoter at approximately 75% of endogenous huntingtin expression level. R6/2 mice recapitulate several symptoms of human HD, including motor dysfunctions (J. Y. Li et al. 2005; Garland et al. 2016) and neuropathological changes such as atrophy of the striatum and cortex, progressive loss of cortical projections (Gatto et al. 2015). Transgenic expression of a huntingtin fragment by the exogenous human huntingtin promotor in R6/2 mice seems to cause and earlier pathology and faster progressing pathology than HD in human patients, where clinical symptoms typically develop between 30-50 years old and progression occurs over 15-20 years. In contrast, R6/2 mice have progressive motor dysfunctions starting as early as 4-6 weeks of age and the lifespan of around 3-4 months (Li et al. 2005).

In addition to transgenic mice that express either full-length or a fragment of the human huntingtin gene by an exogenous promoter, there are knock-in mouse models of HD that were generated by replacing parts of the endogenous mouse huntingtin gene with the corresponding domains of the human huntingtin gene with varying CAG repeats lengths. An advantage of knock-in mice is the expression fidelity as mutant huntingtin gene expression is driven by endogenous mouse huntingtin promoter. Some of the disadvantages of using knock-in mice are mild phenotypes—sometimes no phenotypes in heterozygous mice—and slower disease progression, which makes the research efforts more time-consuming and costly. There are several knock-in mouse models of HD such as Hdh111 (Wheeler et al. 1999; Lloret et al. 2006), CAG140 (Menalled et al. 2003; Rising et al. 2011), Hdh 50, Hdh 100, Hdh 150, Hdh250 (Sathasivam et al. 2013) and zQ175 (Menalled et al. 2012; Peng et al. 2016). One of the key differences among these models is whether or not the exon 1 region is humanized. Hdh150 and Hdh250 mice have completely murine huntingtin gene with increased CAG repeats while others such as Hdh111, CAG140 and zQ175 have an *exon* 1 that features varying degrees of humanization, resulting in a chimeric mouse-human huntingtin.

More recently, zQ175 has gained popularity among HD researchers. Germ line expansions of the CAG track in an older knock-in mouse model with 140 CAG repeats called CAG140 mice (Menalled et al. 2003; Rising et al. 2011) gave rise to a new subline zQ175 with approximately 190 CAG repeats. This zQ175 model was the first knock-in mouse model to exhibit clear disease phenotypes as heterozygotes (Menalled et al. 2012). Although the phenotypes are still not as severe as R6/2 transgenic mice and their lifespan is unaffected, zQ175 mice and its variations are gaining increasing attention within HD research community as most human HD patients are heterozygous for the mutant allele.

#### 2.1.3 Dying-back neurodegeneration in HD

Historically, research efforts on HD therapeutics largely focused on preventing neuronal cell death (Vila and Przedborski 2003; Portera-Cailliau et al. 1995; Estrada Sánchez et al. 2008; Zeron et al. 2001; Hickey and Chesselet 2003; Jakel and Maragos 2000; Chen et al. 2000). However, a growing body of evidence suggest that axonal pathology and synaptic dysfunctions occur prior to neuronal cell death and HD symptoms begin to manifest before cell loss, including previously published data from our lab reporting no neuronal cell death in R6/2 mice even at P90, which is a late stage nearing death in these mice (Gatto et al. 2015). These synaptic dysfunctions include severe deficiencies in dopamine signaling characterized by loss of several components of dopamine signaling such as DARPP-32, ARPP-16, and ARPP-21 (Bibb et al. 2000), increased excitotoxicity due to changes in NMDA receptor functions (Cepeda et al. 2001; Laforet et al. 2001; Klapstein et al. 2001) as well as loss and mislocalization of synaptic proteins (Diprospero et al. 2004; Modregger et al. 2002). Along with synaptic dysfunctions, axonal pathology that long precedes neuronal cell death has been extensively described by several groups. Marked reduction in enkephalin immunoreactivity was reported in (Waters et al. 1988) and GPe (Reiner et al. 1988; Albin et al. 1990) without loss of MSNs, suggesting that degeneration of MSN axons projecting to SN and GP. More recent studies using magnetic resonance imaging (MRI) show white matter abnormalities in early stage HD patients that correlated with cognitive dysfunction (Beglinger et al. 2005). A second imaging modality, diffusion tensor imaging (DTI), revealed white matter disorganization and decreased white matter integrity before significant cell loss in early stage HD patients (Reading et al. 2005; Weaver et al. 2009; Rosas et al. 2010; Ross and Tabrizi 2011). Consistent with findings from early stage HD patients, published work from our lab also demonstrated the pre-symptomatic axonal pathology of transcallosal axons in the R6/2 mouse model of HD by correlating morphometric light microscopy of axons expressing a yellow fluorescent protein (YFP)

reporter with DTI imaging (Gatto et al. 2015). The evidence accumulated over two decades strongly suggests that loss of neuronal connectivity is an early pathogenic event in HD and neuronal death in HD follows the dying-back pattern of neurodegeneration where synaptic terminals and distal portion of the axons degenerate before neuronal apoptosis (Han et al. 2010).

#### 2.1.4 Axonal transport defects in HD

Consistent with evidence supporting the the dying-back pattern of neurodegeneration in HD and the causal relationship between impaired FAT and such degeneration, defects in FAT have been reported in several experimental models of HD. Work from our lab demonstrated that perfusion of mutant huntingtin fragment in squid axoplasms results in inhibition of axonal transport in both anterograde and retrograde directions (Szebenyi et al. 2003; Morfini et al. 2009). Similar results were observed in vivo in drosophila where exon 1 fragment of mutant huntingtin lead to reduced rate of axonal transport as well as accumulation of vesicles and mitochondria in the axon (Gunawardena et al. 2003; Lee et al. 2004; Sinadinos et al. 2009). In addition, studies of transgenic mice expressing full-length huntingtin with polyQ expansion reported impaired transport of vesicles and mitochondria both in vitro and in vivo using retrograde axonal tracer FluoroGold and fluorescent-labeling of mitochondrial proteins (Trushina et al. 2004; Orr et al. 2008). These reports from various experimental models of HD both in vitro and in vivo clearly demonstrate that mutant huntingtin causes FAT impairments, and that exon *1* of huntingtin with expanded CAG repeats is sufficient to cause such impairments.

#### 2.1.5 <u>Alterations in mitochondrial transport</u>

Studies of axonal transport defects in HD often examine the movement of mitochondria that are fluorescently labeled with lipophilic fluorescent dyes (MitoTracker) or expression of mitochondria-targeted proteins with a fluorescent tag. Several groups have reported defects in mitochondrial transport with mutant huntingtin (mHtt) expression (Trushina et al. 2004; Chang et al. 2006; Orr et al. 2008; Shirendeb et al. 2012; Tian et al. 2014). However, recent studies by two independent group reported that mitochondria in mature neurons are predominantly stationary (over 90%) both in primary neurons and *in vivo* (Lewis et al. 2016; Smit-Rigter et al. 2016). Much of the work on mitochondrial transport defects by mHtt is done with either short-term cultures of primary neurons or focus primarily on the transport of mobile mitochondria. Since only a small fraction of mitochondria is mobile in mature neurons, the true contribution of alterations in the mitochondria transport to mHtt-mediated neuronal dysfunction and degeneration remains unclear. Therefore, studying impairments in axonal transport of highly-mobile vesicles seems more critical in elucidating the pathogenic mechanism of HD.

#### 2.1.6 Proposed mechanisms underlying axonal transport defects in HD

#### 2.1.6.1 Loss-of-function upon polyQ expansion of huntingtin

Huntingtin (Htt) is a relatively large protein (350ka) with no enzymatic activity. The functions of wildtype Htt remain elusive but global knockout of Htt in mice leads to early embryonic lethality (Nasir et al. 1995; Zeitlin et al. 1995), indicating that Htt plays a critical role during development. Htt is enriched in the brain but is expressed in all tissues beyond embryonic development (The Human Protein Atlas). Several potential roles of Htt have
been proposed with the hypothesis that polyQ expansion in mHtt results in loss of the proposed functions, leading to HD phenotypes.

Many of the proposed functions of Htt are related to axonal transport either by direct interaction between Htt and motor proteins or by interactions of Htt with adapter proteins such as huntingtin-associated protein 1 (HIP1) that thought to interact with motor proteins. (Caviston et al. 2007) suggested that Htt binds to dynein in a complex with HIP1 and facilitates dynein-mediated vesicle transport. Another group indicated that Htt and HAP1 regulates autophagosome transport and polyQ expansion or knockout of Htt disrupts autophagosome transport (Wong and Holzbaur 2014). While these interactions have been proposed and some have been accepted for decades, essentially all of data identifying protein complexes were generated by artificial methods such as overexpression of the potential interaction proteins followed by co-immunoprecipitation, two-yeast hybridization and co-localization in confocal microscopy (DiFiglia et al. 1995; Velier et al. 1998; Harjes and Wanker 2003; McGuire et al. 2006; Caviston et al. 2007; Caviston and Holzbaur 2009; Deng et al. 2014; White et al. 2015). Methods such as coimmnoprecipitation of overexpressed protein and two-yeast hybridization are prone to type 1 errors (false positives) as they rely on ectopic overexpression of target proteins, and co-localization using confocal microscopy cannot determine protein-protein interaction because of the resolution limit of ~200nm. While techniques such as Förster resonance energy transfer (FRET) increases the resolution of protein-protein interaction to <10nm, it has the same disadvantage of reliance on overexpression of proteins with fluorescent tags.

With identification of more and more protein-protein interactions, the proposed protein complexes have become larger and larger, and a critical review of these "megaprotein complexes" is needed to address the biological feasibility of such complexes. For instance, one of the widely cited motor protein complexes involving huntingtin is a complex comprising dynein, HAP1, Htt, dynactin, and kinesin associated with membranebound cargo. Dynein complex, even without other accessory proteins, includes two heavy chains (530kDa each), two intermediate chains (74kDa each), two light intermediate chains (55kDa each) and two light chains (8kDa each). Dynactin complex is another multisubunit protein complex with more than 20 subunits ranging from 22 to 150kDa each and has molecular weight around 1MDa. Kinesin complex consists of two heavy chains (~100kDa each) and two light chains (64kDa each). Combining dynein complex (1.2MDa), dynactin complex (1MDa), kinesin complex (320kDa), with HAP1 (75kDa) and Htt (350kDa) results in a >3MDa protein complex, even without including other accessary proteins, that associates with membrane-bound cargo and moves at a speed of 1-4µm/sec. No such complexes have been detected on the surface of vesicles by electron microscopic methods. As mentioned, such "mega-complexes" were inferred from multiple experiments using overexpression of one or two parts of the complex and their existence as a whole complex has never been demonstrated in vivo with endogenous proteins. In fact, *lack* of interaction between Htt and motor proteins without overexpression has been shown in vivo. Morfini et al. (2009) showed that endogenous Htt does not interact with molecular motors by co-immunoprecipitation of endogenous Htt, kinesin, or dynein. Kinesin light chains co-immunoprecipitate with kinesin heavy chain but not with dynein subunits, and dynein heavy chains co-immunoprecipitate with dynein intermediate chain

but not with kinesin subunits as they are *true* and *independent* complexes. However, Htt does not co-immunoprecipitate with either kinesin or dynein and *vice versa*, indicating that either endogenous Htt does not form a protein complex with motor proteins or such complex exists only transiently.

Alternatively, Colin et al. (2008) proposed that Htt is a positive regulator of fast axonal transport and a molecular switch that can determine the direction of cargo transport, and this function is lost with the polyQ expansion in HD. The same group later proposed another role of Htt as a scaffold protein that brings the full set of glycolytic enzymes to complex with motor proteins for transporting vesicles (Zala et al. 2013), suggesting that glycolysis provides ATP for the transport of vesicles. The reasoning being that mHtt fails to bring the glycolytic enzymes to the vesicles thus inhibiting axonal transport of those vesicles. The brain is the most energy-dependent organ in the body which consumes 20% of the energy while being only 2% of the body weight. Not surprisingly, the brain critically depends on oxidative phosphorylation to generate the most amount of ATP rather than glycolysis (Magistretti and Allaman 2015), and glucose is almost fully oxidized in the brain (Allaman and Magistretti 2013). Further, the fact that local anoxia will block fast axonal transport has been known for over four decades (Ochs 1971; Leone and Ochs 1978), demonstrating the importance of oxidative metabolism for axonal transport. Therefore, it seems unlikely that the inhibition of axonal transport by mHtt is due to failure of localizing glycolytic enzymes to motor proteins. Furthermore, the relative abundance of Htt is likely to be far less than that of glycolytic enzymes such as glyceraldehyde 3-phosphate dehydrogenase (GAPDH). While the exact intracellular molar concentration of Htt in the brain is not known, comparisons of mRNA levels of Htt and GAPDH within the same sample by three different projects (HPA, GTEx and FANTOM5) reporting in three different dataset (transcripts per million, reads per kilobase per million mapped reads and cap analysis of gene expression tags per million) revealed that Htt mRNA level in the brain is over 100-fold lower than GAPDH mRNA level (The Human Protein Atlas), which suggests that Htt protein is expressed at a far over 100-fold lower level than GAPDH. Combining the low ATP yield by glycolysis and the mismatched stoichiometry of proposed interaction between Htt and GAPDH, the contribution of diminished localization of glycolytic enzymes to vesicles in mHtt-mediated axonal transport defects and even the proposed role of Htt as a scaffold for glycolytic enzymes seem biologically unlikely.

While Htt knockouts are embryonic lethal (Nasir et al. 1995; Zeitlin et al. 1995), a recent and somewhat controversial study using conditional knockout of neuronal Htt in mice reported that the Htt knockout in adult mice did not lead to neurodegeneration (Wang et al. 2016). In addition, gene silencing of mutant Htt allele using antisense oligonucleotides (ASO) has recently passed a Phase 1/2a clinical trial and it demonstrated dose-dependent reduction of mHtt level as well as safety in human HD patients (IONIS-HTTRx; Kordasiewicz et al. 2012; Liu and Zeitlin 2017). These results challenge proposed roles of Htt that are essential for basic neuronal functions in adult neurons. Instead, the suggest that pathogenic mechanism of mHtt-mediated neurodegeneration is more likely to be via gain-of-function upon polyQ expansion rather than loss-of-function. The gain-of-function hypothesis of huntingtin mutation in HD pathogenesis is further supported by transgenic mouse models such as R6/2 mice where

transgenic expression of *exon 1* fragment of mutant huntingtin, without disrupting the expression of mouse huntingtin, is sufficient to cause HD pathology.

#### 2.1.6.2 Kinase-dependent mechanism of fast axonal transport inhibition

In addition to mutations in motor proteins, abnormal kinase signaling has been shown to impair FAT. Molecular motors exist as phosphoproteins and phosphorylation of their subunits can regulate their activity. Works from our lab and others have demonstrated that pathogenic proteins implicated in several unrelated adult-onset neurodegenerative diseases cause aberrant activation of a specific kinase pathway, leading to FAT impairment by abnormal phosphorylation of motor proteins (Morfini et al. 2009; Brady and Morfini 2017).

In isolated axoplasms, perfusion of mHtt induced inhibition of both anterograde and retrograde fast axonal transport (Morfini et al. 2009). This inhibition was prevented by co-perfusion of mHtt with pharmacological inhibitors of c-Jun N-terminal kinases (JNKs) SP600125 or SB203580, indicating that the activation of JNKs by mHtt was necessary for the mHtt-mediated axonal transport inhibition. Further study with perfusions of active recombinant JNK1, 2 and 3 in the isolated axoplasms revealed that JNK3 mediates the inhibition of fast axonal transport by mHtt as perfusion of JNK3 mimics the effect of mHtt on fast axonal transport (Morfini et al. 2009). Active JNK3 can directly phosphorylate kinesin heavy chain subunit of the conventional kinesin at S176 residue, and this this phosphorylation causes detachment of kinesin from microtubules, leading to inhibition of kinesin-based anterograde axonal transport (Morfini et al. 2009). Mechanisms by which mHtt inhibit dynein-based retrograde axonal transport remain unknown, but it is likely to involve JNK activation since co-perfusion of mHtt with pharmacological inhibitors of JNKs rescues both anterograde and retrograde fast axonal transport. In addition, perfusion of JNK3, but not JNK1 or JNK2, in isolated axoplasms leads to retrograde fast axonal transport, suggesting that JNK3 also mediates the inhibition of retrograde fast axonal transport by mHtt (Morfini et al. 2009).

#### 2.1.7 Rationale and hypothesis

Based on the previous work that identified JNK3 as the mediator of the toxic effect of mHtt on fast axonal transport in squid axoplasms (Morfini et al. 2009), we have generated a mouse model of HD with genetic deletion of JNK3 by crossing R6/2 mice with JNK3<sup>-/-</sup> mice (R6/2-JNK3<sup>-/-</sup>). R6/2 mice recapitulate many of the hallmark behavioral and neuropathological phenotypes of HD such as striatal and cortical degeneration. Recent work from our lab has documented pre-symptomatic axonal degeneration of transcallosal axons in R6/2 mice with a YFP reporter (Gatto et al. 2015). As impairments in axonal transport lead to a dying-back pattern of neuropathy and JNK3 is critical for mHtt-mediated axonal transport defects, we hypothesize that JNK is aberrantly activated by mHtt, and genetic deletion of JNK3 will ameliorate HD phenotypes observed in R6/2 mice.

# 2.2 Methods and materials

# 2.2.1 <u>Recombinant huntingtin proteins</u>

Recombinant huntingtin proteins used in this study have been provided by CHDI Foundation. GST-tagged N-terminal fragment of human huntingtin protein corresponding to amino acids 1-548 with either 16 (Htt-Q16) or 55 glutamines (Htt-Q55) were produced in E. Coli, purified, and reconstituted in 20mM HEPES by Dr. Andrea Caricasole (IRBM Science Park, Italy). The quality and relative amounts of each construct were assessed prior to use by immunoblotting 20ng of each construct with anti-Htt antibody clone 4C9 (1:10,000 dilution) **(Figure 1)**.



**Figure 1. Recombinant huntingtin proteins used in this study.** 20ng of each construct was loaded on 4-12% Bis-Tris gel and analyzed by immunoblotting with anti-Htt antibody clone 4C9. Western blot image shows comparable amount of proteins.

# 2.2.2 Mice

Female mice with ovary transplanted from heterozygous R6/2 mice expressing ~1kb of human huntingtin gene with 160 +/- 5 CAG repeats in CBA X C57BL/6J were purchased from The Jackson Laboratory (cat #002810). The ovarian transplanted female mice were paired with wild-type C57BL/6J mice (The Jackson Laboratory cat #000664) to generate wild-type and heterozygous R6/2 mice used in the study. Female JNK3 knockout (JNK3<sup>-/-</sup>) mice in C57BL/6J background were purchased from The Jackson Laboratory (cat #004322) and paired with R6/2 males to generate R6/2-JNK<sup>+/-</sup> males, then paired with JNK3<sup>-/-</sup> females to generate R6/2-JNK3<sup>-/-</sup> mice. Both male and female mice were used in the study. All mice were housed in the barrier facility at University of Illinois at Chicago (UIC) and the protocols involving animal use have been approved by Institutional Animal Care and Use Committee at UIC.

#### 2.2.3 Mouse brain dissection and preparation of mouse brain lysate

Upon euthanasia by CO2, mouse brain was obtained and sliced using ice-cold sagittal slicing matrix with 1.0mm intervals (Zivic Instruments cat #BSMAS001-2). From ML +/-1-3mm slices, cortex, striatum and cerebellum tissues were collected using biopsy punch with 2.0mm diameter (Miltex #33-31-P/25) in fresh lysis buffer (1% SDS in 50mM HEPES with 2mM NaF and 10mM Na<sub>3</sub>VO<sub>4</sub>). Collected tissues were quickly boiled at 90°C for 2 minutes, homogenized using plastic pestle, then sonicated (20% amplification, 6 cycles; 1 cycle = 5s on, 2s off). Sonicated samples were centrifuged at 21130 x g in Eppendorf 5424 tabletop centrifuge (15000 rpm) at 4°C for 15 minutes twice, transferring the supernatant to a new tube each time. The protein concentrations of the prepared

Iysates were measured by BCA protein assay using Pierce BCA protein assay kit (ThermoFisher #23225). Following BCA assay, sample concentrations were adjusted to  $1\mu g/\mu L$  by mixing appropriate amount of the lysate, lysis buffer and 6X Laemmli sample buffer.

# 2.2.4 Isolated squid axoplasm preparation and perfusion

Detailed descriptions of isolated squid axoplasm preparation and perfusion can be found in published work from our lab (Song et al., 2016; Kang et al., 2016) (Figure 2) and an example of the methods of validating antibodies for use in squid axoplasms and detecting changes in kinase activity in isolated squid axoplasms are provided in **Figure 3**. Briefly, pairs of "sister" axons were dissected from the Atlantic squid *Loligo pealeii* at Marine Biological Laboratory in Woods Hole. After removing connective tissues, the axoplasms were extruded on glass slides (Corning cat #2948-75X25) and a hydrophobic boundary was drawn along the contour of the axoplasm to keep perfusion solution on the slides. One of the sister axoplasm was perfused with 200nM recombinant Htt-Q16 (described above) in Buffer X/2 and the other sister axoplasm was perfused with 200nM recombinant Htt-Q55. After 50 minutes of incubation, the axoplasms were lysed with 1% SDS and the lysates were collected into 1.5mL Eppendorf tubes and 6X Laemmli sample buffer was added and stored in -20°C until analysis by western blotting with antibodies validated to recognize squid variants of their target. A non-exhaustive list of antibodies validated in the squid axoplasm is provided in **Table 1**.

Antigen	Host	Clone	Source	
Kinesin-1A, 1B, 1C	Mouse monoclonal	H2	Chemicon	
Kinesin light chains	Mouse monoclonal	63-90	In-house	
Kinesin light chains	Mouse monoclonal	KLC-All In-house		
$\alpha$ -Tubulin	Mouse monoclonal	DM1A	Sigma-Aldrich	
Phosphorylated neurofilament	Mouse monoclonal	SMI-31	BioLegend	
Phosphorylated neurofilament	Mouse monoclonal	RMO55	EMD Millipore	
SNAP-25	Mouse monoclonal	71.1	Synaptic Systems	
p-JNK (Thr183/Tyr185)	Mouse monoclonal	G9	Cell Signaling #9255	
p-JNK (Thr183/Tyr185)	Rabbit polyclonal		Cell Signaling #9251	
p-JNK (Thr183/Tyr185)	Rabbit monoclonal	81E11	Cell Signaling #4668	
p-MKK3 (Ser189)/MKK6 (Ser207)	Rabbit monoclonal	22A8	Cell Signaling #9236	
p-MKK7 (Ser271/Thr275)	Rabbit polyclonal		Cell Signaling #4171	
p-p38 (Thr180/Tyr182)	Rabbit monoclonal	3D7	Cell Signaling #9215	
p-GSK3β (Ser9)	Rabbit monoclonal	D85E12 Cell Signaling #5558		
p-ERK (Tyr204)	Mouse monoclonal	E-4	Santa Cruz Biotech sc-7383	

Table 1. Validated antibodies that cross-react with squid versions of their targetproteins. (Table originally published in Kang et al. 2016)

# 1.1 AXOPLASM PREPARATION



**Figure 2. Outline of procedures in isolated squid axoplasms.** Owing to intrinsic differences between different squid, two "sister" axons need to be dissected from the same squid, extruded, and placed on the glass coverslips. One axoplasms is perfused with control perfusion mix and its "sister' axoplasms with experimental perfusion mix. Metabolic labeling experiments require perfusion mixes containing P32-radiolabeled adenosine triphosphate. After 50-min incubation, axoplasms are lysed and processed for immunoblotting. For metabolic labeling procedures, radiolabeled axoplasmic proteins are immunoprecipitated and analyzed by autoradiography. (Figure originally published in Kang et al. 2016)



Figure 3. An example of biochemical analysis of axoplasms upon perfusion. Axonautonomous effects of properly folded, wild type (SOD1-WT) and oxidized (SOD1-ox) forms of superoxide dismutase 1 on p38 mitogen-activate kinase (MAPK) activity. (A) A schematic of the use of the liquid blocker pen (i.e. Super Pap Pen). A liquid blocking line is drawn along the contour of the axoplasm on the glass slide approximately 3 mm away from the axoplasm. (B) Using a P100 or P200 pipette, perfusion mixes are placed within the boundary drawn with the Pap Pen. If needed, coverslips are tilted to ensure thorough perfusion of the axoplasm. (C) Validation of rabbit monoclonal antibody clone 3D7 (p-p38 antibody; Cell Signaling #9215) in squid axoplasm. Two axoplasms were homogenized in Buffer X/2 with ATP using a pipette. The homogenate was briefly centrifuged and similar aliquots of the supernatant were incubated with (+MKK7) or without (Control) recombinant mitogen-activated kinase kinase (MKK7) (purchased from EMD Millipore), a kinase that directly phosphorylates and activates p38 MAPK. After a 30-min incubation, samples were processed for immunoblotting with antibody 3D7. As expected, increased immunoreactivity was observed in the aliquot incubated with MKK7, compared to its control. (D) "Sister" axoplasms were dissected from six squid (Squid 1-6) and perfused with recombinant forms of superoxide dismutase 1 (SOD1, 5µM). One axoplasm was perfused with SOD1-WT and its "sister" axoplasm with SOD1-ox associated with sporadic forms of amyotrophic lateral sclerosis (Bosco et al., 2010). After a 50-min incubation, axoplasms were lysed, separated by SDS-PAGE and processed for immunoblotting using monoclonal antibody 3D7 (as in C). Note the variable levels of active (phosphorylated) p38 among different squid. Despite this variability, p-p38 immunoreactivity is consistently higher in axoplasm perfused with SOD1-ox than their "sister" counterparts perfused with SOD1-WT. A band recognized by a polyclonal antibody against TrkB (Santa Cruz, sc-11, Lot E0708) provided an internal control for protein loading. A protion of the p-p38 immunoblot (Squid 1-3) was shown in Boscoe et al, 2010. (Figure originally published in Kang et al. 2016)

# 2.2.5 Post-mortem tissues

Human post-mortem cortex tissues from non-HD and HD patients were provided by Dr. Jeffery Kordower at Rush University (originally obtained from New York Brain Bank at Colombia University). Subjects included both male and female with age ranging from 28 to 75. HD patients were diagnosed as HD stage 3/4 and CAG repeat lengths ranged from 42 to 47. Detailed information for each subject is listed in **Table 2**.

Case ID	Age	Sex	Cold PMI (HH:MM)	Frozen PMI (HH:MM)	Diagnosis	PolyQ Length
4915	62	М	04:00	04:30	Encephalopathy of hypoxic-ischemic type, moderate	N/A
4523	62	F	04:33	22:38	Encephalopathy of hypoxic-ischemic type, acute	N/A
320	28	F	02:09	05:57	Control	N/A
4518	56	М	N/A	08:50	Control	N/A
2476	60	М	00:00	22:55	HD 3/4	43
4225	72	F	00:15	48:35	HD 3/4	42
4340	75	М	02:45	08:20	HD 3/4	43
4921	47	М	N/A	34:45	HD 3/4	46
4988	56	М	00:05	15:25	HD 3/4	47
5109	64	М	00:06	38:01	HD 3/4	43
5124	57	М	00:48	18:38	HD 3/4	43

**Table 2. Demographic information of human samples used in this study.** PMI: Postmortem interval, which indicates the interval between the time of death and the time cadavers were placed in cold or frozen. Huntington's disease clinical progression follows 5 diagnostic stages based on symptoms: HD 1 – Preclinical/Prodromal Stage, HD 2 – Early Stage, HD 3 – Middle Stage, HD 4 – Late Stage, HD 5 – End of Life.

#### 2.2.6 Western blotting

For western blotting, 10-20µg of brain lysate samples prepared as described above were loaded on 4-12% Bis-Tris gels (Invitrogen cat #NP0336) and ran in MOPS running buffer at 120V for 2 hours. Following electrophoresis, the proteins were transferred onto a 0.45µm Immobilon-P PVDF membrane (Millipore cat #IPVH00005) or Immobilon-FL (Millipore cat #IPFL00005) in Towbin buffer (25mM Tris, 192 mM glycine and 10% MeOH) at 400mA for 2 hours with cooling system maintained at 4°C. After transfer, the membranes were incubated in blocking buffer (1% non-fat milk in tris-buffered saline with 0.1% Tween-20; TBS-T) for 1hr in room temperature. After blocking, membranes were washed three times with TBS-T for 5 minutes each wash. Then the membranes were incubated overnight with primary antibodies diluted in 1% BSA in tris-buffered saline (TBS) with following dilutions: anti-phospho-JNK (Cell Signaling #9251, 1:500), anti-GAPDH (Sigma #G8795, 1:300,000), anti-JNK1 (BD Biosciences #554286, 1:1000), anti-JNK2 (Cell Signaling #4672, 1:500), anti-JNK3 (Cell Signaling #2305, 1:6000) for human samples; anti-DARPP32 (Cell Signaling #2306, 1: 2,000,000), anti-GAPDH (Sigma #G8795,1:200,000), anti-PSD95 (BD Biosciences #610495, 1:4000), anti-TH (Pel-Freez #P40101-0, 1:200,000), anti-JNK1 (BD Biosciences #554286, 1:500), anti-JNK2 (Cell Signaling #4672, 1:500), anti-JNK3 (Cell Signaling #2305, 1:10,000), anti-phospho-JNK (Cell Signaling #4668, 1:30,000) for mouse samples; anti-KHC (H2, In-house, 1:10,000), anti-phospho-JNK (Cell Signaling #4668, 1:10,000), anti-phospho-MKK7 (Cell Signaling #4171, Lot 3, 1:500) and anti-Htt (4C9, CHDI Foundation, 1:100,000) for isolated squid axoplasm samples. Characterization of antibodies used in this study is shown in Figure 4. The next day, the membranes were washed three times with TBS-T for 5 minutes each wash and incubated with secondary antibodies diluted in 1% milk in TBS for 1 hour in room temperature with following dilutions: goat anti-mouse IgG-HRP conjugate (Jackson Laboratories #115-035-146, 1:30,000), goat anti-rabbit IgG-HRP conjugate (Jackson Laboratories #111-035-144, 1:30,000). After incubation with secondary antibodies, membranes were washed three times with TBS-T for 5 minutes each wash and the signals were detected via chemiluminescence using WesternSure PREMIUM chemiluminescent substrate (LI-COR) and HyBlot CL autoradiography film (Denville Scientific). Some immunoblots were analyzed using LI-COR Odyssey CLx/Fc nearinfrared (NIR) imaging systems. Electrophoresis and transfer procedures for LI-COR NIR imaging was identical as chemiluminescence. Following transfer, the PVDF membranes were incubated with blocking buffer without tween-20 (1% non-fat milk in TBS). Primary antibody incubation procedure for LI-COR NIR imaging was identical as chemiluminescence. Secondary antibodies were diluted in 1% milk in TBS-T with 0.01% SDS and incubated for 45 minutes to 1 hour in room temperature with following dilutions: goat anti-mouse IgG IRDye 680RD (LI-COR #925-68070, 1:10,000) and goat anti-rabbit IgG IR Dye 800CW (LI-COR #925-32211, 1:10,000).



**Figure 4. Characterization of antibodies used in this study. (A)** Characterization of antibodies used in post-mortem human cortex samples. **(B)** Characterization of antibodies used in mouse prefrontal cortex (Ms PFC) and mouse striatum (Ms STR) samples. JNK1 (mouse monoclonal, BD Biosciences #554286), JNK2 (rabbit polyclonal, Cell Signaling #4672), JNK3 (Rabbit monoclonal, Cell Signaling #2305), pJNK 9251 (rabbit monoclonal, Cell Signaling #9251), pJNK 4668 (rabbit monoclonal, Cell Signaling #4668), GAPDH (mouse monoclonal, Sigma #G8795), PSD-95 (mouse monoclonal, Cell Signaling #36223), DARPP-32 (rabbit monoclonal, Cell Signaling #2306), TH (rabbit polyclonal, Pel-Freeez #40101-0)

# 2.2.7 Statistical analysis

Western blot images from chemiluminescence were scanned via negative film scanning and analyzed by densitometry tool in ImageJ. Western blot images from LI-COR near-infrared imaging system were analyzed by LI-COR ImageStudio software. Statistical analyses were performed using Prism 7 software for all experiments. For the comparisons of non-HD and HD human post-mortem tissues, two-tailed unpaired t-tests were performed to assess statistical significance between groups. For the analysis of isolated squid axoplasms, a two-tailed paired t-test was performed to compare two experimental conditions within sister axoplasm pairs due to variability among squid. For the comparisons of different genotypes in mice, two-tailed unpaired t-tests were performed for comparisons between two groups, and one-away analysis of variance (ANOVA) was performed for comparisons among three groups. Following statistically significant one-way ANOVA results, Tukey's post-hoc analysis was performed in order to reveal the statistically significant comparisons.

#### 2.3 <u>Results</u>

#### 2.3.1 Activation of JNK in HD

Previous work from our lab demonstrated activation of JNK in the cell lysates of NSC34 cells transfected with Htt-Q56 compared to those transfected with Htt-Q18 (Morfini et al. 2009). Here, we report activation of JNK in post-mortem cortex of HD patients as well as experimental models of HD: isolated squid axoplasms used in previous study (Morfini et al. 2009) and R6/2 mice used in current study.

#### 2.3.1.1 Increased activation of JNK in post-mortem cortex of HD patients

Western blot analysis of post-mortem cortex samples from non-HD controls (n=4) and HD patients (n=7) showed increased level of pJNK normalized to that of GAPDH in HD patient samples compared to control (Figure 5A, 5B). Non-parametric unpaired two-tailed t-test revealed that this difference between non-HD controls (M<sup>1</sup>=0.07425, SD<sup>2</sup>=0.04648, 95% Cl<sup>3</sup> [<0.001, 0.1482]) and HD patients (M=0.9389, SD=0.5975, 95% Cl [0.3863, 1.491]) was statistically significant (p=0.0061, 95% Cl [0.149, 1.524]). Non-parametric unpaired two-tailed t-test analysis found no significant difference in the level of total JNK3 normalized to that of GAPDH between non-HD controls (M=2.49, SD=0.3368, 95% Cl [1.954, 3.025]) and HD patients (M=2.292, SD=0.6394, 95% Cl [1.701, 2.883]) (p=0.4121, 95% Cl [-0.825, 0.596]) (Figure 5A, 5C). The demographic information regarding the human samples used in this study is listed in Table 2.

<sup>&</sup>lt;sup>1</sup> M: mean

<sup>&</sup>lt;sup>2</sup> SD: standard deviation

<sup>&</sup>lt;sup>3</sup> CI: confidence interval



**Figure 5.** Increased activation of JNK in the cortex of HD patients. (A) Western blot analysis of the levels of pJNK and JNK3 in the cortices of non-HD controls and HD patients. GAPDH is provided as a loading control. (B) Two-tailed t-test revealed a statistically significant increase in the level of pJNK normalized to that of GAPDH in HD patients compared to non-HD controls, \*\*p=0.0.0061. (C) Two-tailed t-test revealed no significant difference between the level of JNK3 normalized to that of GAPDH in non-HD controls compared to HD, p=0.4121. Error bars represent SD.

#### 2.3.1.2 Activation of JNK by mHtt in isolated squid axoplasms

Activation of JNK by mHtt was analyzed in two different experimental models of HD used in this study: isolated squid axoplasms and R6/2 mice. Axoplasms were isolated from squid giant axons as described in 2.2. A total of 7 pairs of isolated squid axoplasms were used, with one axon of each pair perfused with recombinant Htt-Q16 (Htt) and the other with Htt-Q55 (mHtt) proteins described in 2.2 at a concentration of 200nM and analyzed by western blotting and imaged on a LI-COR Odyssey Fc near-infrared imaging system. Following image acquisition, the signals for KHC and pJNK were obtained using LI-COR Image Studio software. Non-parametric paired two-tailed t-test using Prism 7 software revealed a statistically significant increase in the level of pJNK that were normalized to that of KHC in axoplasms perfused with Htt-Q55 (M=0.0239, SD=0.007671, 95% CI [0.01629, 0.03048]) compared to their Htt-Q16 perfused sister axoplasms (M=0.02066, SD=0.008452, 95% CI [0.01284, 0.02847]), p=0.0156 (Figure 6). Due to the inherent differences among wild-caught squid (see Figure 3), the differences between sister axoplasms are represented as % change in Htt-Q55 from Htt-Q16 instead of raw normalized values (Figure 6B).



**Figure 6.** Increased activation of JNK in isolated squid axoplasms perfused with mHtt. (A) A representative immunoblot from 3 pairs of isolated squid axoplasms perfused with either recombinant Htt-Q16 or Htt-Q55 (200nM). Axoplasms perfused with Htt-Q55 shows increased level of pJNK compared to their sister axoplasms perfused with Htt-Q16. KHC is provided as a loading control and Htt demonstrates comparable level of perfused recombinant Htt-Q16 and Q55. (B) Two-tailed paired t-test of 7 pairs of axoplasms revealed a statistically significant increase in the level of pJNK normalized to that of KHC in axoplasms perfused with Htt-Q55 compared to their sister axoplasms perfused with Htt-Q16, \*p=0.0156. The difference between sister axoplasms are represented as % change in Htt-Q55 from Htt-Q16. Error bars represent SD.

#### 2.3.1.3 Activation of JNK in R6/2 mouse model of HD

To evaluate the activation of JNK by mHtt *in vivo*, cortices and striata from postnatal day 50 (P50) wildtype (n=5) and R6/2 (n=5) mice, which is a symptomatic age for R6/2 mice, were collected and analyzed by western blot as described in **2.2**. Unpaired two-tailed t-test with Welch's correction revealed a statistically significant increase in the level of pJNK normalized to that of GAPDH loading control in the prefrontal cortex (PFC) of R6/2 mice (M=1.556, SD=0.2809, 95% CI [1.207, 1.905]) compared to that of wildtype mice (M=1.098, SD=0.2697, 95% CI [0.7634, 1.433]), t(7.987)=2.63, p=0.0302 (**Figure 7A, 7C**), as well as in the striatum (STR) of R6/2 mice (M=0.8432, SD=0.2357, 95% CI [0.2667, 0.6393]), t(6.785)=3.122, p=0.0175 (**Figure 7B, 7D**).



**Figure 7. Increased activation of JNK in R6/2 mouse model of HD.** R6/2 mice (P50) shows increased level of pJNK compared to age-matched wildtype mice in both prefrontal cortex (PFC) **(A)** and striatum (STR) **(B)**. Unpaired two-tailed t-test with Welch's correction revealed a statistically significant increase in pJNK in PFC, \*p=0.0302 **(C)**, and STR, \*p=0.0175 **(D)**. Error bars represent SD.

#### 2.3.2 Characterization of R6/2 mice

R6/2 mice begin to show defects in motor functions around P45 and typically die around P100. Before investigating the effect of JNK3 knockout in these mice, we characterized the biochemical pathology of R6/2 mice at P45-P50, which have been previously reported by others. R6/2 mice at this age do not have significant neuronal cell loss (Gatto et al. 2015), but several reports demonstrate reduced levels of synaptic markers in the striatum, indicating synaptic dysfunction and loss prior to cell death.

# 2.3.2.1 Biochemical analysis of loss of synaptic connectivity in the striatum of R6/2 mice

Mice were euthanized and cortex and striatum samples were collected as described in **2.2**. Total levels of two synaptic markers, postsynaptic density protein (PSD-95) and dopamine- and cyclic-AMP-regulated phosphoprotein of molecular weight 32,000 (DARPP-32), were determined in the striata of wildtype (n=5) and R6/2 (n=7) mice at P45. Unpaired two-tailed t-test with Welch's correction revealed a statistically significant reduction in the level of PSD-95 normalized to that of GAPDH in R6/2 mice (M=0.1754, SD=0.03074, 95% CI [0.1469, 0.2038]) compared to wildtype mice (M=0.6852, SD=0.2848, 95% CI [0.3316, 1.039]), t(4.067)=3.986, p=0.0158 (Figure 8A, 8B) as well as the level of DARPP-32 normalized to that of GAPDH in R6/2 mice (M=0.223, SD=0.1031, 95% CI [0.1277, 0.3184]) compared to wildtype mice (M=0.7239, SD=0.3197, 95% CI [0.3269, 1.121]), t(4.599)=3.38, p=0.0224 (Figure 8A, 8C).



**Figure 8.** Loss of synaptic markers in the striatum of R6/2 mice. (A) Western blot image of synaptic markers PSD-95, DARPP-32 in the striatum of R6/2 mice at P45. GAPDH is provided as a loading control. Unpaired two-tailed t-test with Welch's correction revealed a statistically significant reduction in the level of PSD-95, \*p=0.0158, (B) and DARPP-32, \*p=0.0224, (C) in R6/2 mice. Error bars represent SD.

# 2.3.3 Characterization of JNK3<sup>-/-</sup> mice

Genetic deletion of one isoform of can lead to alterations in the expression levels of other isoforms in order to compensate for the deletion. To test whether or not the deletion of JNK3 in mice affect the expression levels of JNK isoforms as well as the expression levels of biochemical markers of interest, we compared striatum of wildtype and JNK3<sup>-/-</sup> mice at P50.

# 2.3.3.1 JNK isoform expression in JNK3<sup>-/-</sup> mice

Mice were euthanized and striatum samples from wildtype (n=3) and JNK3<sup>-/-</sup> mice (n=3) were collected and analyzed by western blot with antibodies for JNK1, JNK2 and JNK3. As expected, no JNK3 was detected in JNK3<sup>-/-</sup> mice, confirming the genetic deletion in these mice (**Figure 9A, 9D**). No statistical analysis could be done for the comparison of JNK3 levels between wildtype and JNK3<sup>-/-</sup> mice as their values in JNK3<sup>-/-</sup> mice were zero. Unpaired two-tailed t-test with Welch's correction revealed a statistically significant increase in the level of JNK1 normalized to that of GAPDH in the striata of JNK3<sup>-/-</sup> mice (M=0.878, SD=0.02536, 95% CI [0.815, 0.941]) compared to wildtype mice (M=0.369, S=0.09642, 95% CI [0.1295, 0.6085]), t(2.275)=8.843, p=0.0083 (**Figure 9A, 9B**), but there was no significant difference between the level of JNK2 between wildtype (M=0.4967, SD=1.064, 95% CI [0.2325, 0.7609]) and JNK3<sup>-/-</sup> mice (M=0.474, SD=0.2671, 95% CI [-0.1895, 1.138]), t(2.619)=0.1366, p=0.9012 (**Figure 9A, 9C**).



**Figure 9. Expression of JNK isoforms in the striatum of JNK3**<sup>-/-</sup> **mice. (A)** Western blot image of JNK1, JNK2 and JNK3 expression in the striatum of P50 wildtype and JNK3<sup>-/-</sup> mice. GAPDH is provided as a loading control. Unpaired two-tailed t-test with Welch's correction revealed a statistically significant increase in the amount of JNK1 (B), \*\*p=0.0083, but not JNK2 (C) in JNK3<sup>-/-</sup> mice compared to wildtype mice. No JNK3 expression was detected in JNK3<sup>-/-</sup> mice (D). Error bars indicate SD.

# 2.3.3.2 <u>Comparison of the expression of synaptic and neuronal connectivity</u> <u>markers in the striatum of JNK3<sup>-/-</sup> mice</u>

Mice were euthanized and striata from wildtype (n=3) and JNK3<sup>-/-</sup> mice (n=3) were collected and analyzed by western blot with antibodies for PSD-95, DARPP-32 and tyrosine hydroxylase (TH). TH is a rate-limiting enzyme for the production of dopamine and is used as a marker for dopaminergic neurons. As resident neurons in the striatum are GABAergic and do not express TH, the amount of TH detected in the striatum is an indirect measure of processes stemming from the dopaminergic neurons in substantia nigra. Unpaired two-tailed t-test with Welch's correction showed no significant difference in the levels of PSD-95 (M<sub>wildtype</sub>=0.9433, SD<sub>wildtype</sub>=0.368, 95% Cl<sub>wildtype</sub> [0.02917, 1.858]; Mknockout=1.06, SDknockout=0.1078, 95% Clknockout [0.7921, 1.328], t(2.341)=0.5269, p=0.6440), DARPP-32 (M<sub>wildtype</sub>=0.6147, SD<sub>wildtype</sub>=0.1844, 95% Cl<sub>wildtype</sub> [0.1566, 1.073]; Mknockout=0.8077, SDknockout=0.1521, 95% Clknockout [0.4297, 1.186], t(3.861)=1.398, p=0.2370) and TH (M<sub>wildtype</sub>=0.4623, SD<sub>wildtype</sub>=0.1791, 95% Cl<sub>wildtype</sub> [0.0174, 0.9073]; M<sub>knockout</sub>=0.5123, SD<sub>knockout</sub>=0.0.3506, 95% Cl<sub>knockout</sub> [-0.3586, 1.383], t(2.977)=0.22, p=0.8401) normalized to that of GAPDH in the striata of wildtype and JNK3<sup>-/-</sup> mice (Figure 10).



**Figure 10. Levels of synaptic and neuronal connectivity markers in the striatum of JNK3**<sup>-/-</sup> **mice. (A)** Western blot image of PSD-95, DARPP-32 and TH in the striatum of P50 wildtype and JNK3<sup>-/-</sup> mice. (B) Unpaired two-tailed t-test with Welch's correction revealed no statistically significant differences in the levels of PSD-95, DARPP-32 and TH between wildtype and JNK3<sup>-/-</sup> mice. Error bars represent SD.

# 2.3.4 Amelioration of HD phenotypes in R6/2-JNK3<sup>-/-</sup> mice

# 2.3.4.1 <u>Recovery of biochemical markers of synaptic connectivity</u>

With the establishment of baseline by comparing potential differences between wildtype and R6/2 mice as well as between wildtype and JNK3<sup>-/-</sup>, we next examined the effects of JNK3 knockout in the R6/2 mice to investigate the contribution of JNK3 in HD phenotypes observed in R6/2 mice. Striata from P50 wildtype (n=4), R6/2 (n=4), R6/2-JNK3<sup>-/-</sup> (n=4) mice were collected as described in 2.2. One-away ANOVA revealed statistically significant differences in the level of PSD-95 normalized to that of GAPDH among three groups (F(2, 9)=18.38, p=0.0007). Tukey's post-hoc analysis confirmed statistically significant differences in the normalized PSD-95 level between wildtype and R6/2 (p<0.001) and between wildtype and R6/2-JNK3<sup>-/-</sup> (p<0.01), but not between R6/2 and R6/2-JNK3<sup>-/-</sup> (Figure 11A, 11B). One-way ANOVA revealed statistically significant differences in the level of DARPP-32 normalized to that of GAPDH among three groups (F(2, 9)=10.53, p=0.0044). Tukey's post-hoc analysis confirmed statistically significant differences in normalized DARPP-32 level between wildtype and R6/2 (p<0.01), but not between wildtype and R6/2-JNK3<sup>-/-</sup> and between R6/2 and R6/2-JNK3<sup>-/-</sup> (Figure 11A, **11C)**. One-way ANOVA revealed statistically significant differences in the level of TH normalized to that of GAPDH among three groups (F(2, 9)=7.143, p=0.0139). Tukey's post-hoc analysis confirmed statistically significant differences in normalized TH level between wildtype and R6/2 (p<0.05), but not between wildtype and R6/2-JNK3<sup>-/-</sup> and between R6/2 and R6/2-JNK3<sup>-/-</sup> (Figure 11A, 11D).



**Figure 11. Amelioration of hallmark biochemical phenotypes of HD in R6/2-JNK3**<sup>-/-</sup> **mice. (A)** Western blot image shows the loss of synaptic markers PSD-95 and DARPP-32 as well as TH, marker of dopaminergic innervation into the striatum in P50 R6/2 mice. This loss is partially and fully restored to normal levels in R6/2-JNK3<sup>-/-</sup>. One-way ANOVA followed by Tukey's post-hoc analysis found **(B)** a statistically significant reduction in PSD-95 level in R6/2 (\*\*\*p<0.001, compared to wildtype) and a partial rescue in R6/2-JNK3-/- (\*\*p=0.01, compared to wildtype), **(C)** a statistically significant reduction in DARPP-32 level in R6/2 (\*\*p<0.01, compared to wildtype), which is restored to normal level—non-significant difference from wildtype—in R6/2-JNK3<sup>-/-</sup> mice, and **(D)** a statistically significant reduction in TH level in R6/2 (\*p<0.05, compared to wildtype), which is restored to normal level in R6/2-JNK3<sup>-/-</sup> mice. Error bars represent SD.

#### 2.3.4.2 Expression of JNK isoforms in R6/2-JNK3<sup>-/-</sup> mice

The expression levels of different JNK isoforms were analyzed in R6/2-JNK3<sup>-/-</sup> mice to examine potential compensatory increase in other isoforms and interaction between Htt transgene expression and JNK3 knockout. The same set of samples used in **2.3.4.1** were analyzed by immunoblotting with antibodies for each of the JNK isoforms. One-way ANOVA revealed statistically significant differences in the level of JNK1 normalized to GAPDH among three groups (F(2, 9)=7.393, p=0.0126). Tukey's post-hoc analysis identified a significant difference in JNK1 level between wildtype and R6/2-JNK3-/- mice (p<0.05) as well as between R6/2 and R6/2-JNK3-/- (p<0.05) but no difference between wildtype and R6/2 mice (Figure 12A, 12B), indicating that increase in level JNK1 is most likely from genetic deletion of JNK3, which was also observed in JNK3-/- mice (Figure 9). One-way ANOVA showed no significant differences in the level of JNK2 normalized to GAPDH among three groups (F(2, 9)=3.048, p=0.0976) although there was a trend for increased level of JNK2 in R6/2-JNK3<sup>-/-</sup> (Figure 12A, 12C). One-way ANOVA revealed significant differences in the level of JNK3 normalized to GAPDH among three groups (F(2, 9)=8.254, p=0.0092). As expected from genetic knockout of JNK3, Tukey's post-hoc analysis identified a significant reduction in the level of JNK3 in R6/2-JNK3<sup>-/-</sup> mice compared to wildtype (p < 0.01) but only a trend compared to R6/2 mice (p = 0.0614), and there was no significant difference between wildtype and R6/2 mice (p=0.4150) although there may be a trend for reduced level of JNK3 in R6/2 mice (Figure 12A, 12D).



**Figure 12. Expression of JNK isoforms in R6/2 and R6/2-JNK3**<sup>-/-</sup> **mice. (A)** Western blot image shows levels of JNK1, JNK2 and JNK3 expression in the striatum of P50 wildtype, R6/2 and R6/2-JNK3<sup>-/-</sup> mice. GAPDH is provided as a loading control. **(B)** R6/2-JNK3<sup>-/-</sup> mice have a significant increase in the level of JNK1 compared to wildtype (\*p<0.05) and R6/2 (†p<0.05). **(C)** There is no significant difference in the level of JNK2 although there is a trend for increased level of JNK2 in R6/2-JNK3<sup>-/-</sup> mice. **(D)** R6/2-JNK3<sup>-/-</sup> mice, as expected, do not express JNK3 (\*\*p<0.01, compared to wildtype), and there is no significant difference in the level of JNK3 between wildtype and R6/2. Error bars represent SD.

#### 2.3.5 Activation of JNK upstream kinase by mHtt in isolated squid axoplasms

JNK is a member of the mitogen-activated protein kinase (MAPK) family. Phosphorylation of the activation loop of MAPK by upstream kinases, mitogen-activated protein kinase kinases (MAPKKs), activate MAPK. MAPKKs themselves are also activated by phosphorylation of the activation loop by further upstream kinases, mitogenactivated protein kinase kinase kinases (MAPKKs). To determine whether mHtt activates JNK via upstream kinases we examined activation of MAPKKs by mHtt.

Mitogen-activated protein kinase kinase 7 (MKK7) is one of the MAPKKs known to phosphorylate and activate JNK. Using the recombinant Htt-Q16 and Htt-Q55 proteins used in **Figure 6**, mHtt-mediated activation of MKK7 in isolated squid axoplasms was analyzed by western blot with an antibody that recognizes the active form of MKK7 (phospho-MKK7). The level of phospho-MKK7 in 6 pairs of isolated squid axoplasms were analyzed by non-parametric two-tailed paired t-test, and the analysis revealed a statistically significant increase in the level of phospho-MKK7, normalized to that of KHC loading control, in the axoplasms perfused with Htt-Q55 (M=0.01574, SD=0.007287, 95% CI [0.008091, 0.02338]) compared to their sister axoplasms perfused with Htt-Q16 (M=0.01258, SD=0.007089, 95% CI [0.005144, 0.02002]), p=0.0312 (**Figure 13**).



**Figure 13. mHtt-mediated activation of MKK7 in isolated squid axoplasms. (A)** A representative immunoblot image demonstrating the activation of MKK7 in isolated squid axoplasms perfused with mHtt (Htt-Q55). KHC is provided as a loading control. **(B)** Non-parametric two-tailed paired t-test of 6 pairs of axoplasms found a statistically significant increase in the level of pMKK7 in the axoplasms perfused with Htt-Q55 compared to Htt-Q16, \*p=0.0312. The differences between sister axoplasms are represented as % change from Q16. Error bars indicate SD.

# 2.4 DISCUSSION

Experiments presented in this chapter were designed based on the previously published work from our lab demonstrating the activation of JNK3 by mHtt underlies mHttmediated axonal transport defects (Morfini et al. 2009; Morfini et al. 2006). To address the extent of the contribution that JNK3 activation plays in HD pathology, R6/2 mice, a transgenic mouse model of HD, were crossed with JNK3<sup>-/-</sup> mice. Based on our knowledge that defects in axonal transport lead to neurodegeneration (Reid et al. 2002; Karle et al. 2012; Crimella et al. 2012; López et al. 2015; Puls et al. 2005; Hafezparast 2003; Farrer et al. 2009; Konno et al. 2017), we hypothesized that correcting mHtt-mediated axonal transport deficits by genetic deletion of JNK3 would be beneficial in preserving dying-back neuropathy and loss of axonal connectivity as shown in our recent work (Gatto et al. 2015) and that it would alleviate mHtt-mediated neurodegeneration and HD symptoms recapitulated in R6/2 mice.

# 2.4.1 Increased activation of JNK in HD patients and various experimental models of HD

Western blot analysis of post-mortem cortex tissues collected from non-HD donors and HD patients showed a significant increase in the level of phosphorylated (active) JNK in cortices of HD patients (**Figure 5**). The demographic of the donors varied widely in the age of death as well as post-mortem intervals (**Table 2**), which contributed to the variability within the experimental groups, especially for the HD group. Nonetheless, nonparametric two-tailed t-test determined that the difference was statistically significant (\*\*p<0.01). While activation of JNK has been shown in many animal and cellular models
of HD (Morfini et al. 2009; Morfini et al. 2006; Perrin et al. 2009; Taylor et al. 2013; Apostol et al. 2006; Liu 1998), this is the first demonstration of elevated level of active JNK in HD patients to our knowledge. This is an important finding because it suggests that increased activation of JNK is relevant to human HD and that any amelioration of HD phenotypes observed by inhibiting JNK in animal and cellular models may also apply to HD patients.

We also found increased activation of JNK in experimental models of HD used in this study: isolated squid axoplasms perfused with recombinant mHtt (Figure 6) and R6/2 mice (Figure 7). The antibodies used in the analysis of pJNK in mouse and isolated squid axoplasms (Cell Signaling, #4668) and human tissue (Cell Signaling, #9251) were raised against the two phosphorylation sites within the activation loop (Thr183/Tyr185), which are conserved among all three isoforms of JNK (JNK1/2/3). Therefore, they detect all three isoforms of JNK and it is not clear whether or not they have same affinity for all isoforms. While some efforts can be made to discern isoform-specific activation of JNK based on their molecular weight (Figure 4) between JNK1 and JNK2/3, it is not yet possible to selectively detect activation of JNK3 with immunoblotting due to the lack of antibody that selectively recognizes active form of JNK3 but not other JNK isoforms, and it is unlikely that such antibody will be available in the future due to the conserved activation sites among JNK isoforms. Potential approaches to measure activation of JNK3 in an isoform-selective manner are an enzyme-linked immunosorbent assay (ELISA) using a JNK3 antibody to capture JNK3 in the lysate followed by detection of active JNK using a pJNK antibody (or vice versa), and immunoprecipitation of JNK3 followed by immunoblotting with a pJNK antibody (or vice versa). However, both approaches require JNK3 antibody and pJNK antibody to be generated from different hosts. We have

characterized many commercial JNK3 and pJNK antibodies. Unfortunately, JNK3 and pJNK antibodies validated in our lab are all from rabbit. If JNK3 and/or pJNK antibodies from hosts other than rabbit become available in the future, the proposed techniques could be utilized to examine isoform-specific activation of JNK3 in HD.

## 2.4.2 Changes in expression of JNK isoforms in JNK3<sup>-/-</sup>, R6/2 and R6/2-JNK3<sup>-/-</sup> mice

When expression of one or more genes are disturbed by genetic manipulations such as knockouts and knockdowns, upregulation of other isoforms of the same gene or genes that encode for proteins with similar cellular functions is often observed in a compensatory response. Indeed, we observed upregulation of JNK1 in JNK3-/- (Figure 9) as well as R6/2-JNK3-/- mice (Figure 12). JNK1 is ubiquitously expressed in all tissues, and JNK2 is expressed in many tissues and enriched in muscles. JNK3 has the most tissue-selective expression among the three JNK isoforms, mainly expressed in the brain and to a lesser extent in the heart, the pancreas and the testis (Yarza et al. 2016; Coffey 2014). A compensatory increase in JNK1 expression upon genetic deletion of JNK3 suggests some functional redundancy between JNK1 and JNK3 although tissue-specific expression of JNK3 indicates JNK3 has cellular functions distinct from JNK 1 and JNK2. In addition, JNK2/3 have been shown to be activated in response to stimuli such as stress while JNK1 is constitutively active in neurons (Coffey et al. 2002), indicating that the loss of JNK3 may not be well compensated by upregulation of JNK1.

There seemed to be a trend for a reduction in the expression of JNK3 in R6/2 mice, which could be a compensatory mechanism for increased activation of JNK3 with the transgenic expression of mHtt. Although the reduction in JNK3 expression in R6/2 mice

did not reach statistical significance in this study, results from another study involving a larger number of animals indicate a decreased expression of JNK3 in R6/2 mice (Kang et al. *in preparation*).

## 2.4.3 Alleviation of HD pathology by genetic deletion of JNK3 in R6/2 mice

Based on our previous results identifying JNK3 as the critical mediator of axonal transport defects by mHtt (Morfini et al. 2009; Morfini et al. 2006) and preliminary data demonstrating the rescue of transcallosal connectivity in R6/2-JNK3<sup>-/-</sup> mice (Kang et al. in preparation), we hypothesized that deletion of JNK3 would alleviate many of HD phenotypes observed in R6/2 mice. Indeed, R6/2-JNK3<sup>-/-</sup> mice showed normal or near normal levels of synaptic proteins PSD-95 and DARPP-32 as well as TH, an indirect marker of nigrostriatal dopaminergic projections to the striatum, at a symptomatic age (P50) (Figure 11), indicating that neuronal connectivity has been spared in these mice. Behavioral phenotypes that are unmistakably observed in R6/2 mice such as deficits in rotarod performance, clasping test and nesting behavior also improved in R6/2-JNK3<sup>-/-</sup> mice, demonstrating functional recovery along with spared neuronal connections (Kang et al. in preparation). However, R6/2-JNK3<sup>-/-</sup> mice eventually succumb to the disease phenotypes in the late stage (P75 and beyond), and their lifespan is approximately P125, which is about 25% longer than that of R6/2 mice in our colony (Kang et al. in preparation), and 25% increase in the survival of R6/2 mice one of the most efficacious results with any treatments in these mice (Li et al. 2005). As an exaggerated model of HD, R6/2 mice have a very early disease onset and severe symptoms, and the global expression of the mHtt transgene confounds potential causes of death in these mice due to non-neuronal

complications such as metabolic syndromes and cardiac dysfunctions. We are currently investigating the effect of JNK3 deletion in a different mouse model of HD, Q175, which has much slower disease progression.

JNKs are traditionally described as stress-activated kinases and indeed they are activated in response to various stress stimuli such as ultraviolet irradiation, hypoxia, and cytokines. While the amelioration of HD pathology in R6/2-JNK3<sup>-/-</sup> mice may be in part due to potentially diminished stress responses from the genetic deletion of JNK3, our hypothesis and previously published data provide a specific mechanism of *one* of the roles JNK3 plays in the axonal transport impairment and subsequent neurodegeneration in HD.

In sum, the data presented in this chapter demonstrate that loss of neuronal connections was prevented and significant improvements in motor functions and survival were observed in R6/2-JNK3<sup>-/-</sup> mice, indicating that activation of JNK3 by mHtt is a critical pathogenic event in HD, and inhibiting JNK3 could be a promising therapeutic strategy for HD.

## 2.4.4 <u>Potential effects of mHtt-mediated aberrant JNK activation in synaptic</u> <u>transmission</u>

As shown in this chapter, synaptic connections vulnerable in HD were spared in R6/2-JNK3<sup>-/-</sup> mice, presumably from preventing dying-back neuropathy by rescuing axonal transport. While we have demonstrated that the *levels* of synaptic proteins are restored, whether or not the synaptic transmission is rescued in R6/2-JNK3<sup>-/-</sup> mice was not directly addressed in this study. A collaboration through CHDI Foundation is currently

underway to examine recovery of synaptic transmission in these mice. Furthermore, unpublished preliminary work in squid giant synapses demonstrated that microinjection of mHtt into squid giant synapses leads to dysfunctions in synaptic transmission, and the effect of mHtt was prevented by co-injection of a pharmacological inhibitor of JNK, SP600125, along with mHtt (Ivannikov et al, *unpublished*). This finding suggests that JNK3-mediated toxic effects of mHtt on neuronal connections may involve direct effects of JNK3 on synaptic function as well as on axonal transport.

#### 2.4.5 Potential mechanism of activation of JNK by mHtt via upstream kinases

JNKs, as members of mitogen-activated protein kinase (MAPK) family, are activated by upstream kinases mitogen-activated protein kinase kinases (MKKs) such as MKK4/MKK7, which are activated by further upstream kinases mitogen-activated protein kinase kinase kinases (MAPKKS). Data from this chapter shows activation of MKK7, an upstream kinase of JNKs, by mutant huntingtin (mHtt) in isolated squid axoplasms (Figure 13), suggesting that mHtt may activate JNK via upstream kinases. Furthermore, studies using co-expression of mHtt and mixed-linage kinase 2 (MLK2), a member of MAPKKKs that is upstream of MKK7, in non-neuronal cell lines demonstrated a direct interaction between Htt and MLK2 (Liu et al. 2000). Preliminary result from our lab using mouse brain lysates show a direct interaction of Htt with MLK by co-immunoprecipitation, indicating that the Htt-MLK interaction occurs in the brain at endogenous levels. These results suggest that Htt may act as a scaffold for MAPK signaling components.

## 2.4.6 Future directions

As we further our understanding of the pathogenic mechanism of HD and regulation of axonal transport, there are many outstanding questions that warrant future studies. One of those questions is the mechanism of the inhibition of cytoplasmic dynein (CDyn)-based retrograde axonal transport by mHtt. It is clear that mHtt inhibits both anterograde and retrograde axonal transport of membrane-bound cargoes. Previous work from our lab has identified phosphorylation of kinesin heavy chain by JNK3 is the mechanism of anterograde axonal transport inhibition by mHtt. While the mechanism underlying the inhibition of retrograde axonal transport remains unknown, our data from isolated squid axoplasms strongly suggests that JNK3 may also mediate the toxic effect of mHtt on retrograde axonal transport as perfusion of recombinant JNK3 inhibits retrograde axonal transport and co-perfusion of mHtt with JNK inhibitor SP600125 rescues both anterograde and retrograde axonal transport (Morfini et al. 2009; Morfini et al. 2006).

Our ongoing research effort is focused on determining the interaction of Htt and MLKs, and the effects polyQ expansion on such interaction, as well as addressing the effect of JNK3 in another mouse model of HD, Q175 mice, which better represent human HD progression. Based on our findings described in this chapter, if a compound that can isoform-selectively inhibit JNK3 becomes available in the future, it could be a very promising therapeutic compound for HD patients.

#### CHAPTER III.

# III. REGULATION OF RETROGRADE AXONAL TRANSPORT BY NEUROTROPHIN SIGNALING

#### 3.1 Background

#### 3.1.1 Discovery of neurotrophins

Neurotrophins are a family of secreted proteins that are critical for neuronal development, function, and survival (Hefti 1997; Binder and Scharfman 2004). Classic studies in 1930s using chick embryos have demonstrated that target cells innervated by neurons produce trophic signals that promote the survival of innervating neurons (Hamburger 1934), introducing the neurotrophic factor hypothesis. A couple of decades following this finding, the first neurotrophin was identified and named nerve growth factor (NGF) (Levi-Montalcini and Hamburger 1951; Levi-Montalcini 1966). Decades later, another neurotrophin was identified based on its effects on promoting survival of dorsal root ganglion neurons. This protein was eventually purified from pig brain and was named brain-derived neurotrophic factor (BDNF) (Barde et al. 1982). Following the discovery of NGF and BDNF, other neurotrophins such as neurotrophin-3 (NT-3) (Maisonpierre et al. 1990) and neurotrophin-4/5 (NT-4/5) (Hallböök et al. 1991; Ip et al. 1992; Davies et al. 1993) were also identified as a member of a neurotrophin family.

## 3.1.2 <u>Classification of neurotrophic factors</u>

Since the discovery of neurotrophins, other soluble proteins have been identified to exert trophic effects on neurons and have been classified into a larger family of proteins called *neurotrophic factors*. Neurotrophic factors are commonly classified into three main families based on structural and functional similarities: neurotrophins, ciliary neurotrophic factor (CNTF) family (also known as neuropoietic/neurotrophic cytokine family), glial cell line-derived neurotrophic factor (GDNF) family (also known as transforming growth factor beta (TGF- $\beta$ ) superfamily) (Sato 2017; Kalinowska-Lyszczarz and Losy 2012). In addition to the three main families, the list of proteins that have been identified to have neurotrophic effects continues to grow, which includes epidermal growth factor (EGF), neuregulins, vascular endothelial growth factor (VEGF), and fibroblast growth factor (FGF) (Malenka et al. 2009). A non-exhaustive list of neurotrophic factor families and their members are provided in **Table 3**.

Neurotrophic factors		
Neurotrophins	GDNF Family (TGF-β superfamily)	CNTF family (Neurotrophic cytokines)
<ul> <li>NGF</li> <li>BDNF</li> <li>NT-3</li> <li>NT-4/5</li> </ul>	<ul> <li>GDNF family</li> <li>TGF-β family</li> <li>BMP family</li> <li>Neuturin</li> <li>Artemin</li> <li>Persephin</li> <li></li> </ul>	<ul> <li>CNTF</li> <li>Leukemia inhibitory factor</li> <li>IL-6</li> <li>IL-11</li> <li>EGF family</li> <li>FGF</li> <li>VEGF</li> <li>Neuropoetin</li> <li></li> </ul>

**Table 3. Classification of neurotrophic factors.** NGF: nerve growth factor, BDNF: brain-derived neurotrophic factor, NT-3: neurotrophin-3, NT-4/5: neurotrophin-4/5, GDNF: glial-derived neurotrophic factor, TGF- $\beta$ : transforming growth factor, BMP: bone morphogenic protein, CNTF: ciliary neurotrophic factor, IL-6: interleukin 6, IL-11: interleukin 11, EGF: epidermal growth factor, FGF: fibroblast growth factor, VEGF: vascular endothelial growth factor.

#### 3.1.3 Synthesis and release of neurotrophins

Neurotrophins are typically released from post-synaptic cells that receive inputs from neurons, neurons in case of neuron-neuron interaction, and from muscle cells, in case of neuron-muscle interaction at the neuromuscular junction. They bind to neurotrophin receptors on the innervating, pre-synaptic neurons. Neurotrophins are synthesized as a precursor form of pre-pro-neurotrophins (i.e. preproBDNF, preproNGF, ...), which are cleaved into pro-neurotorphins (i.e. proBDNF, proNGF, ...), which are cleaved into pro-neurotorphins (i.e. proBDNF, proNGF, ...), which are then cleaved to produce mature neurotrophins (ie.g. BDNF, NGF, ...). Mature neurotrophins exist as homodimers (Pirvola and Ylikoski 2003; Al-Qudah and Al-Dwairi 2016) although a BDNF/NT-3 heterodimer with 10-fold less affinity to their receptors has been reported in an artificially overexpressed setting (Jungbluth et al. 1994).

## 3.1.4 <u>Neurotrophin receptors</u>

Despite the fact that neurotrophins share more than 50% sequence homology, secreted neurotrophins isoform-specifically bind to their receptors called either tropomyosin receptor kinase or tyrosine receptor kinase A/B/C (TrkA/B/C). NGF binds to TrkA, BDNF and NT-4 binds to TrkB, and NT-3 binds to TrkC but it also binds to TrkA and TrkB with low affinity. All neurotrophins can also bind to another receptor called p75 neurotrophin receptor (p75<sup>NTR</sup>) albeit with low affinity (Chao 2003; Skaper 2008) (**Figure 14**). Trk receptors are members of receptor tyrosine kinase (RTK) family with a single transmembrane domain and a cytoplasmic tyrosine kinase domain surrounded by multiple tyrosine residues. p75<sup>NTR</sup> is thought to form a complex with Trk receptors and modulate their specificity and kinetics of ligand binding (Chao 2003; Skaper 2008).

Interestingly, p75<sup>NTR</sup> binds to pro-neurotrophins with much higher affinity than mature neurotrophins (R. Lee 2001). In addition, binding of pro-neurotrophins to p75<sup>NTR</sup> leads to apoptotic signaling via its cytosolic death domain rather than trophic signaling (R. Lee 2001; Beattie et al. 2002), indicating that neurotrophin signaling can be modulated by regulation of pro-neurotrophin cleavage and the balance of pro-neurotrophin and mature neurotrophin can affect the biological outcome of neurotrophin signaling. Researchers have reported differential expressions of Trk receptors and neurotrophins depending on neuronal subtypes as well as developmental stages (Ylikoski et al. 1993; McMahon et al. 1994; Fariñas et al. 1998; Huang and Reichardt 2001; Pirvola and Ylikoski 2003; Kemi et al. 2006), suggesting that each neurotrophin has unique functions as well as overlapping functions in different cell types and developmental stages.



**Figure 14. Receptor-specificity of neurotrophins.** NGF binds to TrkA, BDN and NT-4 binds to TrkB, and NT-3 binds to TrkC. Receptors form a homodimer and trans-phosphorylate multiple tyrosine residues within and around the kinase domain of the other subunit upon ligand binding. Pro-neurotrophins (ProNGF, ProBDNF, ...) bind to p75<sup>NTR</sup> receptor. All four mature neurotrophins (NGF, BDNF, ...) can also bind to p75<sup>NTR</sup> but at lower affinity compared to pro-neurotrophins. Unlike Trk receptors, ligand binding to p75<sup>NTR</sup> leads to activation of pro-apoptotic signaling cascades via its death domain.

## 3.1.5 Neurotrophin signaling cascade

Upon binding of neurotrophins to their receptors, Trk receptors transphosphorylate several tyrosine residues within (Tyr705, Tyr706, and Tyr707 in case of TrkB) and around the kinase domain (Tyr515 and Tyr816) of the other subunit, then become activated. Active Trk receptors have similar downstream signaling cascades although there are differences in the extent of activation of specific signaling pathways depending on neuronal cell types and the dominant neurotrophin type. Phosphorylation of different tyrosine residues on Trk receptors leads to activation of different pathways. For instance, phosphorylation of Tyr515 on TrkB, which is located just outside of the kinase domain on the N-terminal side, recruits Shc (Src homology 2 domain-containing transforming protein) which acts as an adapter protein for Grb2<sup>4</sup>-Sos<sup>5</sup> protein complex. Sos is a guanine nucleotide exchange factor (GEF) which promotes the exchange of guanosine diphosphate (GDP) to guanosine triphosphate (GTP) and activates a small GTPase protein Ras, leading to activation of Ras-Raf-MEK<sup>6</sup>-ERK<sup>7</sup> pathway as well as PI3K<sup>8</sup>-PDK1<sup>9</sup>-Akt<sup>10</sup> pathway. Phosphorylation of Tyr816 on TrkB, which is located adjacent to the kinase domain on the C-terminal side, recruits phospholipase C gamma (PLC<sub>γ</sub>), leading to subsequent activation of PLC<sub>γ</sub>-IP3<sup>11</sup>-CAMK<sup>12</sup> and PLC<sub>γ</sub>-DAG<sup>13</sup>-PKC<sup>14</sup>

<sup>8</sup> PI3K: phosphatidylinositide 3-kinase

<sup>&</sup>lt;sup>4</sup> Grb2: growth factor receptor-bound protein 2

<sup>&</sup>lt;sup>5</sup> Sos: Son of Sevenless

<sup>&</sup>lt;sup>6</sup> MEK: mitogen-activated protein kinase kinase

<sup>&</sup>lt;sup>7</sup> ERK: extracellular signal-regulated protein kinase

<sup>&</sup>lt;sup>9</sup> PDK1: phosphoinositide-dependent kinase 1

<sup>&</sup>lt;sup>10</sup> Akt: protein kinase B

<sup>&</sup>lt;sup>11</sup> IP3: inositol triphosphate

<sup>&</sup>lt;sup>12</sup> CAMK: Ca2+/calmodulin-dependent protein kinase

<sup>&</sup>lt;sup>13</sup> DAG: diacylglycerol

<sup>&</sup>lt;sup>14</sup> PKC: protein kinase C

pathways (as reviewed in Duman and Voleti 2012). Src family kinases (SFKs), which are non-receptor tyrosine kinases, are also found to be activated by TrkB upon neurotrophin binding. Interestingly, active SFKs can also directly phosphorylate and activate TrkB receptors, suggesting mutual regulation of SFKs and TrkB (Huang and McNamara 2010; Boltaev et al. 2017) (Figure 15).

Activation of several signaling cascades, including ones described above, upon neurotrophin signaling promotes survival and growth of neurons as well as synaptic plasticity. Some of these effects are locally mediated by direct and indirect interaction between Trk receptors and ion channels at the synapse (Takasu et al. 2002; Li et al. 1999; Balkowiec et al. 2000; Nagano et al. 2003). For instance, autocrine neurotrophin signaling at the synapse can activate PKC and CaMK, which can directly modulate local synaptic transmission by phosphorylation of AMPA<sup>15</sup> and NMDA<sup>16</sup> receptors (I. Song and Huganir 2002; Nagy 2008). On the other hand, other effects are mediated by transcriptional activation of pro-survival genes in the nucleus via activation of transcription factors such as cAMP response element-binding protein (CREB) (Duman and Voleti 2012; Ito and Enomoto 2016; Cunha 2010) upon target-derived neurotrophin signaling (Figure 15).

<sup>&</sup>lt;sup>15</sup> AMPA: α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid

<sup>&</sup>lt;sup>16</sup> NMDA: N-methyl-D-aspartate



**Figure 15. BDNF signaling cascade.** Upon BDNF binding, TrkB receptors autophosphorylate at Tyr705/706/707 residues within its kinase domain as well as Tyr515 and Tyr816. Phosphorylation of these residues lead to activation of several kinase signaling cascades which may include SFKs (red), Ras-Raf-MEK-ERK (blue), PI3K-PKD1-Akt (pink), PLC-IP3/DAG-PKC/CaMK (yellow). PKC and CaMK can phosphorylate AMPA and NMDA receptors to modulate their functions. Other pathways can activate transcription of pro-survival genes by phosphorylation of transcription factors such as CREB.

#### 3.1.6 <u>Retrograde transport of neurotrophins</u>

Some aspects of trophic effects by neurotrophins, such as transcriptional activation at the nucleus, require the active Trk receptors to be transported along the axon, sometimes over an extreme distance, to reach the neuronal soma (Heerssen et al. 2004; Ye et al. 2003). Upon activation, neurotrophin-bound Trk receptors are internalized by both clathrin-dependent endocytosis (Zheng et al. 2008) and clathrin-independent pinocytosis (Shao et al. 2002; Valdez et al. 2005). The endocytosed active neurotrophin-Trk receptor complex is transported to the cell body by cytoplasmic dynein (CDyn) in a membrane-bound organelle called signaling endosome with its neurotrophin-bound Nterminus contained in the lumen of the signaling endosome and the C-terminal kinase domain exposed to the cytoplasm during transport (Zweifel et al. 2005).

## 3.1.7 <u>Alterations in BDNF expression and transport in neurodegenerative diseases</u>

Brain-derived neurotrophic factor (BDNF) is a neurotrophin that promotes development, survival, and functions of neurons (Zuccato and Cattaneo 2009). Impaired neurotrophin signaling has been reported in several neurodegenerative diseases such as Alzheimer's disease (AD) (Phillips et al. 1991), Parkinson's disease (PD) (Murer et al. 2001), and Huntington's disease (HD) (Ferrer et al. 2000). Multiple groups have reported reductions in BDNF levels in HD (Ferrer et al. 2000; Zuccato et al. 2001, 2005; Gharami et al. 2008) as well as mHtt-mediated defects in transport of BDNF (Gauthier et al. 2004; del Toro et al. 2006). Several groups have proposed to alleviate HD pathology by enhancing BDNF signaling in various mouse models of HD. Systemic injection of recombinant BDNF in R6/2 resulted in increased level of BDNF expression and reduced

striatal atrophy (Giampá et al. 2013), and a similar result has been shown in N171-82Q HD mice treated with small molecule TrkB agonists (Jiang et al. 2013), but it is not clear whether the reduction in BDNF associated with HD is a direct or indirect effect of the pathology.

## 3.1.8 Rationale and hypothesis

The pro-survival signaling cascades activated by neurotrophins and the evidence for defective neurotrophin signaling in neurodegeneration prompted many scientists to use them as potential therapeutics for several neurodegenerative diseases such as AD, PD, HD, and amyotrophic lateral sclerosis. Unfortunately, these attempts were met with lack of efficacy and substantial side effects in dozens of clinical trials (Thoenen and Sendtner 2002). Even after decades of clinical trials with various neurotrophins including NGF and BDNF, there is currently no FDA-approved clinical use of neurotrophins in treating neurodegeneration, indicating that there is a need for deeper understanding of neurotrophin signaling is the regulatory mechanism underlying transport of signaling endosomes, which must contain active neurotrophin receptors for transcriptional activation by neurotrophin signaling. While numerous downstream signaling cascades of neurotrophin signaling have been identified, mechanisms underlying the activation of signaling endosome transport upon neurotrophin signaling remain elusive.

Based on evidence that regulation of axonal transport could involve phosphorylation of motor proteins, we hypothesized that activation of signaling endosome transport is regulated by phosphorylation of CDyn. Among several subunits of CDyn, dynein intermediate chain (DIC) is particularly of interest because it has been associated with cargo-binding function of CDyn and shown to be phosphorylated *in vivo* (Dillman and Pfister 1994). Preliminary data from our lab using radiometric labeling of rat primary cortical neurons with <sup>32</sup>P followed by immunoprecipitation of CDyn and autoradiography indicates selective increase in the phosphorylation of DIC upon BDNF stimulation of rat primary cortical neurons (Morfini et al. *unpublished*). Based on this preliminary result and previously identified mechanisms of axonal transport regulation by phosphorylation of motor proteins, we hypothesized that neurotrophin signaling, in the context of BDNF, leads to phosphorylation of DIC, and that this phosphorylation of DIC activates retrograde transport of signaling endosomes upon neurotrophin signaling.

#### 3.2 Methods and materials

#### 3.2.1 Rat primary cortical neuronal culture

All procedures involving animals have been approved by the Institutional Animal Care and Use Committee (IACUC) at University of Illinois at Chicago (UIC). Timedpregnant female Sprague-Dawley rats were ordered from Charles River Laboratories, and embryos were collected on embryonic day 18 (E18). Cortices from the embryos were dissected using fine forceps and collected in cold 1X Hank's balanced salt solution (HBSS, Gibco cat. 14185-052). Cortex tissues were trypsinized for 15 minutes in 37°C water bath with manual swirling every 5 minutes using trypsin (Gibco cat. 1509-046) at 0.5% final concentration. Trypsin was washed from the tissues by 3 washes with 1X HBSS then deactivated by adding Dulbecco's modified eagle medium (Gibco cat. 11995-065) supplemented with 10% fetal bovine serum (FBS, Gibco cat. 16000-044) and 1X penicillin/streptomycin (Pen/Strep, Gibco cat. 15140-122) (DMEM++). Trypsinized tissues were manually dissociated with a glass Pasteur pipet then triturated into singlecell suspension with a flame-polished Pasteur pipet with 50% smaller diameter. The number of cells were measured by hemocytometer, and the cell stocks were diluted to desired concentration for plating in DMEM++. Cells were plated onto plasma-treated tissue culture dishes that were coated with 0.5mg/mL poly-L-lysine (Sigma cat. P2636) in borate buffer overnight prior to plating and washed for 30 minutes 3 times with sterile water. 2 x  $10^6$  cells ere plated on P60 dishes and 5 x  $10^6$  cells were plated on P100 dishes. After plating, cells were incubated in a humidified CO<sub>2</sub> incubator with 5% CO<sub>2</sub> at 37°C for 3 hours to make sure they were attached to the dish, and the media was

completely exchanged with Neurobasal medium (Gibco cat. 10888-022) supplemented with 1X B27 (Gibco cat. 17504-044), 0.5mM GlutaMax (Gibco cat. 35050-061) (NB+++).

#### 3.2.2 BDNF stimulation and inhibitor treatment

Recombinant human brain-derived neurotrophic factor (BDNF) was purchased from Alomone Labs (cat. B-250). For BDNF stimulation of rat primary cortical neurons, 25ng/mL of BDNF was added in the media and incubated in 37°C CO<sub>2</sub> incubator for 10-20 minutes after 3 days in vitro (3DIV). For experiments involving kinase inhibitors, cells were pre-treated with inhibitors for 20 minutes prior to BDNF stimulation at following concentrations in NB+++: 200nM k252a (Millipore cat. 420297), 50µM SU6656 (Millipore cat. 572636), 30µM A419529 (Tocris cat. 3914), 30µM CRT 0066101 (Tocris cat. 4975), 10µM HIV TAT PKD1 substrate peptide (synthesized at UIC Research Resources Center; Sequence: GRKKRRQRRRPPAALVRQMSVAFFFK), 10µM HIV TAT PKCô substrate peptide (synthesized at UIC Research Resources Center; Sequence: GRKKRRQRRRPPAKRKRKGSFFYGG). After inhibitor treatment and BDNF stimulation, the media was completely aspirated, and cells were scraped in 1% SDS. Cell lysates were sonicated (20% amplification, 6 cycles; 1 cycle = 5s on, 2s off), and centrifuged at 21130 x g in Eppendorf 5424 tabletop centrifuge (15000 rpm) at 4°C for 15 minutes. Following centrifugation, clarified supernatant was transferred to a new Eppendorf tube and the same volume of 6X sample buffer was added for final concentration of 3X for western blot and Phos-tag SDS-PAGE.

## 3.2.3 Metabolic labeling of rat primary cortical neurons

For metabolic labeling of rat primary cortical neurons with <sup>32</sup>P, neurons were plated and cultured in as described above. On 2DIV, the 3/4 of media was exchanged with DMEM without phosphate (Gibco cat. 11971-025) to promote <sup>32</sup>P incorporation. On 3DIV, <sup>32</sup>P (PerkinElmer cat. NEX053H001MC) was added to the media, and cells were stimulated with BDNF for 20 minutes as described above.

#### 3.2.4 <u>Immunoprecipitation of dynein from rat primary cortical neurons</u>

Endogenous dynein complex was immunoprecipitated from rat primary cortical neurons using a monoclonal antibody against dynein intermediate chain (DIC). This antibody, clone 74.1, immunoprecipitates DIC as well as co-immunoprecipitating other subunits of dynein complex including dynein heavy chain and light intermediate chains. For immunoprecipitation, rat primary cortical neurons were scraped in a non-denaturing lysis buffer ROLB (50mM HEPES pH=7.4, 100mM NaCl, 0.5% Triton X-11, 0.1% sodium deoxycholate, 50mM NaF, 80mM  $\beta$ -glycerophosphate, 1mM EDTA) supplemented with phosphatase inhibitor cocktail II (Calbiochem cat. 524625, 1:200 dilution), protease inhibitor cocktail (Sigma cat. P8340, 1:200 dilution), okadaic acid (Calbiochem cat. 459620, 100nM), microcystin (Calbiochem cat. 475816), and Na<sub>3</sub>VO<sub>4</sub> (Sigma cat. S6508). Cell lysates were manually homogenized with a plastic pestle in 1.5mL Eppendorf tubes, then centrifuged at 21130 x g in Eppendorf 5424 tabletop centrifuge (15000 rpm) at 4°C for 15 minutes twice, transferring the supernatant to new Eppendorf tubes each time. The clarified supernatant was pre-cleared by incubation with pre-clearing mix containing protein G agarose beads (ThermoScientific cat. 20399), mouse IgG agarose beads

(Jackson Immunoresearch cat. 015-000-052), and 0.1% bovine serum albumin (Jackson Immunoresearch cat. 001-000-162) for 1 hour in 4°C. After pre-clearing, samples were centrifuged at 1,000RPM for 1 minute in Eppendorf 5424 tabletop centrifuge to pellet the agarose beads, and the supernatant was transferred to 1.5mL Eppendorf tubes containing protein G agarose beads and 74.1 antibody, and incubated for 3 hours with rotation in 4°C. After immunoprecipitation, samples were centrifuged at 1,000RPM for 1 minute in Eppendorf 5424 tabletop centrifuged at 1,000RPM for 1 minute in Eppendorf 5424 tabletop centrifuge to pellet the agarose beads, and washed with wash buffer (10mM HEPES pH=7.4, 200mM NaCl, 0.5% Triton X-100) 3 times, and a final wash with 20mM HEPES pH=7.4 to remove Triton X-100. After final wash, samples were centrifuged at 1,000RPM for 1 minute in Eppendorf 5424 tabletop centrifuge, and the agarose beads were dried with a 27G needle attached to a vacuum trap. Appropriate volume of 3X sample buffer was added to the beads for SDS-PAGE.

## 3.2.5 <sup>32</sup>P autoradiography

Metabolically labeled dynein complex was immunoprecipitated from the rat primary cortical neurons treated with BDNF in the presence of <sup>32</sup>P as described, and separated by gel electrophoresis on 4-12% Bis-Tris gels (Invitrogen cat. NP0336) in MOPS running buffer at 120V for 2 hours. Following electrophoresis, the gels were stained with Coomassie brilliant blue R-250 solution (Bio-Rad cat. 1610436), detained with destaining solution (10% acetic acid, 25% MeOH in water), and dried using a gel dryer. Dried gels were scanned on Typhoon 9410 phosphoimager to measure the incorporation of <sup>32</sup>P on the phosphorylated subunits of dynein complex.

## 3.2.6 PKD1 in vitro kinase assay

Active recombinant PKD1 (Sigma-Aldrich cat. K4268 Lot# SLBR2717V) with an Nterminal GST tag was used to phosphorylate recombinant full-length rat DIC 1A (produced by UIC Research Resources Center in 2007 then reconstituted to 30µM in 20mM HEPES; stored in -80°C). 100nM PKD1 was incubated with 3µM DIC 1A in kinase assay buffer (50mM K•Aspartate, 10mM MgCl<sub>2</sub>, 1mM DTT, 20mM HEPES pH=7.4) with 0.5mM ATP and 0.1mCi radiolabeled ATP [ $\gamma$ -<sup>32</sup>P] (PerkinElmer cat. NEG035C010MC) for 1 hour. The reaction was stopped by adding 6X sample buffer to final concentration of 3X sample buffer. The samples were separated by gel electrophoresis on a 4-12% Bis-Tris gel (Invitrogen cat. NP0336) in MOPS running buffer at 120V for 2 hours. Following electrophoresis, the gel was stained with Coomassie brilliant blue R-250 solution (Bio-Rad cat. 1610436), detained with destaining solution (10% acetic acid, 25% MeOH in water), and dried using a gel dryer. The dried gel was exposed to HyBlot CL autoradiography film (Denville Scientific cat. NC9550782) for 3 hours, and the film was developed using a film developer.

## 3.2.7 Western blotting

For western blotting, rat primary cortical neuronal lysates prepared as described above were loaded on 4-12% Bis-Tris gels (Invitrogen cat #NP0336) and ran in MOPS running buffer at 120V for 2 hours. Following electrophoresis, the proteins were transferred onto a 0.45µm Immobilon-P PVDF membrane (Millipore cat #IPVH00005) or Immobilon-FL (Millipore cat #IPFL00005) in Towbin buffer (25mM Tris, 192 mM glycine, 10% MeOH) at 400mA for 2 hours with cooling system maintained at 4°C. After transfer, the membranes were incubated in blocking buffer (1% non-fat milk in TBS-T) for 1hr in room temperature. After blocking, membranes were washed three times with TBS-T for 5 minutes each wash. Then the membranes were incubated overnight with primary antibodies diluted in 1% BSA in TBS with following dilutions: anti-phospho-TrkA/TrkB (Tyr706/Tyr707) (Cell Signaling #4621, 1:500), anti-TrkB (Cell Signaling #4603, 1:200), anti-phospho-PKD1 (S916) (Cell Signaling #2051, 1:500), anti-PKD1/PKCµ (Clone C-20, Santa Cruz #sc-639, 1:200), anti-phospho-(Ser/Thr) PKD substrate (Cell Signaling #4381, 1:500), anti-phopshotyrosine (clone PY99, Santa Cruz #sc-7020, 1:200), anti-DIC (clone 74.1, Santa Cruz #sc-13524, 1:500), and anti-GAPDH (Sigma cat. G8795, 1:2000). The next day, the membranes were washed three times with TBS-T for 5 minutes each wash and incubated with secondary antibodies diluted in 1% milk in TBS-T with 0.01% SDS, and incubated for 45 minutes to 1 hour in room temperature with following dilutions: goat anti-mouse IgG IRDye 680RD (LI-COR #925-68070, 1:10,000) and goat anti-rabbit IgG IR Dye 800CW (LI-COR #925-32211, 1:10,000). After incubation with secondary antibodies, membranes were washed three times with TBS-T for 5 minutes each wash, and one final wash with TBS to remove Tween-20, then analyzed using LI-COR Odyssey CLx/Fc near-infrared (NIR) imaging systems.

#### 3.2.8 Phos-tag SDS-PAGE

For analysis of dynein intermediate chain phosphorylation using gel motility shift on Phos-tag SDS-PAGE, 50µM of Phos-tag acrylamide (Wako Chemicals cat. AAL-107) and 10mM MnCl2 were added to the resolving gel solution (7% w/v acrylamide, 0.1% w/v SDS, 375mM Tris-HCl pH=8.8, 0.001% v/v TEMED, 0.0004% v/v ammonium persulfate). Stacking gel solution did not differ from typical recipe (4.5% w/v acrylamide, 125mM Tris-HCl pH=6.8, 0.1% w/v SDS, 0.001% v/v TEMED, 0.0004% v/v ammonium persulfate). To separate phosphorylated dynein intermediate chain, samples were loaded on the Phostag gels and electrophoresed at 25mA for 2 hours and 15 minutes. After SDS-PAGE, gels were incubated in towbin buffer (25mM Tris, 192mM glycine, 10% MeOH) supplemented with 10mM Na•EDTA with gentle agitation on a rocker for 1 hour (fresh buffer every 20 minutes), followed by 20 minute wash with Towbin buffer without 10mM Na•EDTA. After EDTA washes, gels were transferred and proceeded with western blot protocol for LI-COR Odyssey CLx near-infrared imaging system as described above.

## 3.2.9 <u>Vesicle motility assay in isolated squid axoplasms</u>

Isolated squid axoplasms were prepared and perfused as described in **2.2**. For vesicle motility assays, a video-enhanced contrast differential interference contrast (VEC-DIC) microscopy system equipped with was Zeiss Axiomat with a 100x, 1.3 n.a. objective, Hamamatsu Argus 20 and Model 2400 CCD camera, and Hamamatsu Photonics Microscopy C2117 video manipulator was used to visualize the movement of vesicular cargoes in isolated squid axoplasms. Detailed method for vesicle motility assay is described in a published protocol from our lab (Y. Song et al. 2016).

## 3.2.10 Primary neuronal culture in microfluidic chambers

Our microfluidic chamber (MFC) design consists of three individual somatodendritic compartments (SDC) that are each a 7x7 mm square and one axon terminal compartment (ATC) that is 20 mm in length at its maximum. A polydimethyl-

siloxane (PDMS) wall that is 1 mm in width separates the three SDC from one another. Our microfluidic chamber system has an open-top design with a 6 mm hole punched into each of the SDC squares and three 4 mm holes punched into the ATC. There are 106 microchannels (Ax) that connect each SDC to the shared ATC, and a single microchannel is 500 µm in length, 8 µm in width, and 2.5 µm in height (**Figure 16**).

Prior to plating neurons into our custom microfluidic chambers (MFCs), the chambers were sterilized with 70% ethanol for 15 minutes, placed into sterile 100 mm culture dishes, and each of the compartments were washed three times with autoclaved diH<sub>2</sub>O for 1 hr each in a sterile laminar flow hood. The microfluidic chamber compartments were coated with 1 mg/mL poly-L-lysine (Sigma cat. P2636) in 0.1 M borate buffer (pH 8.5) over-night at room temperature, and washed three times with autoclaved diH<sub>2</sub>O for 2 hr each. The compartments were then filled with DMEM(++), and placed inside an incubator at 37°C and 5% CO<sub>2</sub>. Fluidic isolation is maintained within our custom MFC for over 96 hours, which can be sustained over longer periods of time with media changes occurring every 3 days to keep the fluidic height between the compartments stable. After preparation of MFCs, rat primary cortical neurons were prepared as described in **3.3.1**, and 70,000 neurons were plated in each SDC and cultured for 12 days with fluidic isolation.



**Figure 16. Schematic of microfluidic chambers.** Chambers made with PDMS feature somatodendritic (SDC), axonal (Ax), and axon terminal (ATC) compartments. Neurons are plated in SDC, only neurites can enter Ax due to the narrow width ( $8\mu$ m) of Ax, allowing the separation of axons from neuronal cell bodies. Fluidic isolation of ATC from SDC and Ax can be achieved by maintaining higher fluidic height in SDC compared to ATC.

## 3.2.11 QD-BDNF treatment

To prepare the quantum-dot-BDNF conjugate (QD-BDNF), streptavidinconjugated Quantum-Dot-655 (1 $\mu$ M stock; ThermoFisher cat. Q10123MP) was incubated with biotin-conjugated BDNF (1 $\mu$ M stock; Alomone Labs cat. B-250-B) at a 1:1 volume ratio on ice for 1 hr prior to starting the cellular treatments. On 12 days *in vitro* (12DIV) cortical neuron axon terminals were treated with QD-BDNF with or without inhibitors within the axon terminal compartment (ATC) of MFC. First, the axon terminals were incubated with either 200nM K252a or 30 $\mu$ M CRT 0066101 for 20 min at 37°C. The QD-BDNF (final concentration 1nM) was mixed with the ATC media with or without inhibitors and incubated for an additional 20 min at 37°C. Following QD-BDNF incubation, the ATC media was completely replaced with new NB(+++) to remove free QD-BDNF in the media, and cells were incubated for an additional 30 min. The samples then underwent fixation for immunocytochemistry.

## 3.2.12 Immunocytochemistry

Cortical neurons were fixed within the intact microfluidic chamber in preparation for immunocytochemistry. The media was rinsed out of each main compartment with 37°C 1X phosphate buffered saline (PBS). The neurons underwent microtubule extraction and stabilization with a BRB80 (80mM PIPES, 1mM MgCl<sub>2</sub>, 1mM EGTA) and glutaraldehyde containing extraction buffer (1X BRB80, 0.3% Triton-X, 0.25% glutaraldehyde) for 5 min, followed by fixation with 4% paraformaldehyde in PBS for 1 hr, and washed twice with PBS for 30 min each. Fresh PBS was then added to each of the compartments, and the MFC were stored at 4°C overnight. Autofluorescence was quenched for 30 min with 50 mM NH<sub>4</sub>Cl, and the MFC compartments were washed twice with PBS for 30 min each. The neurons were permeabilized with 0.1% Triton-X for 1 hr, prior to blocking and incubation with the anti-βIII tubulin antibody (Sigma cat. T8660, 1:500 dilution) overnight at 4°C. On the following day, the compartments were washed with PBS twice for 1 hr each, then incubated at room temperature with AlexaFluor-488-conjugated goat antimouse IgG antibody (Invitrogen cat. A11029, 1:800 dilution) for 2 hr. The samples were washed with PBS twice for 1 hr each, and Vectashield anti-fade mounting medium with DAPI (Vector Laboratories cat. H-1200) was added to each SDC and ATC. The MFCs were stored in a parafilm-sealed 1000mm dish wrapped in aluminum foil at 4°C until confocal imaging.

## 3.2.13 Confocal microscopy

Following immunocytochemistry, neurons in the SDC located within the frame bordering the microchannels were imaged by confocal microscopy using Zeiss LSM710 confocal microscope with 40x oil immersion. All images were obtained within the same session, and the acquisition and post-acquisition settings were kept identical for all images.

#### 3.2.14 **Quantification of QD-BDNF accumulation**

To quantify the amount of QD-BDNF in SDC, images were converted to 8-bit with identical threshold, and particle analysis plug-in in ImageJ was used to quantify the number of QD-BDNF particles in each image (particle definition: size = 0-infinity, circularity = 0-1). The number of QD-BDNF particles in each image was normalized to the

number of neuronal cell body determined by DAPI and βIII-tubulin staining. Confocal imaging and quantification of QD-BDNF accumulation was performed by an experimenter blinded to experimental groups.

## 3.2.15 Statistical analysis

Any data point above 1.5 interquartile ranges (IQRs) below the first quartile or above the third quartile were defined as outliers and removed from the analysis. The amount of QD-accumulation in three different experimental groups (BDNF, BDNF+k252a, BDNF+CRT 0066101) was analyzed by one-way ANOVA using GraphPad Prism 7. Following one-way ANOVA, Tukey's post-hoc analysis was performed to reveal statistically significant group comparisons.

#### 3.3 <u>Results</u>

#### 3.3.1 Phosphorylation of DIC upon BDNF stimulation

We first confirmed the phosphorylation of dynein intermediate chain (DIC) upon BDNF stimulation in rat primary cortical neurons using two different methods. First, autoradiographic analysis of dynein complex immunoprecipitated from 3 days in vitro (DIV) rat primary cortical neurons metabolically labeled with <sup>32</sup>P was used to show a selective increase in phosphorylation of DIC subunit of dynein complex with BDNF stimulation (Figure 17A). Second, Phos-Tag SDS-PAGE was used to separate phosphorylated proteins from non-phosphorylated proteins by decreasing the mobility of phosphoproteins on SDS-PAGE gels with a phosphate-binding tag (Phos-Tag) (Kinoshita et al. 2006). Using Phos-Tag eliminates the need for radiometric labeling and immunoprecipitation of dynein complex as phosphorylation of DIC can be examined by running the whole cell lysates on Phos-Tag-containing gels followed by immunoblotting with an antibody against total DIC. To confirm autoradiography results using the Phos-Tag system, whole cell lysates from rat primary cortical neurons treated with BDNF were separated on Phos-Tag gel, then immunoblotted with 74.1 antibody, which recognizes DIC regardless of phosphorylation status. Similar to the autoradiography results, Phos-Tag SDS-PAGE method also showed increased levels of phosphorylated DIC in primary neurons treated with BDNF compared to untreated control (Figure 17B). Technical issues in the electrotransfer of proteins from Phos-Tag SDS-PAGE gels to the PVDF membrane resulted in uneven transfer of phosphoproteins compared to non-phosphorylated proteins where BDNF treated samples appeared to have higher amount of total DIC. Conventional SDS-PAGE was used to verify that the total level of DIC did not change upon BDNF

stimulation in the same samples (**Figure 17C**). Using Phos-Tag gels, we demonstrated that the phosphorylation of DIC by BDNF simulation occurs rapidly, within 5 minutes of stimulation (**Figure 18A**), and persists even up to 2 hours following a 20-minute pulse of BDNF stimulation (**Figure 18B**) in this treatment paradigm.



**Conventional SDS-PAGE** 

**Figure 17. Phosphorylation of DIC upon BDNF stimulation. (A)** Autoradiogram of dynein complex immunoprecipitated from 3DIV rat primary cortical neurons either untreated (control) or treated with BDNF (25ng/mL) in the presence of <sup>32</sup>P. BDNF treatment selectively increase the phosphorylation of DIC subunit. (B) BDNF treatment of 3DIV rat primary neurons increases phosphorylation of DIC that can be examined by Phos-Tag SDS-PAGE. (C) Total level of DIC does not change with BDNF stimulation. GAPDH is provided as a loading control.



Phos-Tag SDS-PAGE

**Figure 18. Characterization of BDNF-induced DIC phosphorylation. (A)** Time course of DIC phosphorylation following BDNF (25ng/mL) stimulation from 1 minute to 20 minutes. Maximum DIC phosphorylation is achieved as early as 5 minutes of BDNF stimulation. **(B)** On 3DIV, rat cortical neurons were treated with BDNF (25ng/mL) for 20 minutes. Following 20-minute BDNF pulse, the media was changed to fresh media without BDNF in order to remove extracellular BDNF. Cells were collected at varying time points following the media change up to 120 minutes. Phosphorylation of DIC persisted for 120 minutes, indicating that this BDNF stimulation paradigm results in rapid and persistent phosphorylation of DIC.

## 3.3.2 BDNF-induced DIC phosphorylation requires activation of TrkB and SFKs

After confirming the phosphorylation of DIC following BDNF stimulation, we used various kinase inhibitors to identify kinase signaling cascade responsible for DIC phosphorylation. Rat primary cortical neurons were pre-treated with one of the following inhibitors for 20 minutes before BDNF stimulation: 200nM k252a, a pharmacological inhibitor of the tyrosine kinase activity of Trk receptors (Tapley et al. 1992), and two different inhibitors of Src family kinases (SFKs), 50µM SU6656 (Blake et al. 2000) and 30µM A419529 (Wilson et al. 2002). Inhibition of TrkB kinase activity by k252a prevents activation of all downstream kinase cascades, and as expected, also prevents phosphorylation of DIC upon BDNF stimulation (**Figure 19A**). Interestingly, inhibitors of SFKs, which are among the downstream kinase pathways activated by TrkB, SU6656 and A419529, also prevented phosphorylation of DIC upon BDNF stimulation (**Figure 19A**). Neither the BDNF nor inhibitor treatments altered the total level of DIC (**Figure 19B**). These data indicate that BDNF-induced phosphorylation of DIC requires activation of TrkB and SFKs.



**Figure 19. BDNF-induced DIC phosphorylation requires activation of TrkB and SFKs. (A)** Pre-treatment with pharmacological inhibitors of TrkB (k252a) and SFKs (SU6656, A419529) prevented phosphorylation of DIC upon BDNF stimulation in 3DIV rat primary cortical neurons. **(B)** Total levels of DIC did not change with BDNF and inhibitor treatments. GAPDH is provided as a loading control.

#### 3.3.3 SFKs activate retrograde fast axonal transport in isolated squid axoplasms

Since the activation of SFKs was necessary for BDNF-induced phosphorylation of DIC, we examined whether SFKs affect cytoplasmic dynein (CDyn), retrograde axonal transport of membrane-bound cargoes, in isolated squid axoplasms using vesicle motility assay described in **3.2**. As this preparation removes the plasma membrane from the axoplasm, the direct effect of BDNF stimulation, which requires a transmembrane receptor TrkB, cannot be studied in isolated axoplasms. In addition, whether or not squid expresses either Trk receptors or BDNF is not known. Therefore, we perfused active recombinant kinases downstream of TrkB to examine their effects on axonal transport.

SFKs are a family of non-receptor tyrosine kinases with several members including, but not limited to, Src, Fyn, Lyn, Hck, and Lck (Filippakopoulos et al. 2009). We perfused recombinant Src (70nM) and Fyn (70nM) in isolated squid axoplasms, and the vesicle motility assays following the perfusion revealed both Src and Fyn activated retrograde fast axonal transport while mildly inhibiting anterograde fast axonal transport (**Figure 20**). These findings suggest that activation of SFKs upon BDNF stimulation, which is required for the BDNF-induced phosphorylation of DIC, may lead to activation of retrograde axonal transport of signaling endosomes.


**Figure 20. SFKs activate retrograde fast axonal transport in isolated squid axoplasms.** Perfusions of recombinant Src **(A)** and Fyn **(B)** in isolated squid axoplasms activate CDyn-driven retrograde axonal transport (*red*) while mildly inhibiting kinesin-driven anterograde axonal transport (*blue*).

#### 3.3.4 Dynein is not phosphorylated on tyrosine residues

The activation of a receptor tyrosine kinase TrkB and the downstream non-receptor tyrosine kinases SFKs is required for the phosphorylation of DIC upon BDNF stimulation, and active SFKs activate retrograde fast axonal transport in isolated squid axoplasms. However, previous report by Dillman and Pfister (1994) showed that DIC is phosphorylated on serine residues, but not tyrosine residues, using phosphoamino acid analysis. We tested whether DIC is phosphorylated on tyrosine residues using immunoprecipitation. Rat primary cortical neurons were cultured and stimulated with BDNF on 3DIV as described in 3.2. Following BDNF stimulation, cells were scraped in a nondenaturing buffer (ROLB) and immunoprecipitated with either DIC antibody or pTyr antibody. Immunoprecipitation using DIC antibody, as expected, showed enriched DIC (74kDa) in the immunoprecipitates compared to input and post-immunoprecipitation supernatant (PIS), while mock immunoprecipitate that contained agarose beads and DIC antibody but not the cell lysates showed no DIC immunoreactivity. In the same samples, immunoblotting with pTyr antibody did not show any immunoreactive bands in the immunoprecipitates at 74kDa molecular weight (Figure 21A). Some immunoreactivity was observed in all immunoprecipitates *including* the mock sample, indicating that there is some background from the antibody used for immunoprecipitation, which was generated from the same host (mouse) as the pTyr antibody used for immunoblotting. Immunoprecipitation using pTyr antibody showed enriched proteins with pTyr in the immunoprecipitates compared to input and PIS as expected. DIC was detected in input and PIS, but not in the pTyr immunoprecipitates (Figure 21B). This result agrees with the previous report demonstrating that DIC is not phosphorylated on tyrosine residues.





**Figure 21. DIC is not phosphorylated on tyrosine residues. (A)** DIC was immunoprecipitated from untreated (Ctrl) and BDNF-treated (BDNF) 3DIV rat primary cortical neurons, then immunoblotted with antibodies against DIC and pTyr. DIC (74kDa) is enriched in the immunoprecipitates but there is no pTyr immunoreactive band at 74kDa molecular weight. **(B)** Proteins phosphorylated at pTyr residues were immunoprecipitated from untreated and BDNF-treated 3DIV rat primary cortical neurons, then immunoblotted with antibodies against DIC and pTyr. DIC is detected in the input and PIS, but not in the pTyr immunoprecipitates.

\* "Mock" lanes indicate a control immunoprecipitate where agarose beads and the antibody used for immunoprecipitation were incubated without cell lysate. \* "PIS" refers to post-immunoprecipitation supernatant.

# 3.3.5 <u>SFKs activate retrograde fast axonal transport by activation of a downstream</u> serine/threonine kinase PKD1.

Activation of non-receptor tyrosine kinases SFKs is required for phosphorylation of DIC upon BDNF stimulation and SFKs activate retrograde fast axonal transport. However, DIC is phosphorylated on serine but not tyrosine residues. Thus, we reasoned that there may be an intermediate serine/threonine kinase between SFKs and phosphorylation of DIC. Previous work from our lab reported that members of the protein kinase C (PKC) family can also activate retrograde fast axonal transport in isolated squid axoplasms (G. Morfini et al. 2007). Previous studies (Senis et al. 2014; Murugappan et al. 2009) have reported that SFKs can activate one or more members of the PKC family. The PKC family can be categorized as including three subfamilies based on their regulatory domains: conventional (cPKCs), novel (nPKCs), and atypical PKCs (aPKCs) (**Table 4**) and we sought to determine whether any of these isoforms were downstream of SFKs.

To evaluate whether any PKC mediates the activation of retrograde fast axonal transport by SFKs in the squid axoplasms by co-perfusion of Fyn, a member of SFK family, with two pharmacological inhibitors of PKC, Gö6983 and Gö6976. Both compounds are inhibitors of PKC, but they inhibit different subsets of PKC isoforms. Gö6983 inhibits PKC $\alpha$ , PKC $\beta$ , PKC $\gamma$ , PKC $\delta$ , and PKC $\zeta$  (IC<sub>50</sub>= 7nM, 7nM, 6nM, 10nM, 60nM, respectively as measured by *in vitro* kinase assay with 35µM ATP) but does not inhibit PKCµ/PKD1 (IC<sub>50</sub> > 20µM) (Gschwendt et al. 1996). Gö6976 inhibits PKC $\alpha$ , PKC $\beta$ , and PKCµ/PKD1 (IC<sub>50</sub>= 2nM, 6nM, 20nM, respectively) (Martiny-Baron et al. 1993; Gschwendt et al. 1996) **(Figure 22A)**. Co-perfusion of 70nM Fyn and 500nM Gö6983 did

not prevent activation of retrograde axonal transport by Fyn (Figure 22B), while coperfusion of 70nM Fyn and 500nM Gö6976 blocked effects on both anterograde and retrograde FAT (Figure 22C), suggesting that PKD1, but not PKC $\alpha$ , PKC $\beta$ , PKC $\gamma$ , PKC $\delta$ , and PKC $\zeta$ , could mediate the activation of retrograde axonal transport by SFKs. In addition, perfusion of active recombinant PKD1 to isolated squid axoplasms activates retrograde fast axonal transport, mimicking the effects of SFKs (Figure 23). Together, these data strongly indicates that PKD1 mediates the activation of retrograde fast axonal transport by SFKs.

Subfamily	Isoforms	Require DAG for activation	Require Ca2+ for activation		
Conventional	ΡΚCα, ΡΚCβ, ΡΚCγ	$\checkmark$	$\checkmark$		
Novel	ΡΚϹδ, ΡΚϹε, ΡΚϹη ΡΚϹθ	$\checkmark$	×		
Atypical	ΡΚϹλ/ι, ΡΚϹζ, *ΡΚϹμ (ΡΚD1)	×	×		

**Table 4. Classification of PKC isoforms.** 1) Conventional PKCs (cPKCs) require both Ca<sup>2+</sup> and diacylglycerol (DAG)/phorbol ester for activation; 2) novel PKCs (nPKCs) require DAG but not Ca<sup>2+</sup> for activation; and 3) atypical PKCs (aPKCs) do not require neither DAG nor Ca<sup>2+</sup> for activation (Mackay and Twelves 2007).

\*PKCµ was initially classified as a member of aPKCs then later re-classified to protein kinase D1 (PKD1) (Manning et al. 2002; Celil and Campbell 2005; Ren 2016).





\*Blue: kinesin-based anterograde fast axonal transport \*Red: CDyn-based retrograde fast axonal transport



**Figure 23. PKD1 activates retrograde fast axonal transport in isolated squid axoplasms.** Perfusion of active recombinant PKD1 in isolated squid axoplasms activates retrograde fast axonal transport (*red*) while inhibiting anterograde fast axonal transport (*blue*), mimicking the effects of SFKs (**Figure 20**).

# 3.3.6 <u>BDNF treatment leads to DIC phosphorylation in rat primary neurons via</u> activation of PKD1

Our data from isolated squid axoplasms strongly suggest that PKD1 mediates the activation of retrograde axonal transport by SFKs, which are activated upon BDNF stimulation and subsequent TrkB activation. To test our hypothesis that PKD1 mediates DIC phosphorylation upon BDNF in mammalian neurons, we pre-treated rat primary cortical neurons with PKD1 inhibitors. The inhibitor of PKD1 used in isolated squid axoplasm, Gö6976, was found to also inhibit the kinase activity of TrkB in nanomolar concentration (Behrens et al. 1999). This off-target inhibition made Gö6976 unsuitable for the use in primary neurons although it can still be used in isolated squid axoplasms where the plasma membrane-which contains TrkB-is removed. Instead, we used a smallmolecule inhibitor of PKD named CRT 0066101 (Harikumar et al. 2010; Ni et al. 2013), as well as PKD1 substrate peptide fused with modified HIV-TAT protein sequence (GRKKRRQRRRPP) in the N-terminus, which enables the peptide to cross the plasma membrane (Green and Loewenstein 1988; Frankel and Pabo 1988). PKCs have wellcharacterized consensus substrate sequences that are specific to different isoforms of PKCs (Nishikawa et al. 1997) (Figure 24A), which can provide better isoform-specific inhibition of PKCs than chemical inhibitors. Excess amounts of exogenous substrates specific to a particular isoform of PKC prevent phosphorylation of the endogenous substrates by that PKC isoform through competitive inhibition. PKC<sup>δ</sup> substrate peptide with the same modification was used as a control for isoform-specificity of PKC inhibition.

BDNF stimulation of 3DIV rat primary cortical neurons increased PKD activation, shown as increased immunoreactivity using an antibody against phospho-PKD at Ser916

residue, which is a PKD1 autophosphorylation site (Figure 24B). Although phosphorylation of S916 is not required for the activity of PKD1, it is a marker for PKD1 activation as PKD1 shows strong autophosphorylation at this site following activation (Matthews et al. 1999; Vertommen et al. 2000). Neurons pre-treated with 30µM CRT 0066101, which inhibits the kinase activity of PKD1, did not show an increase in phospho-PKD (S916) immunoreactivity as expected. Neurons pre-treated with 10µM PKD1 substrate peptide or 10µM PKCδ substrate peptide did still show phosphorylation of PKD1 at S916, indicating activation (Figure 24B). Even though an excess amount of PKD1 substrate peptide inhibits phosphorylation of endogenous substrates by competitive inhibition, it cannot easily compete against the S916 autophosphorylation as this is an intramolecular interaction. Total levels of PKD1 and DIC do not significantly change with inhibitor treatments (Figure 24B). Analysis of DIC phosphorylation in the same samples using Phos-Tag SDS-PAGE revealed that inhibition of PKD1 by either CRT 0066101 or PKD1 substrate peptide, but not PKC<sup>δ</sup> substrate peptide, prevents BDNF-induced phosphorylation of DIC (Figure 24C). These results indicate that activation of PKD1, but not another PKC isoform, is required for BDNF-induced DIC phosphorylation.

4		

ΡΚϹα	R	R	R	R	R	K	G	S	F	R	R	K	K
рксδ	A	K	R	K	R	K	G	S	F	F	Y	G	G
ΡΚϹε	Y	Y	Х	K	R	K	М	S	F	F	Е	F	F
рксζ	R	R	F	K	R	Q	G	S	F	F	Y	F	F
PKD1	А	A	L	V	R	Q	М	S	V	Α	F	F	F



**Figure 24. Activation of PKD1 is necessary for BDNF-induced DIC phosphorylation.** (A) PKC isoforms have unique consensus substrate sequences (Nishikawa et al. 1997). Red "S" denotes the serine residue that gets phosphorylated by active PKCs. Two peptides used in this study, PKC $\delta$  and PKD1 substrate sequences, are highlighted. (B) BDNF treatment of rat primary cortical neurons increases activation of PKD1 measured by S916 autophosphorylation. A small-molecule PKD1 inhibitor CRT 0066101 blocks this activation. Cell-permeable PKD1 substrate peptide prevents phosphorylation of endogenous substrates by PKD1 but does not block PKD1 autophosphorylation. Cell-permeable PKC $\delta$  substrate peptide does not inhibit PKD1 activity. Total levels of PKD1 and DIC do not change with inhibitor treatments. GAPDH is provided as a loading control. (C) Phos-Tag SDS-PAGE of the same samples shows inhibition of BDNF-induced DIC phosphorylation by CRT 0066101 and PKD1 substrate peptide, but not by PKC $\delta$  substrate peptide, indicating that PKD1 is required for the phosphorylation of DIC upon BDNF stimulation.

# 3.3.7 <u>Inhibition of PKD1 reduces retrograde axonal transport of QD-BDNF in rat</u> primary cortical neurons

To determine the role of PKD1 on retrograde axonal transport in mammalian neurons, we cultured rat primary neurons in microfluidic chambers capable of fluidic isolation of the axon terminal compartment (ATC) from axonal (Ax) and somatodendritic compartment (SDC) as described in 3.2. On 12 DIV, we observed that neuronal cell bodies were localized to SDC as the narrow width of microchannels in Ax does not allow neuronal cell body to migrate through. Axons originating from neuronal soma in the SDC successfully entered the microchannels of axonal compartment and reached the ATC where they arborize extensively (Figure 25). Quantum-dot-labeled BDNF (QD-BDNF) was prepared as described in 3.2 and was added to the ATC for a 20-minute pulse at 1nM final concentration. Neurons in control group only received the QD-BDNF treatment while those in experimental groups received a 20-minute pre-treatment of either 200nM k252a (+k252a) or 30µM of CRT 0066101 (+CRT 0066101) prior to QD-BDNF treatment. Following the treatment, neurons were incubated for additional 30 minutes at 37°C before fixation and immunocytochemistry. After fixation and immunocytochemistry, the accumulation of QD-BDNF in the SDC was quantified from confocal images of neurons in SDC as described in 3.2 and normalized to the number of neuronal cell bodies in each image. 53-66 images were taken from 6 separate MFCs (2 MFCs per experimental condition) and analyzed by an experimenter blinded to experimental conditions of each MFC. One-way ANOVA revealed a statistically significant difference among control (n=53), +252a (n=66), and +CRT 0066101 (n=56) group means (F(2, 172)=9.909, p=0.0004). Tukey's post-hoc analysis revealed a statistically significant reduction in the

amount of QD-BDNF accumulation in the SDC of +k252a compared to control (P<0.01) as well as CRT 0066101 compared to control (P<0.001), but not between +k252a and +CRT 0066101 (Figure 26). This result is consistent with our previous finding in the squid axoplasm perfused with SFKs and PKD1 (Figures 20, 22, and 23) that activation of retrograde axonal transport upon neurotrophin signaling requires activation of PKD1, suggesting that phosphorylation of DIC by PKD1 has biological function of retrograde axonal transport activation.



Figure 25. Culturing of rat primary cortical neurons in microfluidic chamber. Confocal images of 12DIV rat primary cortical neurons cultured in microfluidic chamber. Neuronal cell bodies are localized to the somatodendritic compartment (SDC) and axons grew through the axonal compartment (Ax) where cell bodies cannot enter, and reached the axon terminal compartment (ATC) where extensive axonal arborization is observed. Fluidic isolation of was maintained to prevent diffusion of materials from ATC to SDC and Ax. The white dotted lines represent the edges of axonal compartment. Blue: DAPI, Green:  $\beta$ III-tubulin. Scale bar = 200µm



Figure 26. Inhibition of PKD1 reduces retrograde axonal transport of QD-BDNF in rat primary cortical neurons. (A) confocal images of neuronal cell bodies in the SDC compartments of BDNF only control, BDNF + k252a, and BDNF + CRT 0066101 group following the QD-BDNF pulse. *Blue: DAPI, Red: QD-BDNF. Scale bar* =  $100\mu m$ . (B) Box plots of QD-BDNF accumulation in the SDC of BDNF control (Control), BDNF + k252a (+k252a), and BDNF + CRT (+CRT 0066101). One-way ANOVA and Tukey's post-hoc analysis revealed a statistically significant reduction in QD-BDNF accumulation in neurons pre-treated with k252a (\*\*, p<0.01) and CRT 0066101 (\*\*\*, p<0.001). *Line: median, +: mean*.

### 3.3.8 PKD1 phosphorylates DIC in vitro

To test if PKD1 can directly phosphorylate DIC, an *in vitro* kinase assay using recombinant PKD1 and recombinant full-length rat DIC 1A was performed in the presence of radiolabeled ATP [ $\gamma$ -<sup>32</sup>P] as described in **3.2**. Unfortunately, the recombinant DIC had a significant amount of degradation from long-term storage as shown with Coomassie blue stain (**Figure 27A**). Nevertheless, the autoradiogram of the Coomassie blue-stained gel clearly shows phosphorylation of full-length DIC and degraded fragments of DIC by recombinant PKD1, as well as autophosphorylation of PKD1 (**Figure 27B**), identifying PKD1 as a serine/threonine kinase capable of phosphorylating DIC.



Coomassie Blue

Autoradiogram

**Figure 27. PKD1 directly phosphorylates DIC** *in vitro*. Recombinant full-length rat DIC 1A was phosphorylated by recombinant GST-PKD1 *in vitro* in the presence of radiolabeled ATP [ $\gamma$ -32P]. Following in vitro phosphorylation, samples were electrophoresed on an SDS-PAGE gel. (A) Coomassie blue stain of SDS-PAGE gel shows recombinant GST-PKD1 (PKD1), recombinant full-length DIC 1A (FL-DIC), and degraded recombinant DIC. (B) Autoradiogram shows phosphorylation of FL-DIC and degraded DIC, as well as autophosphorylation of PKD1.

#### 3.3.9 PKD1 phosphorylates DIC at different residues than ERK1/2

Mitchell et al. (2012) reported that DIC can be phosphorylated at Ser80/81 (DIC-1/2 isoforms, respectively) by extracellular signal-regulated protein kinase 1/2 (ERK1/2) and that this phosphorylation stimulates recruitment of CDyn to signaling endosomes for retrograde axonal transport. We obtained a polyclonal antibody raised against DIC-1/2 phosphorylated at Ser80/81 from Dr. K. Kevin Pfister (D. J. Mitchell et al. 2012), and tested whether this phosphorylation site was relevant to TrkB-SFKs-PKD1 pathway we identified. Western blot analysis of rat primary cortical neurons showed that inhibitors of TrkB, SFKs, and PKD1 diminished the increase in phosphorylation of DIC at Ser80/81 by BDNF treatment (Figure 28), suggesting that PKD1 may also phosphorylate DIC at Ser80/81. In addition, the antibody against phospho-DIC (Sr80/81) shows fairly high level of immunoreactivity even in untreated control (Figure 28), and BDNF treatment leads to a smaller magnitude of increase in phosphorylation at this site compared to the magnitude of increase in DIC phosphorylation detected by Phos-Tag. In order to test whether PKD1 and ERK1/2 truly phosphorylate DIC at the same residue, we treated rat primary cortical neurons with phorbol 12-myristate 13-acetate (PMA) (Figure 29A). PMA is a phorbol ester that activates conventional and novel PKCs (i.e.  $PKC\alpha$ ,  $PKC\delta$ ), but not atypical PKCs (i.e. PKD1) (Table 4) (Tatin et al. 2006; Mackay and Twelves 2007), and leads to downstream activation of ERK (Lallemend et al. 2005). PMA treatment of rat primary neurons resulted in increases in phosphorylation of DIC at Ser80/81 (Figure 29B) and activation of ERK (Figure 29C) similar to BDNF treatment. However, PMA treatment did not show increase in phosphorylation of DIC detected by Phos-Tag SDS-PAGE (Figure **29D).** Phos-Tag separates phosphorylated proteins from unphosphorylated proteins by

decreasing the gel mobility of phosphorylated proteins. However, Phos-Tag does not separate all phosphorylated proteins, and the separation of phosphoproteins varies depending on phosphorylated residues (Kinoshita and Kinoshita-Kikuta 2011). This suggests that PKD1 phosphorylates DIC at additional residues other than Ser80/81 that can be detected by Phos-Tag SDS-PAGE. Consistent with this, vesicle motility assay in isolated squid axoplasms perfused with active recombinant ERK2 showed no effect of ERK2 on retrograde axonal transport (**Figure 30**), which is in contrast to activation of retrograde axonal transport by PKD1. Taken together, our data suggest that PKD1 phosphorylates DIC at different residues than ERK1/2, and that phosphorylation by PKD1, but not ERK1/2, has biological function of activating CDyn-based retrograde axonal transport.



Figure 28. Inhibition of TrkB-SFKs-PKD1 pathway prevents phosphorylation of DIC at Ser80/81 upon BDNF stimulation. (A) Inhibitors of TrkB (k252a) and SFKs (SU6656 and A419529) prevents BDNF-induced phosphorylation of DIC at Ser80/81. (B) Inhibitors of PKD1 (CRT 0066101 and PKD1 substrate peptide), but not inhibitor of PKC $\delta$  (PKC $\delta$  substrate peptide), prevents BDNF-induced phosphorylation of DIC at Ser80/81.



Figure 29. Phos-Tag SDS-PAGE separates DIC that is phosphorylated at residues other than Ser80/81 by gel mobility shift. (A) Chemical structure of phorbol 12myristate 13-acetate (PMA). PMA is a phorbol ester that activates conventional and novel PKCs (i.e. PKC $\alpha$ , PKC $\delta$ ) but not atypical PKCs (i.e. PKD1) (Table 4). (B) Both BDNF and PMA treatments in 3DIV rat primary cortical neurons increase phosphorylation of DIC at Ser80/81, which is phosphorylated by ERK1/2 (Mitchell et al. 2012). (C) Both BDNF and PMA treatments activate ERK, measured by phosphorylation of ERK (pERK). (D) Gel mobility shift in Phos-Tag SDS-PAGE separated phosphorylated DIC (pDIC) from unphosphorylated DIC with BDNF treatment, but not with PMA treatment even though PMA treatment leads to phosphorylation of DIC at Ser80/81. Gel mobility shift in Phos-Tag SDS-PAGE. This indicates that BDNF treatment increases phosphorylation of DIC at residues other than Ser80/81.



Figure 30. ERK2 does not activate retrograde fast axonal transport in isolated squid axoplasms. Vesicle motility assay in isolated squid axoplasms perfused with active recombinant ERK2 (100nM) shows no activation of retrograde fast axonal transport by ERK2.

## 3.4 Discussion

#### 3.4.1 <u>Activation of retrograde fast axonal transport by neurotrophin signaling</u>

Work presented in this chapter identified a novel kinase pathway that activates retrograde fast axonal transport through phosphorylation of intermediate chain subunit (DIC) of cytoplasmic dynein (CDyn) upon neurotrophin (i.e. BDNF) signaling. We found that BDNF stimulation of primary rat cortical neurons leads to rapid and long-lasting phosphorylation of DIC (Figure 18). From several kinase pathways activated by BDNF signaling (Figure 16), we provided evidence that activation of TrkB-SFK-PKD1 pathway is required for phosphorylation of DIC upon BDNF stimulation in primary rat cortical neurons using a variety of pharmacological and peptide-based kinase inhibitors (Figures 19 and 24), as well as showing that PKD1 can directly phosphorylate DIC (Figure 27). From vesicle motility assays in the squid axoplasms, we discovered that SFKs, a subfamily of non-receptor tyrosine kinases, activate CDyn-based retrograde fast axonal transport by activating a downstream serine/threonine kinase PKD1 (Figures 20, 22, and 23). In addition, the role of PKD1 in activation of retrograde axonal transport by neurotrophin was further demonstrated in mammalian neurons by examining the accumulation of QD-BDNF in rat primary cortical neurons cultured in microfluidic chambers. Inhibition of TrkB with k252a or PKD1 with CRT 0066101 reduced the amount of QD-BDNF accumulation in the cell body, indicating that activation of retrograde transport of signaling endosomes containing TrkB-BDNF is mediated by PKD1. Taken together, the data presented in this chapter indicate that phosphorylation of DIC by PKD1 upon neurotrophin signaling has biological function of activating retrograde fast axonal transport (Figure 31).



Figure 31. Proposed mechanism of activation of retrograde axonal transport by neurotrophin signaling. (1) Neurotrophins (i.e. BDNF) bind to their respective receptors (i.e. TrkB), triggering downstream signaling cascades and endocytosis of active receptors. (2) TrkB activates SFKs, a subgroup of non-receptor tyrosine kinase family. (3) SFKs activate PKD1, a serine/threonine kinase. (4) PKD1 phosphorylates dynein intermediate chain (DIC) on serine residue(s) and activation of retrograde fast axonal transport of signaling endosomes.

#### 3.4.2 Phosphorylation of DIC by ERK1/2 and PKD1

Previously, ERK1/2 has been shown to phosphorylate DIC at Ser80/81 (DIC-1/2 isoforms, respectively), and phosphorylation of DIC at this residue was proposed to recruit CDyn to signaling endosomes for retrograde axonal transport based on experiments using rat primary neurons overexpressing pseudophosphorylated DIC (D. J. Mitchell et al. 2012). However, ERK2 had no effect on retrograde fast axonal transport in isolated squid axoplasms (Figure 30) while SFKs and their downstream kinase PKD1 activated retrograde fast axonal transport (Figures 20, 22, and 23). We further investigated these seemingly conflicting results using PMA which activates conventional and novel PKCs as well as ERK without activating PKD1. Previously, we have shown that the constitutively active catalytic subunit of conventional PKCs such as PKCa and PKCB can activate retrograde axonal transport in isolated squid axoplasms In rat primary cortical neurons (G. Morfini et al. 2007). However, data presented in this chapter clearly demonstrates that the activation of retrograde axonal transport by SFKs are mediated by PKD1, suggesting that activation of retrograde axonal transport by PKCs requires a complex mechanism beyond simple activation of the kinase. Nonetheless, PMA treatment increased activation of ERK and subsequent phosphorylation of DIC at Ser80/81 based on immunoblotting, but it did not lead to DIC phosphorylation that is discernable by Phos-Tag SDS-PAGE (Figure 29). As separation of phosphoproteins by gel mobility shift in Phos-Tag SDS-PAGE varies depending on proteins and phospho-residues, we concluded that BDNF treatment leads to phosphorylation of DIC on residues distinct from Ser80/81 as well as Ser80/81 in a TrkB-SFKs-PKD1-dependent manner. Although we report that PKD1 can directly phosphorylate DIC (Figure 27), further study using mass spectrometry is needed

to identify the exact residues on DIC that are phosphorylated by PKD1. Interestingly, inhibition of PKD1 by a chemical inhibitor CRT0066101 and even by a specific PKD1 substrate peptide reduced the increase in phosphorylation of DIC on Ser80/81 residues (Figure 28B) upon BDNF stimulation, suggesting a potential interaction between phosphorylation of DIC by ERK1/2 and PKD1. One such potential interaction is priming phosphorylation where phosphorylation of a substrate by one kinase enables another kinase to recognize and phosphorylate the same substrate at different residues, which has been shown in several kinases (Cho and Johnson 2003, 2004; Hergovich et al. 2006; G. Huang et al. 2007; St-Denis et al. 2015; Aoki and Yoshida 2017). Although it is not explicitly addressed in this study, it is plausible that PKD1 primes DIC for phosphorylation by ERK1/2 in the context of neurotrophin signaling based on our results. Considering phosphorylation of DIC by PKD1 and ERK1/2 as separate events, our data from isolated squid axoplasm indicate that PKD1, but not ERK1/2, activate retrograde axonal transport while they do not exclude the possibility of different biological consequences of DIC phosphorylation by ERK1/2.

## 3.4.3 Complexity of signaling cascades in different biological contexts

Here, we identified a novel kinase signaling cascade that activates retrograde fast axonal transport upon neurotrophin signaling through activation of TrkB-SFK-PKD1. While this pathway seems hierarchal and linear, that may be true only in the context of neurotrophin signaling. Some signaling cascades such as MAPKKK<sup>17</sup>-MAPKK<sup>18</sup>-MAPK<sup>19</sup>

<sup>&</sup>lt;sup>17</sup> MAPKKK: mitogen-activated protein kinase kinase kinase

<sup>&</sup>lt;sup>18</sup> MAPKK: mitogen-activated protein kinase kinase

<sup>&</sup>lt;sup>19</sup> MAPK: mitogen-activate protein kinase

seem to be hierarchal while others may not be. For instance, activation of TrkB by BDNF in rat primary cortical neurons recruits SFKs via interaction between the autophosphorylated tyrosine residues of TrkB and Src-homology domain 2 (SH2) of SFKs, suggesting that there are SFKs downstream of TrkB (Iwasaki et al. 1998). Our data, also in the context of BDNF stimulation of rat primary cortical neurons, support this claim. However, influx of zinc from glutamatergic synaptic transmission has been shown to activate TrkB in an activity-dependent, but neurotrophin-independent, manner by activation of SFKs through inhibition of C-terminal Src kinase (CSK) in rat primary cortical neurons (Huang et al. 2008), indicating that SFKs can be upstream of TrkB in the context of zinc-mediated activation of TrkB in primary cortical neurons (Figure 32A). Another example of multiple signaling pathway sequences dependent on the specific cellular context is activation of SFKs and PKCs. PKCs have been shown to be upstream of SFKs in the context of platelet activation (Senis et al. 2014), podosome formation (Tatin et al. 2006), and conjunctiva goblet cell proliferation (Li et al. 2013), while PKCs appear to be downstream of SFKs in the context of reactive oxygen species (ROS) signaling (Mu and Liu 2017) and development of primordial follicles (Du et al. 2012) (Figure 32B). In addition, SFKs can activate PKD1 in oxidative stress signaling (Steinberg 2012) while activation of PKD1 appears to be dependent on PKC activation by DAG in cardiomyocytes (Guo et al. 2011) and in vascular endothelial growth factor (VEGF)mediated angiogenesis (Ha and Jin 2009) (Figure 32C), indicating that mechanisms of kinase activation differ based on cell types and contexts.

In addition to differential hierarchy of signaling cascades, activation of the same kinase can have different physiological outcomes depending on the context in which it is activated. For instance, our lab has shown that 1-metyhl-4-phenylpyridinium (MPP+), a neurotoxin that causes Parkinsonian symptoms, activates retrograde fast axonal transport by activation of caspase-3 and subsequent proteolytic activation of PKC $\delta$ . This MPP+-mediated activation of retrograde axonal transport can be blocked by competitive inhibition with the PKC $\delta$  substrate peptide, but not with PKD1 substrate peptide (G. Morfini et al. 2007) even though caspase-3 has also been reported to activate PKD1 by proteolysis of its regulatory domain similarly to PKC $\delta$  (Rybin et al. 2012; Steinberg 2012). Data from our current work indicated that activation of SFKs as a result of neurotrophin signaling leads to activation of retrograde axonal transport in a PKD1-dependent manner even though SFKs can also activate PKC $\delta$  (Senis et al. 2014; Murugappan et al. 2009) in different contexts (Figure 33).

These results suggest that the hierarchy of kinase signaling cascades can vary depending on the cell types and biological contexts, and even the activation of same kinase may result in different biological outcomes based on the context in which it is activated. The mechanisms of these differential signaling cascades remain elusive, but mapping out signaling pathways in various biological contexts provides us with some evidence that differences in localization, post-translational modifications such as ubiquitination (Mohapatra et al. 2013; Ball et al. 2016; Yang et al. 2010; Giannini and Bijlmakers 2004) and SUMOlyation (Simpson-Lavy and Johnston 2013; Wen et al. 2017; Knittle et al. 2017), and interacting scaffolding proteins may explain the differential biological outcome of intracellular signaling. Deeper understanding of these mechanisms is essential when manipulating kinase signaling in therapeutic interventions.



**Figure 32. Differential hierarchy of signaling cascades in different biological contexts.** The sequence of signaling cascades can differ based on the cell types and biological contexts in which they are activated. **(A)** In the context of BDNF signaling, TrkB activates SFKs while SFKs activate TrkB in the context of glutamatergic synaptic transmission-mediated Zn<sup>2+</sup> influx (Huang et al. 2008). **(B)** PKCs activate SFKs in the context of platelet activation (Senis et al. 2014), podosome formation (Tatin et al. 2006), and goblet cell proliferation (Li et al. 2013) while SFKs activate PKCs in the context of follicle development (Du et al. 2012) and ROS signaling (Mu and Liu 2017). **(C)** SFKs activate PKD1 in the context of oxidative stress (Steinberg 2012) and neurotrophin signaling (Figures 19 and 22) while PKD1 is activated by PLC-DAG-PKC pathway in cardiomyocytes (Guo et al. 2011) and VEGF-mediated angiogenesis (Ha and Jin 2009).



Figure 33. Differential biological consequences of identical kinases in specific biological contexts. PKC $\delta$  mediates activation of retrograde axonal transport by MPP+ Although caspase-3 has been shown to proteolytically activate PKD1 similarly to PKC $\delta$ , it is not known whether caspase-3 activates PKD1 upon MPP+ intoxication. On the other hand, PKD1 mediates activation of retrograde axonal transport by BDNF-TrkB-SFKs signaling cascade. While SFKs have been shown to activate PKC $\delta$ , it is not known whether a signaling cascade involving SFKs is required for activation of PKC $\delta$  upon BDNF stimulation.

### 3.4.4 Future directions

Our results identified a novel kinase signaling pathway that activates retrograde fast axonal transport through activation of TrkB-SFK-PKD1 and phosphorylation of DIC by PKD1. Although this work was done in the context of BDNF, neurotrophins have overlapping functions and downstream signaling cascades. Therefore, it is likely that the same pathway may be activated by other neurotrophins. Preliminary data from our lab shows phosphorylation of DIC following NT-3 treatment (data not shown) in rat primary cortical neurons although further experiments with kinase inhibitors and other neurotrophins are needed to test whether they share the same downstream signaling pathway leading to phosphorylation of DIC.

Furthermore, the molecular mechanisms underlying the activation of retrograde axonal transport have not been addressed by the present study. Based on the proposed role of DIC in cargo-binding, we hypothesize that phosphorylation of DIC by PKD1 commits signaling endosomes in the synaptic terminal for retrograde transport to the neuronal soma by recruiting cDyn to the endosome. Identifying the exact residues on DIC that are phosphorylated by PKD1 will facilitate analysis of the effects of DIC phosphorylation by PKD1 and ERK1/2. Introducing phosphomimetic and nonphosphorylatable mutations at those residues may be helpful in studying the molecular mechanisms underlying the retrograde fast axonal transport upon phosphorylation of DIC by PKD1. Understanding such mechanisms may also have relevance to pathological conditions. Aberrant activation of retrograde axonal transport of membrane-bound cargoes by MPP+ depletes membranous profiles from the presynaptic terminal by disturbing the lipid membrane equilibrium, leading to synaptic dysfunctions and dyingback degeneration (Morfini et al. 2007; Serulle et al. 2007). Furthermore, neuroinvasive viruses such as poliovirus, rabies virus, and herpes simples virus may be capable of hijacking this pathway to enhance their retrograde axonal transport to the neuronal cell body for replication. Thus, inhibiting the activation of retrograde axonal transport during neuroinvasive viral infections may be helpful in preventing or minimizing the extend of the infections.

#### CHAPTER IV.

### **IV. CONCLUSIONS**

Data presented in this work supports the main hypothesis in our lab that phosphorylation of motor proteins like conventional kinesin (kinesin) and cytoplasmic dynein (CDyn) regulates fast axonal transport of molecular cargoes. Normal phosphorylation can determine what is transported and where a cargo is delivered. Aberrant phosphorylation of motor proteins and subsequent axonal transport defects in neurodegenerative diseases such as Huntington's disease (HD) leads to dying-back neuropathy of affected neurons. Previous work from our lab has demonstrated that the CAG repeat expansion mutation in huntingtin that causes HD may be a hypermorphic gain-of-function for huntingtin, which results in abnormal activation c-Jun N-terminal kinase 3 (JNK3) and subsequent axonal transport defects. Work described in Chapter II extends this finding by addressing the role of JNK3 in HD pathology using the R6/2 mouse model of Huntington's disease with genetic deletion of JNK3. Our results indicate that deletion of JNK3 ameliorates HD pathology in R6/2 mice by preserving neuronal connectivity, suggesting that inhibition of JNK3 is a promising therapeutic approach for HD. Work presented in **Chapter III** identified a novel kinase signaling pathway that activates retrograde fast axonal transport by neurotrophin signaling. Brain-derived neurotrophic factor (BDNF), a member of neurotrophin family, triggers a signaling cascade involving activation of TrkB-SFK-PKD1. Active PKD1 then phosphorylates

dynein intermediate chain (DIC) subunit of CDyn to activate retrograde fast axonal transport.

The morphology of neurons places a unique challenge on neurons to maintain proper delivery of molecular cargoes to specific subcellular compartments. This evidence suggests that 1) there is a normal physiological role of kinase signaling in regulation of motor proteins and axonal transport; 2) neuropathogenic proteins disrupt this regulation by aberrant activation of specific kinase signaling pathways; and 3) correcting the abnormal kinase signaling can ameliorate axonal transport defects and dying-back neurodegeneration caused by neuropathogenic proteins.

Neurodegenerative diseases inflict immense pain and suffering on patients and their families, and place astronomical burdens on society. Unlike diseases such as cancer, very little success has been achieved in treating neurodegenerative diseases despite tremendous effort by many groups. Recent studies indicate that unrelated neurodegenerative diseases such as Alzheimer's disease, Huntington's disease, and amyotrophic lateral sclerosis may share a common pathology disruption of normal axonal transport function, leading to degeneration of neurons with long axons. I believe that defective axonal transport, termed "dysferopathy", represents a critical pathogenic event in neurodegenerative diseases. Expanding our knowledge on the regulation of axonal transport and the disruptions associated with specific disease mechanisms will help us develop effective therapeutic interventions for these diseases.

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Declaration on STM Publishing, November 2007: http://www.stm-assoc.org/2007\_11\_01\_Brussels\_Declaration.pdf

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December 1, 2011 Revised for PAF

Gerardo Morfini Anatomy & Cell Biology M/C 512 Office of Animal Care and Institutional Biosafety Committees (MC 672) Office of the Vice Chancellor for Research 206 Administrative Office Building 1737 West Polk Street Chicago, Illinois 60612-7227

Dear Dr. Morfini:

The protocol indicated below was reviewed at a convened ACC meeting in accordance with the Animal Care Policies of the University of Illinois at Chicago on 10/18/2011. The protocol was not initiated until final clarifications were reviewed and approved on 11/15/2011. The protocol is approved for a period of 3 years with annual continuation.

Title of Application: Analysis of Axonal Transport and Kinase-based Signaling Mechanisms in Neurodegenerative Diseases

ACC Number: 11-180

Initial Approval Period: 11/15/2011 to 10/18/2012

Current Funding: Portions of this protocol are supported by the funding sources indicated in the table below.

Number of funding sources: 3				
Funding Agency	Funding Title			Portion of Proposal Matched
NIH	Axonal Transport Deficits During Hereditary Spastic Paraplegia			Matched
Funding Number	Current Status	UIC PAF NO.	Performance Site	Funding PI
RO1 NS066942 (A1 version)	Funded	201000275	UIC	Gerardo Morfini
Funding Agency	Funding Title			Portion of Proposal Matched
ALS Therapy Alliance (ALSTA)	Mechanisms Underlying MAPK Activation and Axonal Transport Deficits in Familial ALS			Matched
Funding Number	Current Status	UIC PAF NO.	Performance Site	Funding PI
N/A	Funded	2010-02403	UIC	Gerardo Morfini
Funding Agency	Funding Title			Portion of Proposal Matched

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### Appendix B. IACUC Approvals (continued)

Brain Research Foundation	Effects of Mutant Huntingtin on Cytoplasmic Dynein Phosphorylation and Function			Matched
Funding Number	Current Status	UIC PAF NO.	Performance Site	Funding PI
N/A	Funded	201104500	UIC	Gerardo Morfini

This institution has Animal Welfare Assurance Number A3460.01 on file with the Office of Laboratory Animal Welfare (OLAW), NIH. This letter may only be provided as proof of IACUC approval for those specific funding sources listed above in which all portions of the funding proposal are matched to this ACC protocol.

In addition, all investigators are responsible for ensuring compliance with all federal and institutional policies and regulations related to use of animals under this protocol and the funding sources listed on this protocol. Please use OLAW's "*What Investigators Need to Know about the Use of Animals*" (http://grants.nih.gov/grants/olaw/InvestigatorsNeed2Know.pdf) as a reference guide. Thank you for complying with the Animal Care Policies and Procedures of UIC.

Sincerely yours,

Richard D. Mindeal

Richard D. Minshall, PhD Chair, Animal Care Committee

RDM/*mbb* cc: BRL, ACC File, Rodolfo Gatto, PAF 201000275, 200901463, 201104500

Gerardo Morfini ACC 2011180 Page 2 of 2

12/1/2011

### Appendix b. IACUC Approvals (continued)

This institution has Animal Welfare Assurance Number A3460.01 on file with the Office of Laboratory Animal Welfare (OLAW), NIH. This letter may only be provided as proof of IACUC approval for those specific funding sources listed above in which all portions of the funding proposal are matched to this ACC protocol.

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Sincerely yours,

Bradley Merrill, PhD Chair, Animal Care Committee

BM/mbb cc: BRL, ACC File, Rodolfo Gatto, Scott T. Brady, PAF 201000275, 201400263

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11/4/2014

### Appendix B. IACUC Approvals (continued)



September 11, 2017

Gerardo Morfini Anatomy & Cell Biology M/C 512 1737 West Polk Street Chicago, Illinois 60612-7227

Office of Animal Care and

Institutional Biosafety Committees (MC 672) Office of the Vice Chancellor for Research

206 Administrative Office Building

Dear Dr. Morfini:

The protocol indicated below was reviewed at a convened ACC meeting in accordance with the Animal Care Policies of the University of Illinois at Chicago on 8/15/2017. The protocol was not initiated until final clarifications were reviewed and approved on 9/11/2017. The protocol is approved for a period of 3 years with annual continuation.

Title of Application: Analysis of axonal transport and kinase-based signaling mechanisms in neurodegenerative diseases

ACC Number: 17-140

Initial Approval Period: 9/11/2017 to 8/15/2018

Current Funding: Portions of this protocol are supported by the funding sources indicated in the table below.

Number of funding sources: 2				
Funding Agency	Funding Title			Portion of Proposal Matched
CDHI Fdn. Inc.	Role of the JNK pathway on HD pathogenesis (Institutional #00004208)			All matched
Funding Number	Current Status	UIC PAF NO.	Performance Site	Funding PI
A-11014	Funded	201606069	UIC	Gerardo Morfini
Funding Agency	Funding Title			Portion of Proposal Matched
NIH	Addressing the Contribution of JNK3 to Axonal Pathology in Huntington's Disease (Institutional #00026078)			All matched
Funding Number	Current Status	UIC PAF NO.	Performance Site	Funding PI
R21NS096642 (years 1-2 A1)	Funded	201605902	UIC	Gerardo Morfini

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### Appendix B. IACUC Approvals (continued)

This institution has Animal Welfare Assurance Number A3460.01 on file with the Office of Laboratory Animal Welfare (OLAW), NIH. This letter may only be provided as proof of IACUC approval for those specific funding sources listed above in which all portions of the funding proposal are matched to this ACC protocol.

In addition, all investigators are responsible for ensuring compliance with all federal and institutional policies and regulations related to use of animals under this protocol and the funding sources listed on this protocol. Please use OLAW's "*What Investigators Need to Know about the Use of Animals*" (http://grants.nih.gov/grants/olaw/InvestigatorsNeed2Know.pdf) as a reference guide. Thank you for complying with the Animal Care Policies and Procedures of UIC.

Sincerely yours,

John P. O'Bryan, PhD Chair, Animal Care Committee JPO /mbb cc: BRL, ACC File, Mercedes Priego, Leon Tai

Page 2 of 2

9/11/2017

# VITA

## MINSU KANG

EDUCATION	
<b>University of Illinois, Chicago</b> Ph.D., Anatomy and Cell Biology with a Concentration in Neuroscienc	2013-2018 e
<b>University of Illinois, Urbana-Champaign</b> B.S. with High Distinction, Individual Plan of Study – Neuroscience	2009-2013
TEACHING ACTIVITIES	
<b>University of Illinois, Chicago</b> Teaching Assistant, Human Neuroanatomy	2016-2017
University of Illinois, Urbana-Champaign Tutor, General Chemistry, Organic Chemistry, Molecular and Cellular	2010-2012 Biology
AWARDS AND HONORS	
Harry Monsen and Mildred Monsen Award for Excellence Department of Anatomy and Cell Biology, University of Illinois at Chica	2018 ago
<b>CCTS-PECTS Fellowship</b> Center for Clinical and Translational Science, University of Illinois at C	2016-2018 Chicago
Graduate Student Poster Award Brain Research Foundation	2016
Graduate Student Council Travel Award Graduate Student Council, University of Illinois at Chicago	2016
<b>Student Presenter Award</b> Graduate College, University of Illinois at Chicago	2015
Horace Wu Scholarship Award University of Illinois at Urbana-Champaign	2013

### PUBLICATIONS

Leo, L., Weissmann, C., Burns, M., **Kang, M**., Song, Y., Qiang, L., Brady, S. T., Baas, P. W., Morfini, G. Mutant spastin proteins promote deficits in axonal transport through an isoform-specific mechanism involving casein kinase 2 activation. 2017. *Hum Mol Genet*.

**Kang, M.**, Baker, L., Brady, S. T., Morfini, G. A. Analysis of axon-specific phosphorylation events in isolated squid axoplasms. 2016. *Methods Cell Biol.* 

Song, Y., **Kang, M.**, Morfini, G. A., Brady, S. T. Fast axonal transport in isolated axoplasm from the squid giant axon. 2016. *Methods Cell Biol*.

### PRESENTATIONS

Axonal transport defects and dying-back neuropathy in neurodegenerative diseases. UIC Association for Neuropsychological Student Training Seminar University of Illinois, Chicago, Illinois	2018
Kinase-based regulation of retrograde fast axonal transport by neurotrophin signaling. Departmental Seminar Department of Anatomy and Cell Biology University of Illinois, Chicago, Illinois	2017
Inhibition of fast axonal transport by mutant huntingtin. Departmental Seminar Department of Anatomy and Cell Biology University of Illinois, Chicago, Illinois	2016
<b>Contribution of JNK3 in Huntington's disease pathology.</b> <i>Summer Postdoc and Graduate Student Seminar</i> Marine Biological Laboratory, Woods Hole, Massachusetts	2016
Fast axonal transport deficits in Huntington's disease. Summer Postdoc and Graduate Student Seminar Marine Biological Laboratory, Woods Hole, Massachusetts	2015
Fast axonal transport deficits induced by mutant huntingtin involves activation of a specific MAPK pathway. <i>UIC Neuroscience Day</i> Graduate Program in Neuroscience University of Illinois, Chicago, Illinois	2015

## ABSTRACTS

**Kang, M.**, Klein, A., Morris, S., Ebenezer, K., Zhang, R., Brady, S. T., Morfini, G. A. BDNF activates retrograde fast axonal transport by phosphorylation of cytoplasmic dynein. 2017. Abstract for poster presentation, *Graduate Education in Medical Sciences Research Forum*, Chicago, Illinois, September 2017.

**Kang, M.**, Gatto, R., Weissmann, C., Mesnard-Hoaglin, N., Brady, S. T., Morfini, G. A. Mechanisms underlying axonal transport deficits in Huntington's disease. 2016. Abstract for poster presentation, *Society for Neuroscience*, San Diego, California, September 2016.

**Kang, M.**, Gatto, R., Weissmann, C., Brady, S. T., Morfini, G. A. The role of JNK3 in Huntington's disease pathology. 2016. Abstract for poster presentation, *Graduate Education in Medical Sciences Research Forum*, Chicago, Illinois, September 2016.

**Kang, M.**, Gatto, R., Weissmann, C., Brady, S. T., Morfini, G. A. Genetic deletion of JNK3 ameliorates Huntington's disease pathology. 2015. Abstract for poster presentation. *American Society for Neurochemistry*, Denver, Colorado, March 2016.

**Kang, M.**, Gatto, R., Friedeck, H., Kim, B., Shah, S., Brady, S. T., Morfini, G. A. Contribution of JNK3 in Huntington's Disease Pathology. 2016. Abstract for poster presentation, *Brain Research Foundation Neuroscience Day*, Chicago, Illinois, January 2016.

Gatto, R., Chu, Y., **Kang, M.**, Lopez-Rosas, A., Friedeck, H., Kim, B., Kordower, J., Morfini, G. Addressing the in-vivo contribution of JNK3 to Huntington's disease pathogenesis. 2015. Abstract for poster presentation. *Society for Neuroscience*, Chicago, Illinois, October 2015.

**Kang, M.**, Brady, S. T., Morfini, G. A. Fast axonal transport deficits induced by mutant huntingtin involve activation of a specific MAPK pathway. 2015. Abstract for poster presentation. *Student Research Forum*, Chicago, Illinois, March 2015.

**Kang, M.**, Brady, S. T., Morfini, G. A. Fast axonal transport deficits induced by mutant huntingtin involve activation of a specific MAPK pathway. 2015. Abstract for poster presentation. *American Society for Neurochemistry*, Atlanta, Georgia, March 2015.

**Kang, M.**, Brady, S. T., Morfini, G. A. Fast axonal transport deficits induced by mutant huntingtin involve activation of a specific MAPK pathway. 2015. Abstract for poster presentation. *Society for Neuroscience Chicago Chapter*, Chicago, Illinois, March 2015.

**Kang, M.**, Kriefall, N., Abdelmesih, B., MacVeigh-Fierro, D. Purks, J., Brady, S. T., Morfini, G. A. Fast axonal transport deficits in Huntington's disease. 2014. Abstract for poster presentation. *UIC Neuroscience Day*, Chicago, Illinois, September 2015.

**Kang, M.**, Hedger, J., Krishnamani, T., O'Hearn, D., Sherrill, L. K., Wu, M., Gulley, J. M. Ethanol Oral Self-Administration and the Assessment of Ethanol Intoxication. 2013. Abstract for poster presentation. *Undergraduate Research Symposium*, University of Illinois, Urbana, Illinois, April 2013.

#### **PROFESSIONAL MEMBERSHIP**

Golden Key Honor Society	2018-present
Society for Neuroscience	2014-present
American Society for Neurochemistry	2014-present
International Society for Neurochemistry	2014-present