

# **The Impact of Parkinson's Disease on Mammalian Adult Neurogenesis**

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## **ABSTRACT**

Parkinson's disease (PD) has been reported to negatively affect adult neurogenesis. Mitochondrial dysfunction associated with PD may be involved, given that recent studies have identified mitochondria to be central regulators of neural stem cell (NSC) fate decisions. For this thesis, we sought to characterize adult neurogenesis in PINK1 and parkin knockout (KO) mouse models of PD. Immunohistochemical staining of subventricular zone (SVZ) and subgranular zone (SGZ) tissue sections from 6 month old mice was performed in order to identify and quantify changes in specific cell populations involved with adult neurogenesis. The loss of PINK1 or parkin was found to cause aberrant changes in adult neurogenesis, particularly in the SGZ. Going forward, it would be interesting to determine if the observed changes in adult neurogenesis were the result of mitochondrial dysfunction.

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## LIST OF ABBREVIATIONS

|                         |                                                          |
|-------------------------|----------------------------------------------------------|
| $^{14}\text{C}$         | Carbon-14                                                |
| $^3\text{H}$ -thymidine | Tritiated thymidine                                      |
| 6-OHDA                  | 6-hydroxydopamine                                        |
| aa                      | Amino acid                                               |
| Acetyl-CoA              | Acetyl coenzyme A                                        |
| AIF                     | Apoptosis-inducing factor                                |
| $\alpha$ -KG            | $\alpha$ -ketoglutarate                                  |
| ANOVA                   | Analysis of variance                                     |
| ATP                     | Adenosine triphosphate                                   |
| ATP13A2                 | ATPase Type 13A2                                         |
| BLBP                    | Brain lipid-binding protein                              |
| BNIP3                   | BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 |
| BrdU                    | 5-bromo-2'-deoxyuridine                                  |
| $\text{Ca}^{2+}$        | Calcium ion                                              |
| CBIA                    | Cell Biology and Image Acquisition Core                  |
| CCCP                    | Carbonyl cyanide m-chlorophenyl hydrazone                |
| CD133                   | Prominin-1                                               |
| CIHR                    | Canadian Institutes of Health Research                   |
| CNS                     | Central Nervous System                                   |
| DAPI                    | 4',6-diamidino-2-phenylindole                            |
| DAT                     | Dopamine transporter                                     |
| Dcx                     | Doublecortin                                             |
| DG                      | Dente gyrus                                              |
| DJ-1                    | Daisuke-Junko-1                                          |
| Dlx2                    | Distal-less homeobox 2                                   |
| DNA                     | Deoxyribonucleic acid                                    |
| Drp1                    | Dynamin-related protein 1                                |
| $\Delta\Psi\text{m}$    | Mitochondrial membrane potential                         |
| ECAR                    | Extracellular acidification rate                         |
| EdU                     | 5-ethynyl-2'-deoxyuridine                                |
| EGFR                    | Epidermal growth factor receptor                         |
| ETC                     | Electron transport chain                                 |
| FKBP8                   | FK506-binding protein 8                                  |
| FUNDC1                  | FUN14 domain containing 1                                |
| GAD65                   | Glutamate decarboxylase enzyme 65                        |
| GAPDH                   | Glyceraldehyde 3-phosphate dehydrogenase                 |
| GFAP                    | Glial fibrillary acidic protein                          |
| Gp78                    | Glycoprotein 78                                          |
| GTP                     | Guanosine-5'-triphosphate                                |
| HPRT                    | Hypoxanthine phosphoribosyltransferase                   |
| IBR                     | In-between RING                                          |



|                         |                                                                                           |
|-------------------------|-------------------------------------------------------------------------------------------|
| IF1                     | Inhibitory factor 1                                                                       |
| IMM                     | Inner mitochondrial membrane                                                              |
| KO                      | Knockout                                                                                  |
| Lhx5                    | LIM (Lin11, Isl1, and Mec-3) homeobox 5                                                   |
| LRRK2                   | Leucine-rich repeat kinase 2                                                              |
| MAD                     | Mitochondria-associated degradation                                                       |
| MAO-B                   | Monoamine oxidase B                                                                       |
| Mash1                   | Mammalian achaete scute homolog-1                                                         |
| MCM2                    | Minichromosome maintenance complex component 2                                            |
| Mdivi-1                 | Mitochondrial Division Inhibitor 1                                                        |
| MDV                     | Mitochondria-derived vesicle                                                              |
| MFN1                    | Mitofusin 1                                                                               |
| MFN2                    | Mitofusin 2                                                                               |
| Miro                    | Mitochondrial Rho                                                                         |
| MitAP                   | Mitochondrial antigen presentation                                                        |
| mito-QC                 | mCherry-GFP-FIS1 (mitochondrial fission 1 protein) <sup>101-152</sup> transgenic reporter |
| MPC                     | Mitochondrial pyruvate carrier                                                            |
| MPP                     | Mitochondrial processing peptidase                                                        |
| MPP <sup>+</sup>        | 1-methyl-4-phenylpyridinium                                                               |
| MPTP                    | 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine                                              |
| mRNA                    | Messenger RNA                                                                             |
| MSc                     | Master of Science                                                                         |
| mtDNA                   | Mitochondrial DNA                                                                         |
| mt-Keima                | Mitochondria-matrix targeted Keima                                                        |
| MTS                     | Mitochondria targeting sequence                                                           |
| MUL1                    | Mitochondrial E3 ubiquitin protein ligase 1                                               |
| NAD                     | Nicotinamide adenine dinucleotide                                                         |
| NAD <sup>+</sup>        | Oxidized nicotinamide adenine dinucleotide                                                |
| Neo                     | Neomycin                                                                                  |
| NeuN                    | Neuronal nuclei                                                                           |
| NIX                     | NIP3-like protein X                                                                       |
| Nkx2.1                  | NK2 homeobox 1                                                                            |
| NR                      | Nicotinamide riboside                                                                     |
| NRF2                    | Nuclear factor erythroid 2–related factor                                                 |
| NSC                     | Neural Stem Cell                                                                          |
| OB                      | Olfactory Bulb                                                                            |
| OCR                     | Oxygen consumption rate                                                                   |
| OMM                     | Outer mitochondrial membrane                                                              |
| OMS                     | Outer mitochondrial membrane localization signal                                          |
| Opal                    | Optic atrophy protein 1                                                                   |
| Opal <sup>tg</sup> mice | Opal overexpressing transgenic mice                                                       |
| OXPHOS                  | Oxidative phosphorylation                                                                 |
| PARIS                   | Parkin interacting substrate                                                              |

|                |                                                                                                                                                                                                        |
|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| PARL           | PINK1/PGAM5 (phosphoglycerate mutase family member 5)-associated rhomboid-like protease (formally known as presenilin-associated rhomboid-like protease)                                               |
| PBS            | Phosphate-buffered saline                                                                                                                                                                              |
| PCR            | Polymerase chain reaction                                                                                                                                                                              |
| PD             | Parkinson's disease                                                                                                                                                                                    |
| PDK            | Pyruvate dehydrogenase kinase                                                                                                                                                                          |
| PFA            | Paraformaldehyde                                                                                                                                                                                       |
| PGC-1 $\alpha$ | Peroxisome proliferator-activated receptor (PPAR)- $\gamma$ coactivator-1 $\alpha$                                                                                                                     |
| PGK            | Phosphoglycerate kinase                                                                                                                                                                                |
| PGK-HPRT       | Human hypoxanthine phosphoribosyltransferase gene construct coupled with a phosphoglycerate kinase promoter element                                                                                    |
| PGK-Neo        | Phosphoglycerate kinase-neomycin                                                                                                                                                                       |
| PINK1          | Phosphatase and tensin homolog (PTEN)-induced putative kinase 1                                                                                                                                        |
| PNS            | Peripheral Nervous System                                                                                                                                                                              |
| POLG           | DNA polymerase $\gamma$                                                                                                                                                                                |
| Prox1          | Prospero homeobox protein 1                                                                                                                                                                            |
| REP            | Repressor of park                                                                                                                                                                                      |
| RGL            | Radial glial-like                                                                                                                                                                                      |
| RING           | Really Interesting New Gene                                                                                                                                                                            |
| RING0          | Really Interesting New Gene 0                                                                                                                                                                          |
| RING1          | Really Interesting New Gene 1                                                                                                                                                                          |
| RING2          | Really Interesting New Gene 2                                                                                                                                                                          |
| RMS            | Rostral migratory stream                                                                                                                                                                               |
| RNA            | Ribonucleic acid                                                                                                                                                                                       |
| RNAseq         | RNA sequencing                                                                                                                                                                                         |
| ROS            | Reactive oxygen species                                                                                                                                                                                |
| SD             | Standard deviation                                                                                                                                                                                     |
| Ser65          | Serine at amino acid position 65                                                                                                                                                                       |
| SGZ            | Subgranular zone                                                                                                                                                                                       |
| SIAH1          | Seven in absentia homolog 1                                                                                                                                                                            |
| Sim1           | Single-minded homolog 1                                                                                                                                                                                |
| SN             | Substantia nigra                                                                                                                                                                                       |
| SNpc           | Substantia nigra pars compacta                                                                                                                                                                         |
| SOD1           | Superoxide dismutase 1                                                                                                                                                                                 |
| SOD2           | Superoxide dismutase 2                                                                                                                                                                                 |
| SODPAR         | Compound parkin KO and SOD2 hemizygous KO                                                                                                                                                              |
| Sox2           | SRY (sex determining region Y)-box 2                                                                                                                                                                   |
| SVZ            | Subventricular zone                                                                                                                                                                                    |
| TBK1           | TANK [TRAF (tumor necrosis factor receptor-associated factor) family member-associated NF- $\kappa$ B (nuclear factor $\kappa$ -light-chain-enhancer of activated B cells) activator]-binding kinase 1 |
| Tbr2           | T-box brain protein 2                                                                                                                                                                                  |
| TFAM           | Mitochondrial transcription factor A                                                                                                                                                                   |

|               |                                              |
|---------------|----------------------------------------------|
| TIM23         | Translocase of the inner membrane 23         |
| TMD           | Transmembrane domain                         |
| TOM           | Translocase of the outer membrane            |
| Tom20         | Translocase of the outer membrane subunit 20 |
| TRAK          | Trafficking kinesin protein                  |
| Type I cell   | SGZ neural stem cell                         |
| Type II cell  | SGZ intermediate progenitor cell             |
| Type III cell | SGZ neuroblast                               |
| Type A cell   | SVZ neuroblast                               |
| Type B cell   | SVZ niche specific astrocyte                 |
| Type B1 cell  | SVZ neural stem cell                         |
| Type B2 cell  | Non-neurogenic SVZ niche specific astrocyte  |
| Type C cell   | SVZ transit amplifying progenitors           |
| Type E cell   | Ependymal cell                               |
| Type E1 cell  | Multiciliated ependymal cell                 |
| Type E2 cell  | Bi-ciliated ependymal cell                   |
| Ub            | Ubiquitin                                    |
| Ubl           | Ubiquitin-like                               |
| UCP2          | Uncoupling protein 2                         |
| WT            | Wild-type                                    |
| ZNF746        | Zinc finger protein 746                      |

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## **INTRODUCTION**

### **1.1. Neurogenesis in the Adult Mammalian Brain**

#### **1.1.1. The Early History of Adult Neurogenesis**

A long held belief in the field of neuroscience was the idea that neurogenesis only occurred during embryonic and early postnatal stages of development (Gross, 2000). This view started to change in the 1960's, when <sup>3</sup>H-thymidine labelling experiments identified the presence of newborn neurons in the hippocampus and olfactory bulbs (OBs) of adult rats (Altman, 1969; Altman and Das, 1965). Studies in several different animal models and humans were able to explain these findings with the discovery of two distinct neurogenic niches in the adult mammalian brain: (1) the subgranular zone (SGZ) of the hippocampal dentate gyrus (DG) and (2) the subventricular zone (SVZ) lining the lateral ventricles (Bond et al., 2015; Eriksson et al., 1998; Gage et al., 1995; Lois and Alvarez-Buylla, 1993, 1994; Lois et al., 1996; Palmer et al., 1997). In both of these niches, neural precursor cells, which refer to both neural stem cells (NSCs) and progenitor cells, are able to undergo differentiation and maturation to become mature, post-mitotic neurons. The discovery of continued neurogenesis in the adult mammalian brain offers several promising avenues of research, particularly with respect to neural regenerative medicine (Bond et al., 2015).

For the purposes of this dissertation, the fundamentals of adult neurogenesis in the SVZ and SGZ will be described with respect to rodent animal models. Evidence of adult neurogenesis and its significance in humans will also be discussed.

### **1.1.2. Adult Neurogenesis in the SVZ**

The adult SVZ neurogenic niche is defined by the presence of four major cell populations: type E, B, C, and A cells (Doetsch et al., 1997). Type E cells (ependymal cells) are multiciliated (Type E1) or bi-ciliated (Type E2) cells lining the lateral ventricles that are responsible for regulating cerebrospinal fluid circulation with their cilia (Mirzadeh et al., 2008; Sawamoto et al., 2006). Type B cells are niche-specific astrocytes that can be divided into two subgroups based on their localization in the niche. Type B1 cells span the entire SVZ by making contact with both ependymal cells and SVZ blood vessels, while type B2 cells are only found surrounding type A cells (Doetsch et al., 1997; García-Verdugo et al., 1998). Type B1 cells are considered to be the NSCs of this niche and can exist in a quiescent or activated state (Capilla-Gonzalez et al., 2014; Codega et al., 2014; Doetsch et al., 1999a, 1999b; Mirzadeh et al., 2008; Obernier and Alvarez-Buylla, 2019). Activated type B1 cells undergo differentiation to give rise to type C cells (transit-amplifying progenitors), which in turn become type A cells (neuroblasts) (Doetsch et al., 1997). In rodents, these newly generated neuroblasts migrate along the rostral migratory stream (RMS) in order to reach the OBs to become mature granule or periglomerular cells (Doetsch and Alvarez-Buylla, 1996). These newly integrated neurons are currently thought to be involved with short-term olfactory memory (Breton-Provencher et al., 2009).

### **1.1.3. Adult Neurogenesis in the SGZ**

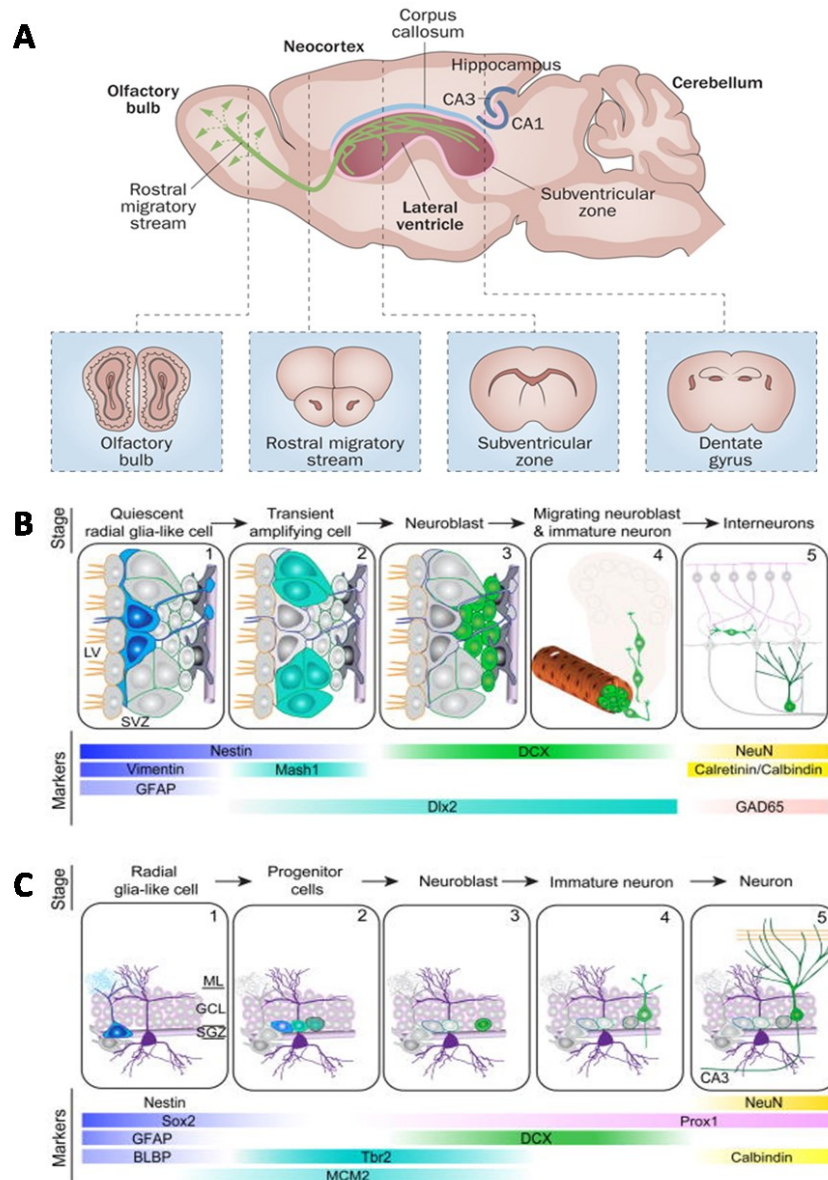
Similar to the SVZ, adult neurogenesis in the SGZ is based on the step-wise differentiation of astrocyte-like NSCs into mature neurons (Seri et al., 2001). The current model of neurogenesis in the adult SGZ argues that the NSCs (Type I cells) of this niche are comprised of a mixed population of SRY (sex determining region Y)-box 2 (Sox2) positive cells that exhibit either radial

glial-like (RGL) or horizontal morphologies (Suh et al., 2007). The RGL cell subpopulation is relatively quiescent, while the horizontal cell subpopulation is comprised of both quiescent and activated cells (Lugert et al., 2010; Shin et al., 2015). Once activated, NSCs will differentiate into intermediate progenitor cells (Type II cells), that later give rise to neuroblasts (Type III cells) (Kronenberg et al., 2003; Seri et al., 2001). Newly generated neuroblasts will undergo radial migration in the granule cell layer and eventually become mature granule cells (Kempermann et al., 2004). While the exact function of these newborn neurons has not been fully elucidated, adult neurogenesis in the SGZ has been shown to affect spatial-temporal memories and pattern-separation ability (Clelland et al., 2009; Ko et al., 2009; Nakashiba et al., 2012; Saxe et al., 2006; Tronel et al., 2012). Figure 1 provides a summary of adult neurogenesis in the SVZ and SGZ.

#### **1.1.4. Adult Neurogenesis in Humans**

Evidence of adult neurogenesis in the human SVZ and SGZ was first obtained from a study analyzing BrdU (5-bromo-2'-deoxyuridine) incorporation in post-mortem brains from cancer patients (Eriksson et al., 1998). Subsequent studies based on immunohistochemistry and the study of cell cultures derived from cells obtained from the human SVZ and SGZ provided additional evidence supporting the existence of human adult neurogenesis (Curtis et al., 2007; Göritz and Frisén, 2012; Johansson et al., 1999; Knoth et al., 2010; Sanai et al., 2004, 2011; Wang et al., 2011a). One interesting finding was that neurogenesis in the human SVZ was found to only meaningfully contribute to the production of new OB neurons until about 18 months of age, as opposed to the lifelong production of OB neurons from neurogenesis in the SVZ of rodents (Sanai et al., 2011). In order to investigate the relevance of adult neurogenesis in humans, researchers





**Figure 1: Overview of adult neurogenesis in the rodent brain.** (A) Diagram of the adult rodent brain from a sagittal viewpoint. Zoomed-in images represent coronal sections of key areas involved with adult neurogenesis in the subventricular zone (SVZ) and the subgranular zone (SGZ). (B) Diagram of the progression of SVZ adult neurogenesis. (C) Diagram of the progression of SGZ adult neurogenesis. Adult neurogenesis in the SVZ (B) and SGZ (C) can be studied using different combinations of biomarkers to identify specific cell populations in both neurogenic niches. BLBP, Brain lipid-binding protein; DCX, doublecortin; Dlx2, Distal-less homeobox 2; GAD65, Glutamate decarboxylase enzyme 65; GFAP, glial fibrillary acidic protein; Mash1, mammalian achaete scute homolog-1; MCM2, Minichromosome maintenance complex component 2; NeuN, neuronal nuclei; Prox1, Prospero homeobox protein 1; Sox2, SRY (sex determining region Y)-box 2; Tbr2, T-box brain protein 2. Adapted from (Ming and Song, 2011; Ziegler et al., 2015).

decided to assess neuronal turnover by using carbon dating (comparing  $^{14}\text{C}$  levels in genomic DNA to atmospheric  $^{14}\text{C}$  levels over time) to retrospectively determine when particular cell populations were born (Bergmann et al., 2012; Ernst et al., 2014; Spalding et al., 2013). By using this carbon dating based retrospective birth-dating approach, it was discovered that approximately 35% of neurons in the human hippocampus (corresponding to the dentate gyrus) are able to undergo neuronal exchange at a relatively consistent rate of approximately 1.75%/year (Spalding et al., 2013). Adult neurogenesis in the human SVZ was also found to contribute to the production of new neurons in the striatum (with approximately 25% of neurons in the striatum able to undergo neuronal exchange at a relatively consistent rate of 2.7%/year) and not in the OBs (Bergmann et al., 2012; Ernst et al., 2014). The presence of significant neuronal turnover in the adult human brain (Ernst et al., 2014; Spalding et al., 2013) supports a potential functional role for adult neurogenesis in humans (Bergmann et al., 2015; Kempermann et al., 2018).

The purpose of studying adult neurogenesis in rodents is to gain a better understanding of endogenous NSCs, which can then be applied for the human brain. At a fundamental level, the process of adult neurogenesis is relatively conserved amongst species (Ernst and Frisén, 2015). The study of adult neurogenesis in humans is difficult due to several technical issues, such as post-mortem tissue sample handling (Boekhoorn et al., 2006) and a lack of reliable cell markers for the quantitative study of human adult neurogenesis (Mathews et al., 2017). In fact, two recent studies published in high impact journals obtained opposite conclusions on the longevity and significance of adult neurogenesis in the human SGZ (Boldrini et al., 2018; Sorrells et al., 2018) as a result of differences between their methodologies (Lee and Thuret, 2018). Future studies will need to focus on resolving technical issues involved with studying adult neurogenesis in humans, in order to

obtain meaningful results that can contribute to the development of novel therapeutic strategies for the brain (Kempermann et al., 2018).

#### **1.1.5. NSC Fate Decisions**

A key area of research in the field of adult neurogenesis is the study of cell fate decisions for NSCs. In the SVZ and SGZ, the differentiation and maturation of NSCs is a tightly regulated process since a balance must be achieved between NSC self-renewal and differentiation. NSCs must undergo differentiation to generate new mature neurons, but NSCs must also undergo self-renewal to prevent the depletion of the NSC pool. This conundrum leads to a simplistic, but nevertheless critical question on what drives NSCs towards self-renewal or differentiation (Ito and Suda, 2014; Shohayeb et al., 2018).

Regulation of NSC fate decisions is achieved through a combination of external and internal signaling mechanisms that alter the expression of genes involved with quiescence, self-renewal, and neuronal differentiation (Faigle and Song, 2013; Shohayeb et al., 2018). NSCs within the brain exist in defined neurogenic niches that provide these cells with a unique microenvironment (Conover and Notti, 2008). These neurogenic niches are comprised of several types of cells (Doetsch et al., 1997; Mirzadeh et al., 2008; Seri et al., 2004) and exhibit extensive vascularization (Shen et al., 2008; Sun et al., 2015; Tavazoie et al., 2008). NSCs receive external signalling cues from their niche, which are known to affect cell fate decisions. These external signals are comprised of morphogens (Choe et al., 2016), growth factors (Oliveira et al., 2013), neurotrophic factors (Vilar and Mira, 2016), and neurotransmitters (Berg et al., 2013). Internal signaling mechanisms that alter NSC fate decisions involve transcription factors and epigenetic modifications (Hsieh, 2012; Hsieh and Zhao, 2016; Semerci and Maletic-Savatic, 2016; Sun et al., 2011). For the purposes of this dissertation, only specific external and internal signalling pathways

involved with the regulation of NSC fate decisions through mitochondrial function will be discussed in detail.

## **1.2. Importance of Mitochondria in NSC Fate Decisions**

### **1.2.1. Mitochondrial Metabolism Regulates Stem Cell Fate Decisions**

Stem cells tend to rely on glycolysis and have globular mitochondria with poorly developed cristae structure, while differentiated cells tend to rely on oxidative phosphorylation (OXPHOS) and have elongated mitochondria with highly organized cristae structure (Chen et al., 2008; Cho et al., 2006; Chung et al., 2007; St. John et al., 2005; Khacho et al., 2016; Kondoh et al., 2007; Piccoli et al., 2005; Varum et al., 2011). As a result, stem cells generate less cellular ATP compared to their differentiated counterparts (Cho et al., 2006; Folmes et al., 2011; Prigione et al., 2010; Varum et al., 2011). Based on these observations, it was initially thought that stem cells had immature and dysfunctional mitochondria, which suggested that the metabolic shift from glycolysis to OXPHOS during differentiation was simply a consequence of specialized cells requiring more cellular energy than stem cells (Cho et al., 2006; Chung et al., 2010; Facucho-Oliveira et al., 2007; St. John et al., 2005; Prigione et al., 2010; Yanes et al., 2010). However, several studies have provided compelling evidence arguing that cellular metabolism plays an activate role in regulating cell fate decisions (Folmes et al., 2011; Khacho et al., 2016; Takubo et al., 2013). Inhibiting glycolysis or enhancing OXPHOS has been demonstrated to promote differentiation, while inhibiting OXPHOS or enhancing glycolysis has been demonstrated to promote pluripotency (Chen et al., 2008; Folmes et al., 2011; Khacho et al., 2016; Mandal et al., 2011; Panopoulos et al., 2012; Pereira et al., 2013; Varum et al., 2011; Yanes et al., 2010; Zhu et al., 2010).

Interestingly, cellular metabolism plays an ATP-independent role in regulating cell fate decisions. As previously mentioned, mitochondria in stem cells were once considered to be immature and defective due to their low bioenergetic output. However, it has been reported that stem cells can be forced into using OXPHOS, suggesting that these cells can generate ATP through the electron transport chain (ETC) (Folmes et al., 2011; Sánchez-Aragó et al., 2013; Zhang et al., 2011, 2012). Several OXPHOS suppression pathways have been identified in stem cells, including the upregulation of uncoupling protein 2 (UCP2), pyruvate dehydrogenase kinase (PDK), and the ATPase inhibitory factor 1 (IF1) (Sánchez-Aragó et al., 2013; Takubo et al., 2013; Zhang et al., 2011). Another example involves the downregulation of the mitochondrial pyruvate carrier (MPC) in order to physically prevent pyruvate from entering the mitochondria (Schell et al., 2017). Taken together, these findings suggest that stem cells need to actively maintain a glycolytic state in order to preserve their pluripotency (Khacho and Slack, 2017).

ATP-independent metabolic reprogramming is achieved through the activity of specific metabolic intermediates and by-products known to affect cell fate decisions (Zhang et al., 2018). Reactive oxygen species (ROS), which were once considered to be a toxic by-product of OXPHOS, have been shown to act as signaling molecules involved with molecular pathways related to stem cell differentiation (Le Belle et al., 2011; Khacho et al., 2016; Lyublinskaya et al., 2015; Owusu-Ansah and Banerjee, 2009; Paul et al., 2014; Tormos et al., 2011). Metabolite intermediates such as  $\alpha$ -ketoglutarate ( $\alpha$ -KG), acetyl coenzyme A (acetyl-CoA), and nicotinamide adenine dinucleotide (NAD) can influence cell fate decisions through epigenetic modifications (Imai and Guarente, 2014; Kaelin et al., 2013; Ryall et al., 2015; Wellen et al., 2009).  $\alpha$ -KG promotes DNA and histone demethylation (Kaelin et al., 2013), while acetyl-CoA and oxidized

NAD (NAD<sup>+</sup>) facilitate histone acetylation and deacetylation, respectively (Imai and Guarente, 2014; Ryall et al., 2015; Wellen et al., 2009).

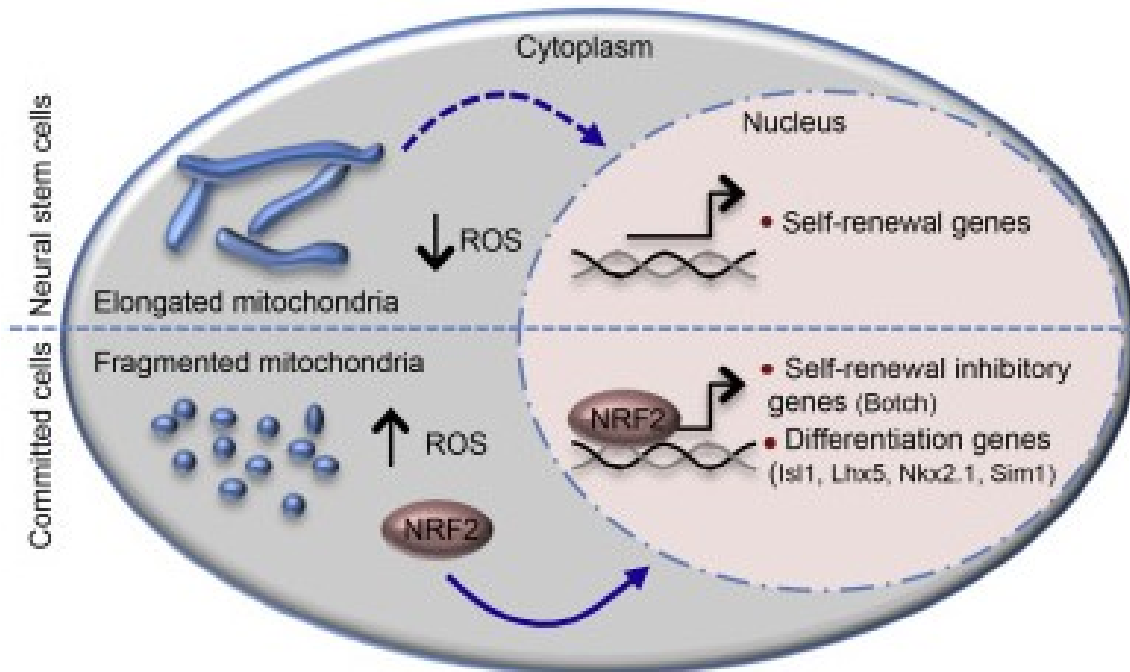
### **1.2.2. Mitochondrial Dynamics and Cellular Metabolism**

Mitochondrial dynamics describe changes in mitochondrial morphology as a result of fusion and fission events. Mitochondrial fusion is achieved by mitofusin 1 (MFN1), mitofusin 2 (MFN2), and optic atrophy protein 1 (Opa1). MFN1 and MFN2 are involved with outer mitochondrial membrane (OMM) fusion, while Opa1 is involved with inner mitochondrial membrane (IMM) fusion and cristae remodelling (Chen et al., 2003; Cipolat et al., 2004; Meeusen et al., 2006; Song et al., 2009). Mitochondrial fission is mediated by dynamin-related protein 1 (Drp1) and other fission factors (Losón et al., 2013; Smirnova et al., 2001). Exposing cells to various stress conditions has been shown to cause changes in mitochondrial morphology (Benard and Rossignol, 2008; Gomes et al., 2011; Tondera et al., 2009). These changes are intended to promote cell survival by not only preventing cell-death by apoptosis (Cipolat et al., 2006; Frank et al., 2001; Germain et al., 2005; Montessuit et al., 2010), but by also ensuring sufficient ATP production (Cogliati et al., 2013; Gomes et al., 2011; Khacho et al., 2014; Patten et al., 2014; Rambold et al., 2011). Mitochondrial fusion enhances OXPHOS efficiency by promoting the formation of respiratory chain supercomplexes, while mitochondrial fission impairs OXPHOS efficiency by disrupting the formation of respiratory chain supercomplexes (Cogliati et al., 2013). These findings suggest a bidirectional relationship between mitochondrial dynamics and metabolism.

### **1.2.3. Mitochondrial Regulation of NSC Fate Decisions**

Given the central role of mitochondria in regulating stem cell fate decisions, we wanted to gain a better understanding of the mitochondrial regulation of NSC fate decisions (Khacho et al., 2016). Characterization of NSCs, progenitor cells, and neurons in the embryonic mouse brain revealed that NSCs and neurons have elongated mitochondria, while progenitor cells have fragmented mitochondria. This finding suggested a potential role for mitochondrial dynamics in neuronal differentiation. Acute genetic modifications of mitochondrial morphology were found to alter NSC fate decisions, independently of ATP production and mitochondrial integrity. Enhancing mitochondrial fusion was found to promote NSC self-renewal, while enhancing mitochondrial fission was found to promote NSC differentiation. These observations were discovered to be the result of an NRF2 (nuclear factor erythroid 2–related factor 2) dependent retrograde gene expression pathway mediated by ROS signaling (Figure 2). According to this pathway, increased mitochondrial fragmentation promotes NSC differentiation by causing increased ROS production, which leads to the NRF2-dependent upregulation of the notch-dependent self-renewal inhibitor *botch* (Chi et al., 2012) and several pro-neuronal transcription factors. This study demonstrated that mitochondrial morphology itself could affect NSC fate decisions (Khacho et al., 2016).

A different team of researchers decided to study mitochondrial regulation of adult hippocampal neurogenesis (Beckervordersandforth et al., 2017). Mitochondria were demonstrated to undergo a characteristic change in both morphology and bioenergetics during NSC differentiation in the adult hippocampus. Adult NSCs have highly fragmented mitochondria and rely primarily on glycolysis. During neuronal differentiation, mitochondria become increasingly elongated and shift towards OXPHOS. Genetic and transgenic approaches to disrupt OXPHOS in NSCs revealed that the shift towards OXPHOS occurs as early as the transition from activated



**Figure 2. Mitochondrial dynamics is a regulator of NSC fate decisions.** This diagram illustrates how mitochondrial dynamics can regulate neural stem cell (NSC) fate decisions through a nuclear factor erythroid 2–related factor 2 (NRF2)-dependent retrograde gene expression pathway mediated by reactive oxygen species (ROS) signalling. Mitochondrial fusion promotes NSC self-renewal by causing a reduction in ROS production. This results in NRF2 remaining inactive, which allows for the continued expression of genes related to self-renewal. Mitochondrial fission promotes NSC differentiation by causing an increase in ROS production. This results in the activation of NRF2, which can then upregulate the expression of genes that promote neuronal commitment and inhibit self-renewal. Lhx5, LIM (Lin11, Isl1, and Mec-3) homeobox 5; Nkx2.1, NK2 homeobox 1; Sim1, Single-minded homolog 1. Adapted from (Khacho et al., 2016).



NSCs to progenitor cells and is required for the proliferation and differentiation of progenitors. The conditional knockout (KO) of the mitochondrial transcription factor A (TFAM) in mice did not affect the NSC population in the adult SGZ, but did cause a decrease in the total number of T-box brain protein 2 (Tbr2)-positive progenitors and doublecortin (Dcx)-positive neuroblasts and immature neurons. The conditional KO of TFAM was also found to impair the dendritic maturation of neurons, demonstrating a role for mitochondria in regulating neuronal maturation. Interestingly, similar results were obtained when comparing adult hippocampal neurogenesis between young and aged mice (Beckervordersandforth et al., 2017). Lastly, the researchers demonstrated that piracetam, a pharmacological agent known to improve mitochondrial function (Costa et al., 2013; Keil et al., 2006; Leuner et al., 2010; Waegemans et al., 2002), could ameliorate many of the observed age-dependent defects in adult NSC differentiation and maturation, provided that these cells had intact ETC components. Compared to the study by Khacho et al. (2016), this study focused entirely on the importance of mitochondria in regulating NSC fate decisions and neuronal maturation in the adult brain (Beckervordersandforth et al., 2017).

Given the importance of mitochondria in regulating NSC fate decisions (Beckervordersandforth et al., 2017; Khacho et al., 2016), we sought to study the long-term impact of mitochondrial dysfunction on neuronal development (Khacho et al., 2017). This was achieved by using conditional apoptosis-inducing factor (AIF) KO mouse models to study the effects of mitochondrial dysfunction on neurogenesis during embryonic and adult stages of development (Cheung et al., 2006; Germain et al., 2013; Khacho et al., 2017; Klein et al., 2002; Vahsen et al., 2004). The loss of AIF during embryogenesis was found to cause decreased NSC self-renewal, increased proliferation of neural progenitor cells, and impaired neuronal commitment and survival. A prolonged loss of AIF in the dorsal telencephalon was found to cause cognitive defects due to a

complete loss of adult neurogenesis in the SGZ. These results suggested that mitochondrial dysfunction could lead to impaired neurogenesis by causing a decrease in NSC self-renewal coupled with a defect in neuronal commitment and survival (Khacho et al., 2017). The findings from this study could provide useful insights into understanding aging and neurodegenerative diseases; two conditions associated with mitochondrial dysfunction and defects in adult neurogenesis (Beal, 2005; Khacho et al., 2017; Seib and Martin-Villalba, 2014; Winner and Winkler, 2015).

### **1.3. Overview of PD**

#### **1.3.1. Pathology and Clinical Aspects of PD**

Parkinson's disease (PD) is a neurodegenerative disorder defined by the progressive loss of dopaminergic neurons within the substantia nigra pars compacta (SNpc). The loss of these neurons causes dopamine deficiency in the striatum, resulting in impaired motor activity. Typical motor symptoms of PD include bradykinesia, rigidity, postural instability, and resting tremors (Kalia and Lang, 2015; Magrinelli et al., 2016). PD also affects other neuronal populations in the central and peripheral nervous systems (CNS and PNS), which leads to the development of non-motor symptoms such as hyposmia, sleep disturbances, constipation, mood changes, and cognitive decline (Braak and Braak, 2000; Braak et al., 2004; Giguère et al., 2018; Schapira et al., 2017; Winkler et al., 2011). Interestingly, these non-motor symptoms have been reported in patients to occur well before the onset of any motor deficits (Winkler et al., 2011). In the majority of PD cases, protein aggregates comprised primarily of alpha-synuclein can be found in the soma (Lewy bodies) and processes (Lewy neurites) of afflicted neurons (Kim et al., 2014; Shults, 2006; Spillantini et al., 1997). There is currently no cure for PD and current treatment options, such as

levodopa therapy and deep brain stimulation, focus on symptomatic relief (Anderson et al., 2017; Schapira et al., 2009).

### **1.3.2. Sporadic vs. Familial PD**

PD can be broadly classified as being either sporadic or familial, depending on the nature of the disease. Sporadic PD accounts for ~90% of all cases of PD and is the result of a combination of genetic and environmental risk factors. Familial PD accounts for the remaining ~10% of PD cases and is caused by mutations in specific genes that follow Mendelian inheritance (Exner et al., 2012). Autosomal dominant PD has been reported as a result of gain-of-function mutations in genes encoding proteins like alpha-synuclein (Chartier-Harlin et al., 2004; Polymeropoulos et al., 1997; Singleton et al., 2003) or leucine-rich repeat kinase 2 (LRRK2) (Funayama et al., 2002; Paisán-Ruiz et al., 2004; Zimprich et al., 2004). Autosomal recessive PD has been reported as a result of loss-of-function mutations in genes encoding proteins like parkin (Kitada et al., 1998), phosphatase and tensin homolog (PTEN)-induced putative kinase 1 (PINK1) (Valente et al., 2004), Daisuke-Junko-1 (DJ-1) (Bonifati et al., 2003), or ATPase Type 13A2 (ATP13A2) (Ramirez et al., 2006). Interestingly, all of these proteins have been shown to be involved in one or more aspects of maintaining proper mitochondrial function (Exner et al., 2012).

### **1.3.3. PD is Associated with Mitochondrial Dysfunction**

The underlying cause of neurodegeneration in PD remains unknown (Giguère et al., 2018). However, numerous studies have shown mitochondrial dysfunction to be associated with PD (Giguère et al., 2018; Park et al., 2018; Pickrell and Youle, 2015). Evidence supporting this relationship was first obtained from observations of human patients that had developed Parkinsonism (displayed motor symptoms typical of PD) and degeneration of dopaminergic

neurons in the SN after accidentally taking 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) (Davis et al., 1979; Langston et al., 1983). MPTP is oxidized by monoamine oxidase B (MAO-B) into 1-methyl-4-phenylpyridinium (MPP<sup>+</sup>), which is able to selectively enter dopaminergic neurons via the dopamine transporter (DAT) and inhibit the activity of complex I of the ETC (Javitch et al., 1985; Nicklas et al., 1985; Ramsay et al., 1986; Vyas et al., 1986). Signs of mitochondrial dysfunction were then found in patients with sporadic PD, such as complex I deficiency (Parker et al., 1989, 2008; Schapira et al., 1989, 1990) and increased mitochondrial DNA (mtDNA) mutations in dopaminergic neurons of the SN (Bender et al., 2006; Kraytsberg et al., 2006). The discovery of familial forms of PD, involving genes related to proper mitochondrial maintenance, has provided even more evidence supporting a link between mitochondrial dysfunction and PD (Exner et al., 2012). Whether mitochondrial dysfunction is causative or simply a symptom of PD is still under investigation (Giguère et al., 2018; Park et al., 2018; Pickrell and Youle, 2015).

## **1.4. Involvement of Parkin and PINK1 in PD**

### **1.4.1. The Parkin and PINK1 Proteins**

The first gene discovered to play a role in autosomal recessive PD was *PARK2*, which encodes the E3 ubiquitin (Ub) ligase parkin (Kitada et al., 1998; Matsumine et al., 1997). This 465 aa (amino acid) protein is composed of an ubiquitin-like (Ubl) domain, three really interesting new gene (RING) domains (RING0, RING1, and RING2), an in-between RING (IBR) domain, and a repressor of parkin (REP) region (Gladkova et al., 2018; Trempe and Fon, 2013; Trempe et al., 2013; Wauer and Komander, 2013). As an E3 ubiquitin enzyme, parkin is responsible for facilitating the transfer of Ub from E2 conjugating enzymes to other proteins (Hristova et al., 2009;

Shimura et al., 2000; Trempe and Fon, 2013). Parkin is found in the cytosol in an auto-inhibited state, which is thought to prevent auto-ubiquitination and its subsequent degradation (Gladkova et al., 2018; Kumar et al., 2015; Rakovic et al., 2013; Sauvé et al., 2018; Trempe and Fon, 2013; Wauer and Komander, 2013).

The second gene discovered to play a role in autosomal recessive PD was *PARK6*, which encodes the serine/threonine kinase PINK1 (Unoki and Nakamura, 2001; Valente et al., 2004). This 581 aa protein is composed of a mitochondria targeting sequence (MTS), an outer mitochondrial membrane localization signal (OMS), a transmembrane domain (TMD), and a kinase domain (Okatsu et al., 2015; Silvestri et al., 2005; Sim et al., 2012; Valente et al., 2004; Zhou et al., 2008). Through its kinase activity, PINK1 can activate parkin (Kane et al., 2014; Kazlauskaitė et al., 2014; Kondapalli et al., 2012; Koyano et al., 2014; Shiba-Fukushima et al., 2012). Figure 3 provides an overview of the domain structures of human parkin and PINK1.

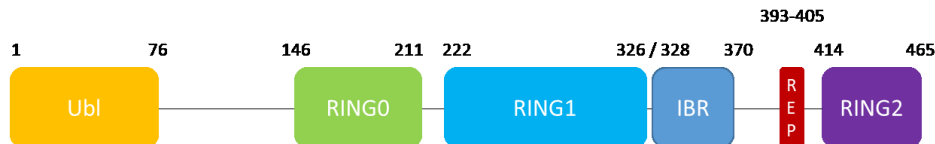
#### **1.4.2. Parkin and PINK1 KO Animal Models**

After discovering the involvement of parkin and PINK1 in familial PD, various animal models were developed in order to study the roles of these proteins in the cell (Pickrell and Youle, 2015). Parkin and PINK1 KO *Drosophila* models demonstrated reduced lifespans, male sterility, flight muscle degradation, loss of specific subsets of dopaminergic neurons, locomotor defects, and aberrant changes in mitochondrial integrity (Clark et al., 2006; Greene et al., 2003; Park et al., 2006; Pesah et al., 2004; Whitworth et al., 2005; Yang et al., 2006). The first parkin and PINK1 KO mouse models failed to recapitulate key aspects of PD pathology, such as a significant loss of dopaminergic neurons in the SN and gross motor impairments (Akundi et al., 2011; von Coelln et al., 2004; Goldberg et al., 2003; Itier et al., 2003; Kitada et al., 2007; Perez and Palmiter, 2005).

### PINK1 (581 aa)



### Parkin (465 aa)



**Figure 3: Domain structure diagrams of human PINK1 and parkin.** PINK1 (581 aa) is a serine/threonine kinase and parkin (465 aa) is an E3 ubiquitin ligase (Gladkova et al., 2018; Sekine and Youle, 2018). Numbers refer to specific aa locations. aa, amino acid(s); IBR, in-between RING; MTS, mitochondria targeting sequence; OMS, outer mitochondrial membrane localization signal; PINK1, phosphatase and tensin homolog (PTEN)-induced putative kinase 1; REP, repressor of parkin; RING, really interesting new gene; RING0, really interesting new gene 0; RING1, really interesting new gene 1; RING2, really interesting new gene 2; TMD, transmembrane domain; Ubl, ubiquitin-like.

Even aged parkin, PINK1, and DJ-1 triple KO mice showed no signs of neurodegeneration in the SN (Kitada et al., 2009). However, signs of altered dopamine metabolism in the striatum and mitochondrial dysfunction have been observed in certain parkin and PINK1 KO mouse models (Gandhi et al., 2009; Gautier et al., 2008; Goldberg et al., 2003; Itier et al., 2003; Palacino et al., 2004; Periquet et al., 2005). PD mouse models based on the inducible KO of PD associated genes (Lee et al., 2017; Shin et al., 2011) or combining germline KO models with an additional cellular stressor (Pickrell et al., 2015), have reported dopaminergic neurodegeneration.

#### **1.4.3. Parkin and PINK1 Maintain Mitochondrial Integrity**

Complementation studies in parkin and PINK1 KO *Drosophila* suggested that these proteins were involved in a common pathway responsible for maintaining proper mitochondrial function and morphology, with PINK1 acting upstream of parkin (Clark et al., 2006; Greene et al., 2003; Park et al., 2006; Yang et al., 2006). A common pathway involving both proteins was soon discovered by a study demonstrating that treatment of cultured cells with carbonyl cyanide m-chlorophenyl hydrazone (CCCP) resulted in parkin translocation to depolarized mitochondria, which leads to the selective removal of these impaired mitochondria through a process of autophagy known as mitophagy (Narendra et al., 2008). PINK1 was later found to be necessary for the activation and translocation of parkin in this process (Matsuda et al., 2010; Narendra et al., 2010; Vives-Bauza et al., 2010). Parkin and PINK1 have also been discovered to be involved with several other pathways related to processes such as mitochondrial quality control (Braschi et al., 2010; McLelland et al., 2014; Soubannier et al., 2012; Vincow et al., 2013; Xu et al., 2011), dynamics (Park et al., 2018), transport (Liu et al., 2012b; Wang et al., 2011c), biogenesis (Lee et al., 2017; Shin et al., 2011), and mRNA processing on the OMM (Gehrke et al., 2015).

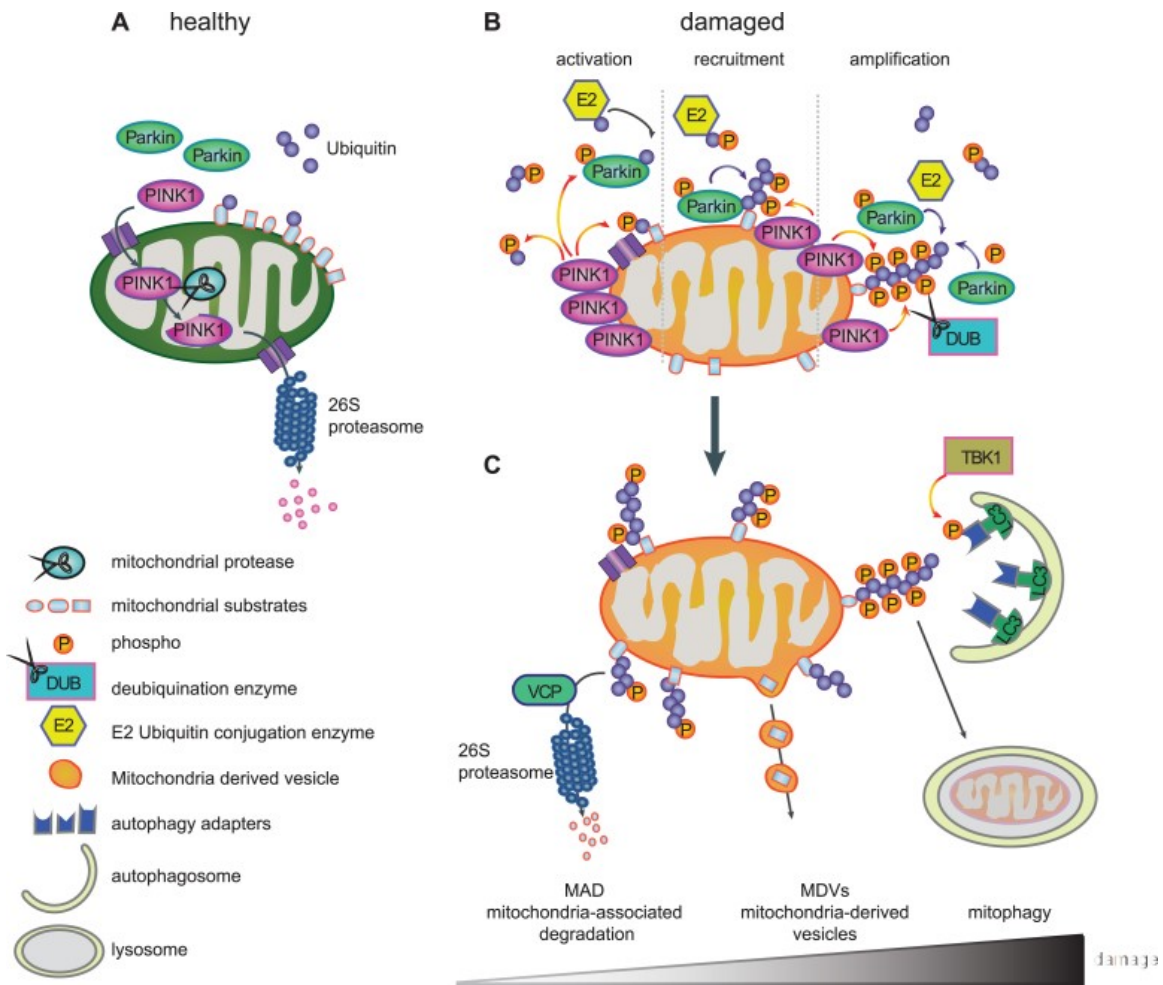
## **1.5. Cellular Functions of PINK1 and Parkin**

### **1.5.1. PINK1 and Parkin Regulation of Mitochondrial Quality Control**

PINK1 and parkin regulate mitochondrial quality control through mitochondria-associated degradation (MAD), mitochondria-derived vesicles (MDVs), and mitophagy (Truban et al., 2017). During MAD, polyubiquitination of OMM proteins selectively targets these proteins for degradation by the proteasome (Karbowski and Youle, 2011; Taylor and Rutter, 2011). Examples of PINK1/parkin-dependent MAD include the degradation of mitofusins during PINK1/parkin-dependent mitophagy (Tanaka et al., 2010; Ziviani et al., 2010) and the mitochondrial Rho (Miro) GTPase during cessation of mitochondrial transportation (Liu et al., 2012b; Wang et al., 2011c). PINK1 and parkin can also facilitate the formation of MDVs that can transport oxidized proteins towards lysosomes for degradation (McLelland et al., 2014; Soubannier et al., 2012). Interestingly, PINK1 and parkin were also discovered to inhibit a novel MDV-mediated mitochondrial antigen presentation (MitAP) pathway, which raises questions regarding the roles of PINK1 and parkin in regulating innate immunity (Matheoud et al., 2016). Lastly, PINK1/parkin-dependent mitophagy involves the removal of entire defective mitochondria through autophagy (Matsuda et al., 2010; Narendra et al., 2008, 2010; Vives-Bauza et al., 2010). Given the interest in PINK1/parkin-dependent mitophagy with respect to PD pathology (Pickrell and Youle, 2015), this process will be described below in greater detail. Figure 4 provides an overview of PINK1/parkin-dependent regulation of mitochondrial quality control.

Under basal conditions, PINK1 is rapidly degraded shortly after being translated (Matsuda et al., 2010; Narendra et al., 2010). This process begins with PINK1 entering the mitochondria through the translocase of the outer membrane (TOM) and translocase of the inner membrane 23





**Figure 4. Overview of PINK1/parkin-dependent regulation of mitochondrial quality control.** (A) Under basal conditions, PINK1 is continuously recruited to the mitochondria to undergo degradation, while parkin remains in an auto-inhibited state in the cytosol. (B) Damage to the mitochondria causes PINK1 to stabilize on the outer mitochondrial membrane (OMM). PINK1 recruits and fully activates parkin by phosphorylating parkin and ubiquitin (Ub). By working in concert, PINK1 and parkin are able to facilitate the rapid polyubiquitination of OMM proteins. (C) Depending on the severity of the mitochondrial damage, mitochondrial homeostasis can be maintained through several different PINK1/parkin-dependent pathways. Individual polyubiquitinated OMM proteins can be selectively degraded through mitochondria-associated degradation (MAD). Localized mitochondrial damage could lead to the degradation of a collection of oxidized proteins through mitochondria-derived vesicles (MDVs). Lastly, OMM polyubiquitin chains can recruit autophagosome components to facilitate the degradation of the entire mitochondria through the process of mitophagy. TBK1, TANK [TRAF (tumor necrosis factor receptor-associated factor) family member-associated NF- $\kappa$ B (nuclear factor  $\kappa$ -light-chain-enhancer of activated B cells) activator]-binding kinase 1. Adapted from (Truban et al., 2017).

(TIM23) complexes (Beilina et al., 2005; Lin and Kang, 2008; Okatsu et al., 2015; Silvestri et al., 2005; Takatori et al., 2008; Valente et al., 2004). During mitochondrial entry, PINK1 is cleaved by the mitochondrial processing peptidase (MPP) in the matrix and the PINK1/PGAM5 (phosphoglycerate mutase family member 5)-associated rhomboid-like protease (PARL) in the IMM (previously named as the presenilin-associated rhomboid-like protease) (Greene et al., 2012; Jin et al., 2010; Meissner et al., 2011; Spinazzi and De Strooper, 2016). The resulting 52 kDa PINK1 fragment is then retro-translocated from the mitochondria back into the cytosol to be ubiquitinated and degraded by the proteasome (Lin and Kang, 2008; Takatori et al., 2008; Yamano and Youle, 2013).

During a cell stress event that causes mitochondrial dysfunction, translocation through the TIM23 complex stops, due to a loss of mitochondrial membrane potential ( $\Delta\Psi_m$ ) (Bertolin et al., 2013; Jin et al., 2010). When PINK1 is unable to translocate through the TIM23 complex, PINK1 is retained in the OMM and forms a complex with another PINK1 protein and components of the TOM complex (Bertolin et al., 2013; Lazarou et al., 2012; Okatsu et al., 2012, 2013, 2015). This leads to the activation of PINK1 through auto-phosphorylation (Okatsu et al., 2012, 2013; Rasool et al., 2018). PINK1 is then able to phosphorylate parkin and OMM protein Ub chains at their Ser65 amino acid residues. The phosphorylation of Ub and parkin is necessary for the recruitment of parkin to impaired mitochondria and to fully activate its ligase activity (Kane et al., 2014; Kazlauskaitė et al., 2014; Kondapalli et al., 2012; Koyano et al., 2014). Parkin is able to create polyubiquitinated chains that can be phosphorylated by PINK1, thereby creating a feed-forward loop that rapidly causes polyubiquitination of OMM proteins (Ordureau et al., 2014; Sarraf et al., 2013). These polyubiquitinated chains act as receptors for autophagy components that will be

recruited to allow for the selective removal of damaged mitochondria (Heo et al., 2015; Lazarou et al., 2015).

Following the characterization of PINK1/parkin-dependent mitophagy, there was debate on the involvement of mitophagy in regulating mitochondrial homeostasis in neurons (Cummins and Götz, 2018; Mouton-Liger et al., 2017). PINK1/parkin-dependent mitophagy was first characterized in artificial cell-culture models that used immortalized cells that primarily rely on glycolysis for ATP production, protonophores to induce significant mitochondrial depolarization, and the overexpression or even exogenous expression of parkin and PINK1. It was also possible to induce a complete loss of the mitochondrial network under these conditions (Matsuda et al., 2010; Narendra et al., 2008, 2010; Vives-Bauza et al., 2010). Neurons rely on OXPHOS to meet their high bioenergetic demands, meaning that a process that could potentially lead to a loss of the entire mitochondrial network seems impractical and unlikely to occur in neurons (Almeida et al., 2001, 2004; Bolaños, 2016). Results from initial studies on mitophagy in neurons were mixed since there were studies that failed to observe PINK1/parkin-dependent mitophagy in neurons (Van Laar et al., 2011; Rakovic et al., 2013; Sterky et al., 2011), while other studies had reported this process to occur in neurons under specific culture conditions (Ashrafi et al., 2014; Cai et al., 2012). A study using a mitochondrial-targeted form of the pH-sensitive fluorescent probe Keima (mt-Keima) was able to demonstrate basal mitochondrial turnover by PINK1/parkin-dependent mitophagy in neurons (Bingol et al., 2014). Transgenic reporter systems based on mt-Keima or mito-QC have since been used to provide *in vivo* evidence of mitophagy in various cell types, including neurons (Cornelissen et al., 2018; McWilliams et al., 2018; McWilliams et al., 2016; Sun et al., 2017; Williams et al., 2017).

Questions regarding the relevance of PINK1 and parkin in mediating mitophagy in neurons have been raised (Cummins and Götz, 2018; Mouton-Liger et al., 2017; von Stockum et al., 2018). In a recent study by McWilliams et al. (2018), basal mitophagy in PINK1 KO mice was reported to be unaffected in almost all analyzed tissues, including those from the brain. PINK1 and/or parkin independent pathways of mitophagy have been discovered and could potentially explain these findings (Cummins and Götz, 2018; McWilliams et al., 2018; von Stockum et al., 2018). E3 Ub ligases other than parkin, such as glycoprotein 78 (Gp78), mitochondrial E3 ubiquitin protein ligase 1 (MUL1), and seven in absentia homolog 1 (SIAH1), have been found to facilitate ubiquitination of OMM proteins and promote mitophagy (Fu et al., 2013; Li et al., 2015; Szargel et al., 2016). Autophagy receptors in the OMM such as NIX (NIP3-like protein X), BNIP3 (BCL2/adenovirus E1B 19 kDa protein-interacting protein 3), FUNDC1 (FUN14 domain containing 1), and FKBP8 (FK506-binding protein 8) can recruit autophagosome components to the mitochondria, independent of OMM protein ubiquitination by an E3 Ub ligase (Bhujabal et al., 2017; Georgakopoulos et al., 2017; Liu et al., 2012a; Novak et al., 2010; Rikka et al., 2011). The presence of cardiolipin in the OMM has been shown to directly recruit autophagosome components to mitochondria (Chu et al., 2013). Iron and glyceraldehyde 3-phosphate dehydrogenase (GAPDH)-mediated pathways of mitophagy have also been suggested (Allen et al., 2013; Hwang et al., 2015; Yogalingam et al., 2013). Therefore, future studies will need to investigate the potential context-dependent roles of PINK1 and parkin in regulating neuronal mitophagy (McWilliams et al., 2018).

### 1.5.2. PINK1 and Parkin Regulation of Mitochondrial Dynamics

Aberrant changes in mitochondrial morphology have been observed in various parkin and PINK1 KO models (Lim et al., 2012). Initial studies in parkin and PINK1 KO *Drosophila* models revealed an increase in mitochondrial fusion (Clark et al., 2006; Greene et al., 2003; Park et al., 2006; Yang et al., 2006). Mitochondrial morphology was found to be relatively unchanged in corresponding early mouse models, except for an increase in mitochondrial elongation in the striatum of PINK1 KO mice (Gautier et al., 2008; Palacino et al., 2004). Interestingly, a number of parkin and PINK1 KO mammalian cell models have shown that a loss of either protein results in an increase in mitochondrial fragmentation (Cui et al., 2010; Dagda et al., 2009; Exner et al., 2007; Lutz et al., 2009). In the study by Lutz et al. (2009), loss of parkin or PINK1 in cultured cells from *Drosophila* was found to cause a transient increase in mitochondrial fragmentation, followed by a sustained increase in mitochondrial fusion. These observations suggest that various factors including the choice of species, time of analysis, presence of compensatory mechanisms, and the method of altering parkin/PINK1 gene expression can impact the study of parkin/PINK1-dependent regulation of mitochondrial dynamics (Lim et al., 2012; Lutz et al., 2009). Several mechanistic studies have provided evidence supporting a role for parkin and PINK1 interacting with components of the mitochondrial fission or fusion machinery in order to promote either mitochondrial fragmentation or elongation (Buhlman et al., 2014; Deng et al., 2008; Gegg et al., 2010; Lutz et al., 2009; Poole et al., 2008, 2010; Pryde et al., 2016; Wang et al., 2011b; Yang et al., 2008; Ziviani et al., 2010). It has been hypothesized that the regulation of mitochondrial dynamics by parkin and PINK1 is important in facilitating mitochondrial quality control, through the efficient separation of defective mitochondria from their healthy counterparts (Buhlman et al., 2014; Pryde et al., 2016; Wang et al., 2011b; Ziviani et al., 2010).

### **1.5.3. PINK1 and Parkin Regulation of Mitochondrial Transportation**

Mitochondria can be transported along microtubules within the cell by utilizing a protein complex consisting of Miro, a trafficking kinesin protein (TRAK)/Milton motor-adaptor protein, and a kinesin or dynein motor protein (Brickley and Stephenson, 2011; Glater et al., 2006; Guo et al., 2005; Stowers et al., 2002; van Spronsen et al., 2013). The binding of  $\text{Ca}^{2+}$  to Miro inhibits mitochondrial motility, which suggests a possible role for mitochondrial transportation in maintaining  $\text{Ca}^{2+}$  homeostasis by promoting the localization of mitochondria to areas with high  $\text{Ca}^{2+}$  concentrations (MacAskill et al., 2009; Saotome et al., 2008; Wang and Schwarz, 2009). PINK1 and parkin have both been implicated in regulating mitochondrial transportation by inhibiting mitochondrial motility through the degradation of Miro (Liu et al., 2012b; Wang et al., 2011c; Weihofen et al., 2009). A loss of PINK1 or parkin can prove detrimental to maintaining mitochondrial homeostasis, since the rapid cessation of mitochondrial transportation is necessary to ensure the efficient removal of defective mitochondria by mitophagy (Hsieh et al., 2016; Liu et al., 2012b).

### **1.5.4. PINK1 and Parkin Regulation of Mitochondrial Biogenesis**

Mitochondrial biogenesis requires the precise coordinated transcription of mitochondrial related genes from both the nuclear and mitochondrial genomes (Jornayvaz and Shulman, 2010). Peroxisome proliferator-activated receptor (PPAR)- $\gamma$  coactivator-1 $\alpha$  (PGC-1 $\alpha$ ) is essential for proper mitochondrial biogenesis since PGC-1 $\alpha$  activates nuclear respiratory factors 1 and 2, which are responsible for the activation of TFAM (Andersson and Scarpulla, 2001; Lin et al., 2002; Meirhaeghe et al., 2003; Puigserver et al., 1998; Virbasius and Scarpulla, 1994; Wu et al., 1999). Parkin was discovered to be involved with regulating mitochondrial biogenesis through the

ubiquitination of the parkin interacting substrate [(PARIS; also known as zinc finger protein 746 (ZNF746)], a transcriptional repressor of PGC-1 $\alpha$  that undergoes degradation following ubiquitination (Shin et al., 2011). PINK1 was later revealed to be involved with this pathway by phosphorylating PARIS in order to facilitate parkin-dependent ubiquitination (Lee et al., 2017). The conditional KO of parkin or PINK1 in mice was noted to result in PARIS-dependent dopaminergic neurodegeneration (Lee et al., 2017; Shin et al., 2011).

#### **1.5.5. PINK1 and Parkin Regulation of mRNA Translation at the Mitochondria**

The translation of mRNA encoding mitochondrial proteins was originally thought to occur in the cytosol and mitochondrial matrix (Schmidt et al., 2010; Wenz et al., 2015). However, numerous studies have provided evidence demonstrating mitochondrial protein mRNA translation at the OMM (Lesnik et al., 2015). PINK1 and parkin have been implicated in regulating the translation of specific nuclear encoded mRNAs at the OMM, by facilitating the removal of several translational repressors (Gehrke et al., 2015).

#### **1.6. Adult Neurogenesis and PD**

Results from animal studies have suggested that the non-motor symptoms of PD could be partially explained by an impairment in adult neurogenesis. Non-motor symptoms of PD such as hyposmia, depression, and cognitive decline have been observed in animal models of dysfunctional adult neurogenesis (Regensburger et al., 2014). Toxin-based PD mouse models using 6-hydroxydopamine (6-OHDA) or MPTP have reported decreased proliferation in the SVZ (Baker et al., 2004; Höglinger et al., 2004; O’Keeffe et al., 2009; Sui et al., 2012; Winner et al., 2006). Interestingly, mice treated with 6-OHDA or MPTP have also been reported to have an

increased number of dopaminergic glomerular neurons in the OBs (Winner et al., 2006; Yamada et al., 2004). Decreased neuronal survival in the SGZ and OBs have been observed in transgenic mouse models overexpressing  $\alpha$ -synuclein (Kohl et al., 2012; Marxreiter et al., 2009, 2013a; May et al., 2012; Nuber et al., 2008; Winner et al., 2004, 2008) or LRRK2 (Winner et al., 2011). A loss of PINK1 in mice was shown to impair neuronal differentiation, possibly due to aberrant changes in mitochondrial function (Agnihotri et al., 2017). There is also some evidence in post-mortem studies on human PD patients that supports the notion that PD can lead to impaired adult neurogenesis in the SVZ and SGZ (Höglinger et al., 2004; O'Keeffe et al., 2009). Studying the impact of PD on adult neurogenesis could prove useful in the development of novel therapeutic strategies involving NSCs.



### 1.7. Rationale for the Hypothesis and Objectives of the Present Study

Based on the literature, mitochondrial function can be considered as a major player in NSC fate decisions and PD pathology (Khacho et al., 2019). This means it would be interesting to study the impact of PD related mitochondrial dysfunction on NSC fate decisions. This type of study would involve the characterization of adult neurogenesis in a suitable model of PD, analysis of mitochondrial dynamics and function in specific cell populations of interest, identification of the molecular pathways behind any observed changes, and a demonstration of a rescue of adult neurogenesis through the restoration of mitochondrial integrity. Given the magnitude of such a project, this thesis will focus on the preliminary characterization of adult neurogenesis in animal models of PD. **I hypothesize that a loss of PINK1 or parkin in mice causes impaired adult neurogenesis.** In order to test this hypothesis, there are two objectives:

**Aim I:** Characterization of SVZ and SGZ adult neurogenesis in PINK1 KO mice.

**Aim II:** Characterization of SVZ and SGZ adult neurogenesis in parkin KO mice.

Assessment of adult neurogenesis will be done using immunohistochemistry to compare differences in specific SGZ and SVZ cell populations between PD mouse models and wild-type (WT) controls.

## MATERIALS AND METHODS

### 2.1. Mice

Three transgenic mouse lines were used for this study: PINK1<sup>-/-</sup>, parkin<sup>-/-</sup>, and SOD2<sup>+/-</sup> (Fournier et al., 2009; Haque et al., 2012; Itier et al., 2003; Kitada et al., 2007; Lebovitz et al., 1996). All mice were examined at 6 months of age. All mice were maintained on a pure C57BL6 genetic background. Littermate controls were used whenever possible (otherwise outsourced C57BL6 mice were used as controls). All experimental protocols involving mice were approved by the University of Ottawa Animal Care Committee.

The PINK1 KO mice were provided by Dr. David Park's lab (University of Ottawa Brain and Mind Research Institute). PINK1 KO was achieved by using a phosphoglycerate kinase-neomycin (PGK-Neo) cassette to cause a deletion of exons 4-7 of PINK1. This disrupts the coding of the PINK1 kinase domain and also introduces a premature stop codon (Kitada et al., 2007). The original PINK1 KO mice had either 129SV/C57BL6 or 129SV/BALBc/C57BL6 mixed genetic backgrounds (Kitada et al., 2007), until being backcrossed onto a pure C57BL6 genetic background (Haque et al., 2012).

The parkin KO mice were provided by Dr. Michael Schlossmacher's lab (Ottawa Hospital Research Institute). Parkin KO was achieved by using a Neo-resistance cassette to cause a deletion of exon 3 of parkin (Itier et al., 2003). The original parkin KO mice had either a pure 129SV or mixed 129SV/C57BL6 genetic backgrounds (Itier et al., 2003), until being backcrossed onto a pure C57BL6 genetic background (Fournier et al., 2009).

The SOD2 (superoxide dismutase 2) hemizygous KO mice were also provided by Dr. Michael Schlossmacher's lab (Ottawa Hospital Research Institute). A complete SOD2 KO is lethal. The SOD2 KO was achieved through the deletion of exons 1 and 2 of SOD2 by using a

human hypoxanthine phosphoribosyltransferase (HPRT) gene construct coupled with a PGK promoter element. The original SOD2 hemizygous mice were developed on a pure 129SV genetic background (Lebovitz et al., 1996). These mice had been backcrossed onto a pure C57BL6 genetic background and can be purchased through The Jackson Laboratory (JAX #002973). Compound parkin KO and SOD2 hemizygous KO mice are referred to as SODPAR mice.

Genotyping was done by PCR using REDExtract-N-Amp™ PCR ReadyMix™ (MilliporeSigma) and following the guidelines from the manufacturer. Primer sequences for genotyping (Table 1) were based off of published protocols (Fournier et al., 2009; Kessova and Cederbaum, 2007; Madeo et al., 2014). Genotyping for SOD2 was done using primers specific for the PGK-HPRT construct, with primers for SOD1 (superoxide dismutase 1) being used as an internal control (Kessova and Cederbaum, 2007). While this would have technically made it impossible to genotype between a hemizygous or homozygous SOD2 KO, any homozygous SOD2 KO mice would not be viable (Lebovitz et al., 1996).

## **2.2. Tissue Fixation, Cryoprotection, and Cryosectioning**

Adult mice that were sacrificed first received an intraperitoneal injection of 0.65mg/g of a diluted Euthanyl solution (65mg/mL pentobarbital sodium USP), before undergoing a transcardial perfusion with 1X phosphate-buffered saline (PBS) followed by a 4% paraformaldehyde (PFA) solution in 1X PBS (pH=7.4). Perfused brains were stored for 24 hours in 4% PFA to ensure complete fixation. Afterwards, the brains were transferred to a 20% sucrose and 0.01% sodium azide solution in 1X PBS for long-term storage. Fixed brains were partitioned into left and right hemispheres, with one hemisphere returned to storage and the other frozen in isopentane (Thermo Fisher Scientific) at a temperature between -35°C and -40°C. Frozen hemispheres were mounted

| Target               | Genotyping Primer Sequences                                                                                                                                                                                                                        |
|----------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| PINK1                | <p>WT-Forward: 5'-AGAGGATGCTAGTCCCTGTGAAGGG-3'<br/>(PINK1-F)</p> <p>WT-Reverse: 5'-ACACTCAGTCCTTGGGCAATGCTA-3'<br/>(PINK1-X)</p> <p>KO-Reverse: 5'-ACCAAAGAAGGGAGCCGGTTG-3'<br/>(NeoA)</p>                                                         |
| Parkin               | <p>WT-Forward: 5'-TGCTCTGGGGTTCGTC-3'</p> <p>KO-Forward: 5'-TTGTTTTGCCAAGTTCTAAT-3'</p> <p>Common-Reverse: 5'-TCCACTGGCAGAGTAAATGT-3'</p>                                                                                                          |
| SOD1 and<br>PGK-HPRT | <p>SOD1-Forward (IMR0878): 5'-TGAACCAGTTGTGTTGTCAGG-3'</p> <p>SOD1-Reverse (IMR0888): 5'-TCCATCACTGGTCACTAGCC-3'</p> <p>PGK-HPRT-Forward (IMR0781): 5'-TGTTCTCCTCTTCCTCATCTCC-3'</p> <p>PGK-HPRT-Reverse (IMR0782): 5'-ACCCTTTCCAAATCCTCAGC-3'</p> |

**Table 1. PCR primer sequences used for genotyping.** Forward and reverse genotyping primers for specific regions of PINK1 (Madeo et al., 2014), parkin (Fournier et al., 2009), SOD1, and PGK-HPRT (Kessova and Cederbaum, 2007).

with Tissue-Tek® O.C.T. Compound (Sakura Finetek) and sectioned using a cryostat (Leica CM 1850) to obtain 30µm thick serial coronal sections of the SVZ and SGZ. Nine wells of serial coronal sections were obtained for each brain structure of interest. Tissue sections were stored at 4°C in a solution of 0.01% sodium azide in 1X PBS.

### **2.3. Immunohistochemistry**

Free-floating tissue sections from an entire well were removed from storage, washed 4x in 1X PBS for 5 minutes each time, and then incubated with primary antibodies (Table 2) diluted in a solution of 0.1% Triton X-100 (MilliporeSigma) and 0.1% Tween-20 (Thermo Fisher Scientific) in 1X PBS overnight. Afterwards, tissue sections were washed 4x in 1X PBS for 5 minutes each time and then incubated with appropriate secondary antibodies conjugated with fluorescent markers (Table 2) and 4',6-diamidino-2-phenylindole (DAPI) diluted in another solution of 0.1% Triton X-100 and 0.1% Tween-20 in 1X PBS for 2 hours (protected from light). DAPI (MilliporeSigma) was diluted at 1:1000 from an original 1µg/mL solution. Tissue sections were then washed 4x in 1X PBS for 5 minutes each time before being mounted onto Fisherbrand™ Superfrost™ Plus Microscope Slides (Thermo Fisher Scientific) with Thermo Scientific™ Shandon™ Immu-Mount™ (Thermo Fisher Scientific). Different antibodies were sometimes used for the same targets depending on antibody combinations and/or commercial availability.

### **2.4. EdU Labelling**

*In vivo* labelling of proliferating cells was achieved by giving an intraperitoneal injection of 10µL/g of a 5 mg/mL EdU (5-ethynyl-2'-deoxyuridine) solution (Clickbase, BCK647-IV-IM-M) to the adult mice, 2.5 hours prior to being sacrificed. Tissue sections from these mice were

| Antibody                       | Host Species | Source                                     | Dilution                       |
|--------------------------------|--------------|--------------------------------------------|--------------------------------|
| <b>Primary Antibodies</b>      |              |                                            |                                |
| Dcx                            | Goat         | Santa Cruz Biotechnology (sc-8066)         | 1:500                          |
|                                | Rabbit       | Cell Signaling Technology (4604S)          | 1:500                          |
| GFAP                           | Mouse        | MilliporeSigma (MAB3402)                   | 1:1000 (SGZ)<br>1:10 000 (SVZ) |
| Ki67                           | Rabbit       | Cell Marque (SP6)                          | 1:500 (SGZ)                    |
| Nestin                         | Goat         | R&D Systems (AF2736)                       | 1:1000                         |
| Sox2                           | Goat         | Neuromics (GT15098)                        | 1:500                          |
|                                | Rabbit       | Abcam (ab97959)<br>MilliporeSigma (AB5603) | 1:500<br>1:500                 |
| <b>Secondary Antibodies</b>    |              |                                            |                                |
| Anti-goat Cy3                  | Donkey       | Jackson ImmunoResearch<br>(705-165-147)    | 1:1000                         |
| Anti-mouse Alexa<br>Fluor 647  | Donkey       | Jackson ImmunoResearch<br>(715-605-151)    | 1:1000                         |
| Anti-rabbit Alexa<br>Fluor 488 | Donkey       | Jackson ImmunoResearch<br>(711-545-152)    | 1:1000                         |

**Table 2. Primary and secondary antibodies used for immunohistochemistry.** Unless otherwise stated, listed antibody dilutions were used for both SVZ and SGZ tissue sections.

processed according to the manufacturer's instructions (Clickbase, BCK647-IV-IM-M). EdU label processing was done on tissue samples after being washed 4x in 1X PHS for 5 minutes each time, following incubation with primary and secondary antibodies for immunohistochemistry.

## **2.5 Microscopy, Cell Quantification, and Statistical Analysis**

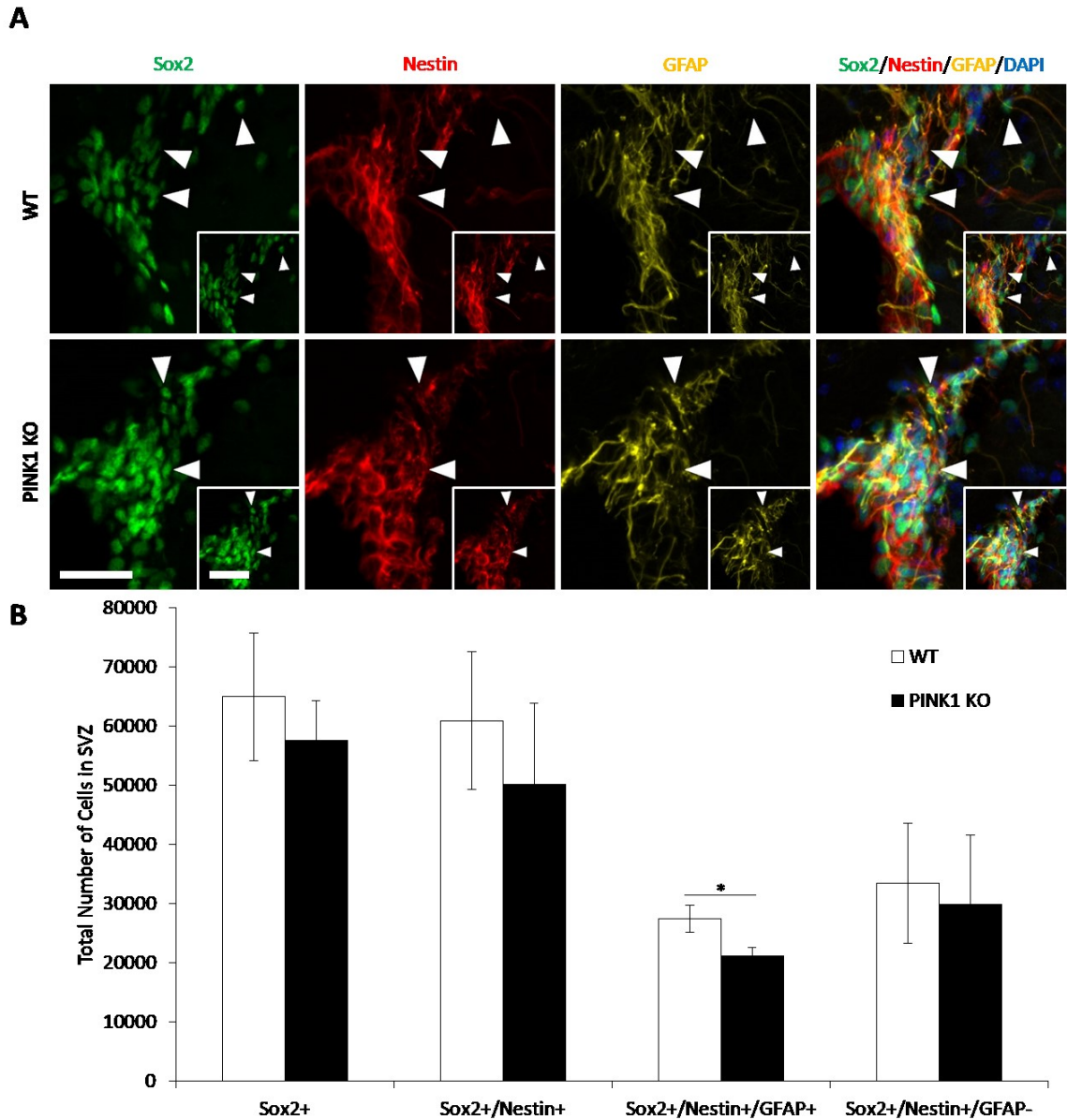
Mounted tissue sections were imaged by a Zeiss LSM800 AxioObserver Z1 confocal microscope using ZenPro (ZEISS) image acquisition software or a GE DeltaVision Elite (with microinjector) epifluorescence microscope using SoftWoRx (GE) image acquisition software. The entire structure of the SVZ or SGZ was imaged using an objective of 20X. Image processing and cell quantification was done using Fiji (ImageJ) software. Total SVZ or SGZ cell counts were extrapolated from cell counts performed on imaged sections. SVZ cell counts were based off of analyzing 2-3 SVZ sections per animal. SGZ cell counts were based off of analyzing 7-11 SGZ sections per animal (depending on the total number of serial sections obtained from each animal). Cell counts are represented as mean  $\pm$  SD. Comparisons between WT and PINK1 groups were done using unpaired, two-tailed Student's t-tests. Comparisons between WT, parkin KO, and SODPAR mice were done using a one-way ANOVA followed by a post-hoc Tukey's test.

## RESULTS

### 3.1. Role of PINK1 in SVZ Adult Neurogenesis

We decided to first examine how the absence of PINK1 affects adult neurogenesis in the SVZ. Immunohistochemical staining of SVZ sections from adult WT and PINK1 KO mice was done using markers for Sox2, nestin, and GFAP (Figure 5). By using this combination of markers, it was possible to identify specific populations of neural precursor cells. For instance, Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup> cells would represent activated NSCs (Type B1 cells), while Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cells would represent transit amplifying progenitors (Type C cells) (Codega et al., 2014; Doetsch et al., 1997; Graham et al., 2003; Imayoshi et al., 2011; Kazanis et al., 2010; Lagace et al., 2007; Lendahl et al., 1990). With respect to the overall number of neural precursor cells (Sox2<sup>+</sup> cells) in the SVZ, no significant difference was found between the WT and PINK1 KO groups (Figure 5B and Table S1). However, the PINK1 KO mice were found to have significantly fewer (~22.77% fewer) activated Type B1 cells than the WT mice (Figure 5B and Table S1). Potential causes for this finding include a defect in NSC self-renewal, decreased cellular proliferation, or increased cell death. However, there was no significant difference in the total number of nestin expressing neural precursor cells (Sox2<sup>+</sup>/Nestin<sup>+</sup> cells) or Type C cells in the SVZ between the WT and PINK1 KO mice (Figure 5B and Table S1). Given that there was no difference between both experimental groups with respect to the total number of nestin expressing neural precursor cells in the SVZ, there should have been an increase in the total number of Type C cells for the PINK1 KO mice to compensate for the decrease in the total number of activated Type B1 cells. It is possible that there was indeed a potential difference in either the total number of neural precursor cells, the subpopulation of neural precursor cells expressing nestin, or Type C cells, which was obscured by high statistical variance.



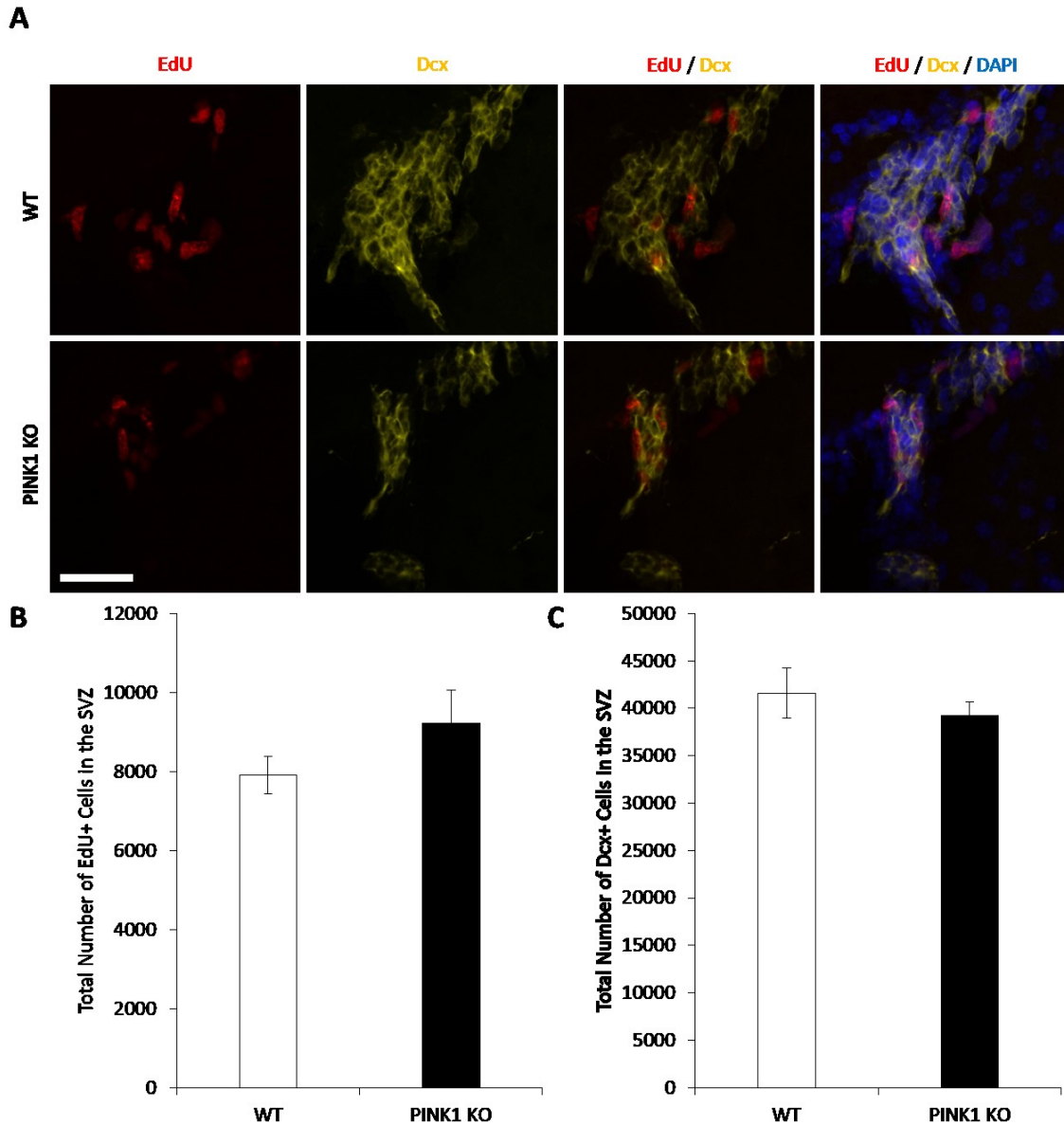


**Figure 5: Loss of PINK1 causes a decrease in the total number of activated Type B1 cells in the adult SVZ.** (A) Representative confocal images of the SVZ from 6 month old WT and PINK1 KO mice stained against Sox2, Nestin, GFAP, and DAPI. (B) Quantification of the Sox2<sup>+</sup>, Sox2<sup>+</sup>/Nestin<sup>+</sup>, Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup>, and Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cell populations in the SVZ. Arrowheads label activated Type B1 cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup>/DAPI<sup>+</sup>). Insets provide a zoomed-in view of the images. Quantitative data is represented as mean ± SD (n=3 per genotype, \*p<0.05, Student's t-test). Scale bars = 50 μm.

In order to investigate the decline in the total number of activated Type B1 cells for the PINK1 KO mice (Figure 5), we decided to examine cellular proliferation in the SVZ (Figure 6). Prior to being sacrificed, the mice used for this study were given a single pulse of EdU, so that it would be possible to later assess cellular proliferation by counting the total number of EdU<sup>+</sup> cells (Chehrehasa et al., 2009). No significant difference was found between the WT and PINK1 KO mice with respect to the total number of EdU<sup>+</sup> cells in the SVZ (Figure 6B and Table S2). This result suggests that the decline in the total number of activated Type B1 cells for the PINK1 KO mice was not caused by a decrease in cellular proliferation.

While there were other possibilities that could have been explored with respect to the decreased number of activated Type B1 cells in the SVZ of the PINK1 KO mice (ie: self-renewal defect or increased cell death), we decided to shift our attention to studying the impact of a loss of PINK1 downstream of the neural precursor cell population in the SVZ. By using a marker for Dcx, a protein primarily expressed in neuroblasts (Type A cells) and newborn neurons (Koizumi et al., 2006; Lagace et al., 2007; Ming and Song, 2011), it was possible to compare the total number of Type A cells in the SVZ between WT and PINK1 KO mice (Figure 6). No significant difference was found between the WT and PINK1 KO mice with respect to the total number of Dcx<sup>+</sup> cells in the SVZ (Figure 6C and Table S2). This would imply that the loss of PINK1 (at least up until 6 months of age) does not affect the normal progression of neural precursor cells into becoming Type A cells in the SVZ.

Our analysis of neurogenesis in the adult SVZ revealed a decrease in the total number of activated Type B1 cells for the PINK1 KO mice (Figure 5). This decline was also found to not be the result of a defect in cellular proliferation (Figure 6). The loss of PINK1 was also found to not affect the total number of Type A cells in the SVZ (Figure 6). It is possible that the defect in the



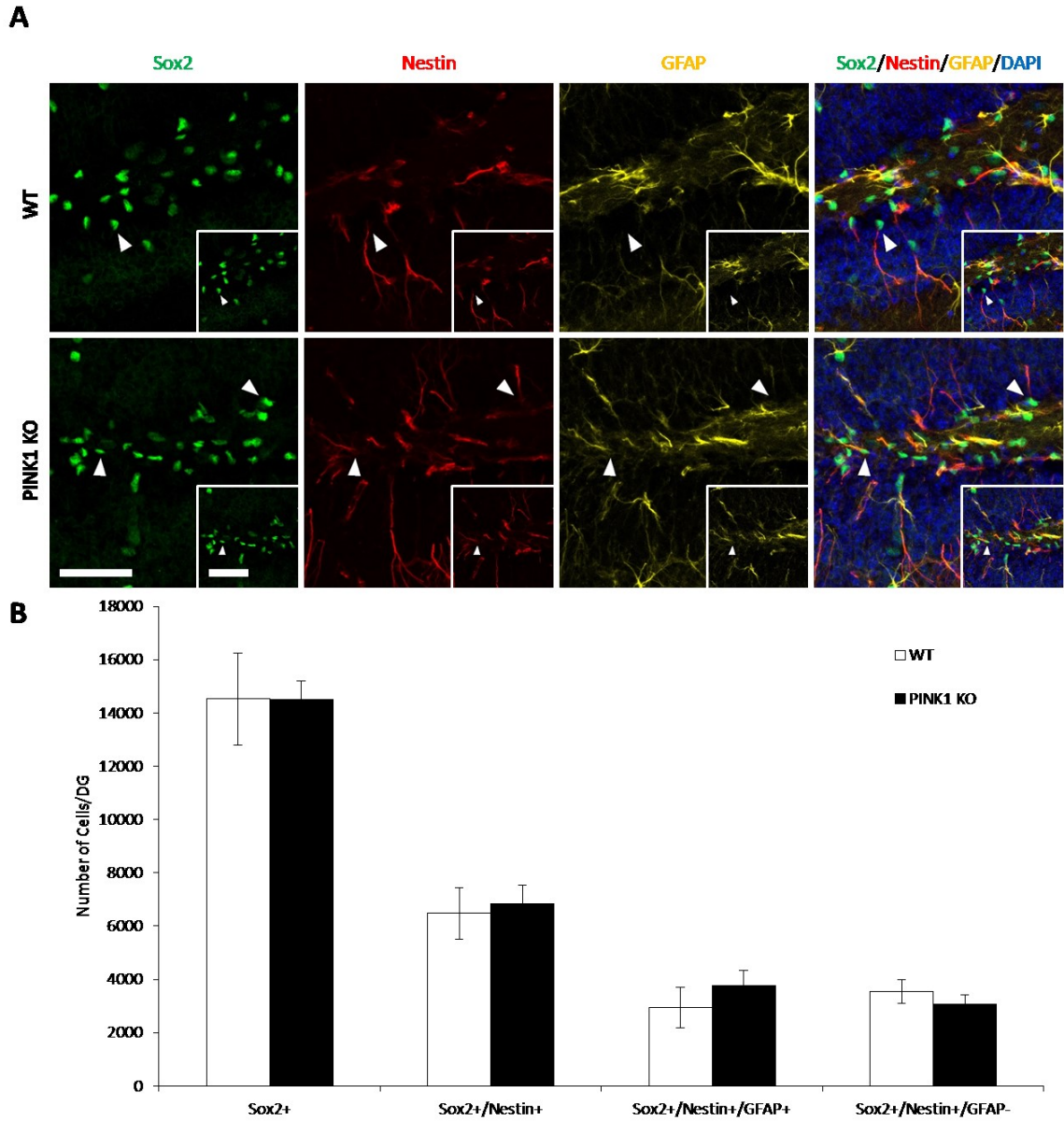
**Figure 6: Loss of PINK1 does not affect cellular proliferation or the total number of Type A cells in the adult SVZ.** (A) Representative confocal images of the SVZ from 6 month old WT and PINK1 KO mice stained against EdU, Dcx, and DAPI. (B) Quantification of the total number of EdU<sup>+</sup> cells in the SVZ. (C) Quantification of the total number of Dcx<sup>+</sup> cells in the SVZ. Quantitative data is represented as mean  $\pm$  SD (n=3 per genotype, Student's t-test). Scale bar = 50  $\mu$ m.

activated Type B1 cells was relatively recent, which would explain why there was no apparent change in the total number of Type A cells between both experimental groups.

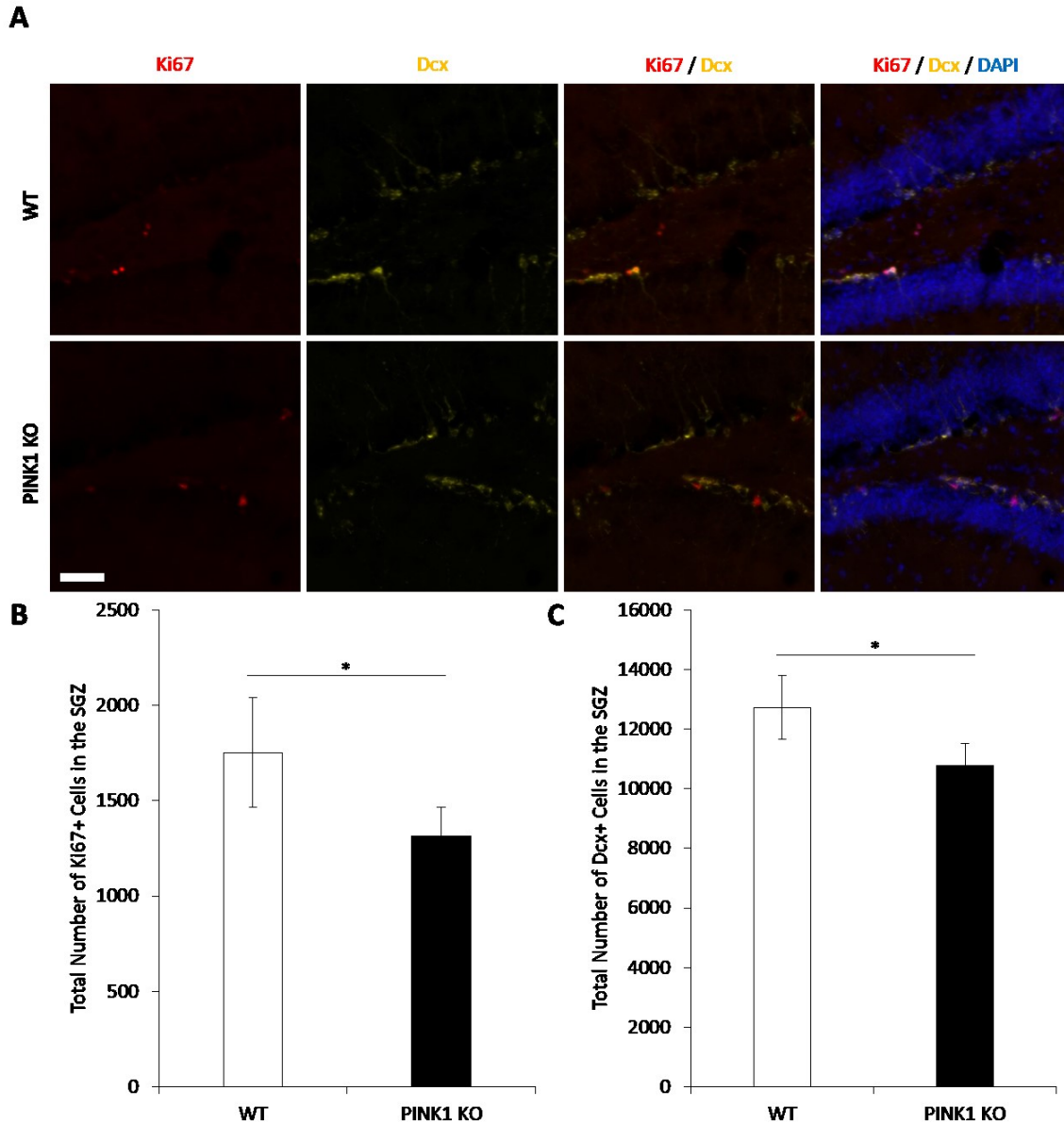
### **3.2. Role of PINK1 in SGZ Adult Neurogenesis**

After investigating the impact of a loss of PINK1 on adult neurogenesis in the SVZ, we decided to examine its impact on adult neurogenesis in the SGZ. The absence of PINK1 could have different effects on adult neurogenesis in the SVZ and SGZ because of niche specific differences (Bond et al., 2015; Ming and Song, 2011). Similar to our analysis in the SVZ, individual neural precursor cell populations in the SGZ were identified using markers for Sox2, nestin, and GFAP (Figure 7). In the SGZ, GFAP is expressed in NSCs (Type I cells), Sox2 is expressed in Type I cells and intermediate progenitor cells (Type II cells), and nestin is expressed in Type I cells and the Type IIa subpopulation of intermediate progenitors (Kronenberg et al., 2003; Lagace et al., 2007; Lugert et al., 2010, 2012; Seri et al., 2004; Shin et al., 2015; Suh et al., 2007). No significant differences were found between the WT and PINK1 KO mice with respect to the total number of neural precursor cells (Sox2<sup>+</sup> cells), nestin expressing neural precursor cells (Sox2<sup>+</sup>/Nestin<sup>+</sup> cells), Type I cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup> cells), or Type IIa cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cells) in the SGZ (Figure 7B and Table S3). Based on these results, PINK1 is not necessary for the maintenance of the neural precursor cell population in the adult SGZ.

To determine if the absence of PINK1 causes aberrant cellular proliferation in the SGZ, we performed immunohistochemical staining of SGZ sections for Ki67 (Figure 8), a well-known marker of cellular proliferation (Scholzen and Gerdes, 2000). The PINK1 KO mice were found to have significantly fewer (~25.09% fewer) Ki67<sup>+</sup> cells in the SGZ than the WT mice (Figure 8B



**Figure 7: Loss of PINK1 does not affect the total number of neural precursor cells in the adult SGZ.** (A) Representative confocal images of the SGZ from 6 month old WT and PINK1 KO mice stained against Sox2, Nestin, GFAP, and DAPI. (B) Quantification of the Sox2<sup>+</sup>, Sox2<sup>+</sup>/Nestin<sup>+</sup>, Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup>, and Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cell populations in the SGZ. Arrowheads label Type I cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup>/DAPI<sup>+</sup>). Insets provide a zoomed-in view of the images. Quantitative data is represented as mean ± SD (n=4 per genotype, Student's t-test). Scale bars = 50 μm.



**Figure 8: Loss of PINK1 causes a decrease in the total number of proliferating cells and newborn neurons in the adult SGZ.** (A) Representative fluorescent images of the SGZ from 6 month old WT and PINK1 KO mice stained against Ki67, Dcx, and DAPI. (B) Quantification of the total number of Ki67<sup>+</sup> cells in the SGZ. (C) Quantification of the total number of Dcx<sup>+</sup> cells in the SGZ. Quantitative data is represented as mean  $\pm$  SD (n=4 per genotype, \*p<0.05, Student's t-test). Scale bar = 50  $\mu$ m.

and Table S4). This suggests that PINK1 is required for proper cellular proliferation in the adult SGZ.

We decided to next investigate how the absence of PINK1 affects cells derived from neural precursor cells. This involved staining SGZ sections for Dcx (Figure 8), which is expressed in Type IIb cells, neuroblasts (Type III cells), and newborn neurons in the SGZ (Kronenberg et al., 2003; Lagace et al., 2007; Nicola et al., 2015). The PINK1 KO mice were found to have significantly fewer (~15.28% fewer) Dcx<sup>+</sup> cells, compared to the WT mice (Figure 8C and Table S4). The decrease in the total number of Dcx<sup>+</sup> cells in the SGZ for the PINK1 KO mice would indicate a decline in the total number of newborn neurons being produced, which would ultimately cause a decrease in the total number of mature neurons being produced by the SGZ over time. It is possible that this decline in the total number of newborn neurons could be caused in part by the previously mentioned deficit in cellular proliferation in the SGZ.

### **3.3. Role of Parkin in SVZ Adult Neurogenesis**

For the second half of this investigation, we focused on studying the role of parkin in adult neurogenesis. While PINK1 and parkin have been shown to work together in several molecular pathways related to mitochondrial quality control, these two proteins have also been demonstrated in other molecular pathways to operate independently of each other (Exner et al., 2012; McWilliams and Muqit, 2017; Mouton-Liger et al., 2017; Park et al., 2018; Truban et al., 2017). This means that the absence of PINK1 or parkin could have different effects on adult neurogenesis. In order to study the role of parkin in adult neurogenesis, WT mice were compared to parkin KO and SODPAR (parkin KO with a hemizygous SOD2 KO) mice. SOD2 is an antioxidant enzyme responsible for reducing mitochondrial ROS in the cell (Lebovitz et al., 1996; Weisiger and

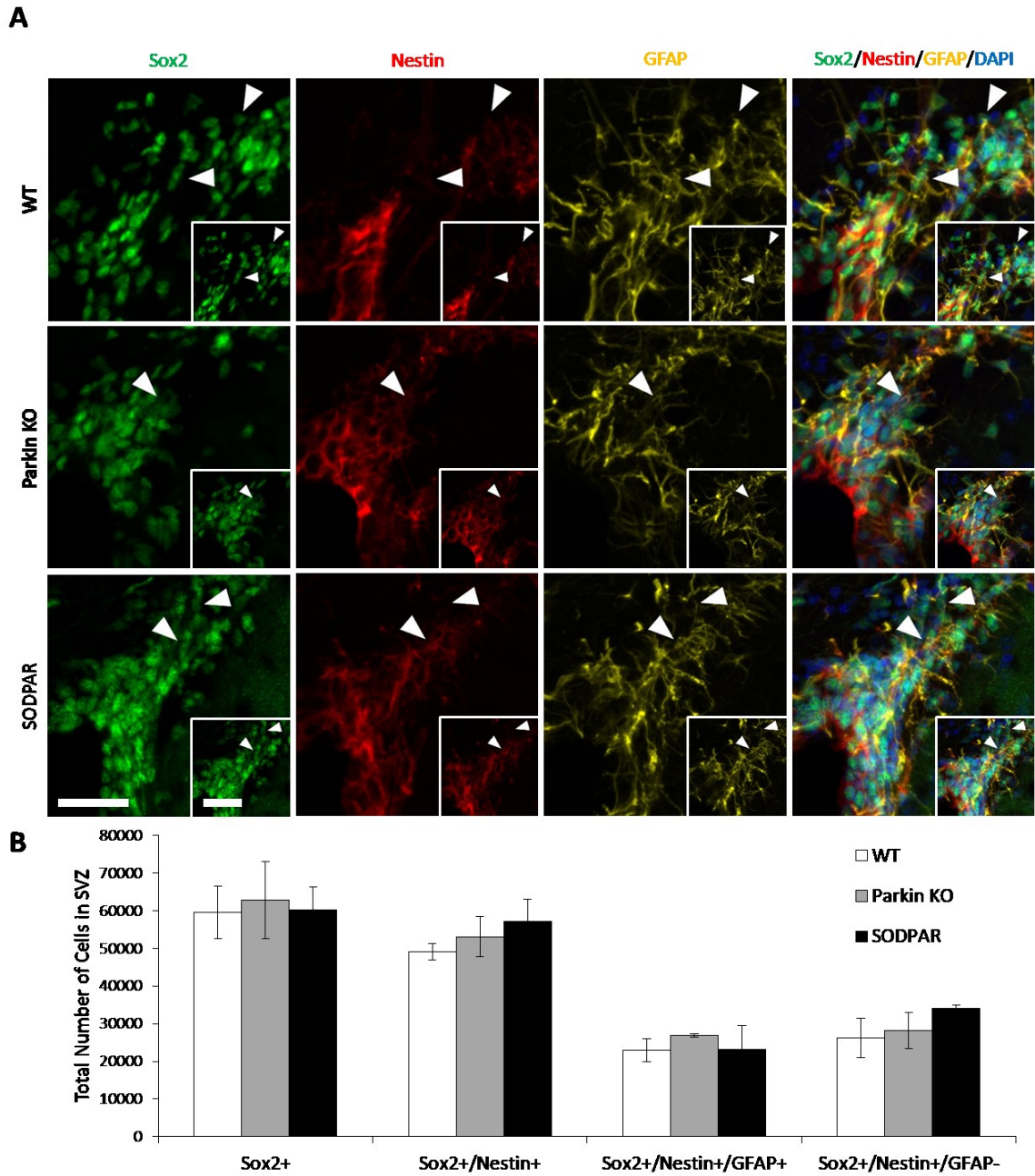
Fridovich, 1973; Zelko et al., 2002). By combining a loss of parkin with a reduction in SOD2, the SODPAR mice could potentially show more pronounced changes in adult neurogenesis than the parkin KO mice, which are known to display only minimal signs of PD pathology (Itier et al., 2003; Periquet et al., 2005). It was not possible to create homozygous SOD2 KO mice since the complete loss of SOD2 is lethal (Lebovitz et al., 1996).

The first question we asked when studying the role of parkin in adult neurogenesis, was how a loss of parkin would affect the neural precursor cell population in the SVZ. As with our analysis of the PINK1 KO mice (Figure 5), SVZ sections from WT, parkin KO, and SODPAR mice were stained with markers for Sox2, nestin, and GFAP (Figure 9) in order to identify specific populations of neural precursor cells. No significant differences were found between the WT, parkin KO, and SODPAR mice with respect to the total number of neural precursor cells (Sox2<sup>+</sup> cells), nestin expressing neural precursor cells (Sox2<sup>+</sup>/Nestin<sup>+</sup> cells), activated Type B1 cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup> cells), or Type C cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cells) in the SVZ (Figure 9B and Table S5). These results suggest that parkin is not necessary for the maintenance of the neural precursor cell population in the adult SVZ.

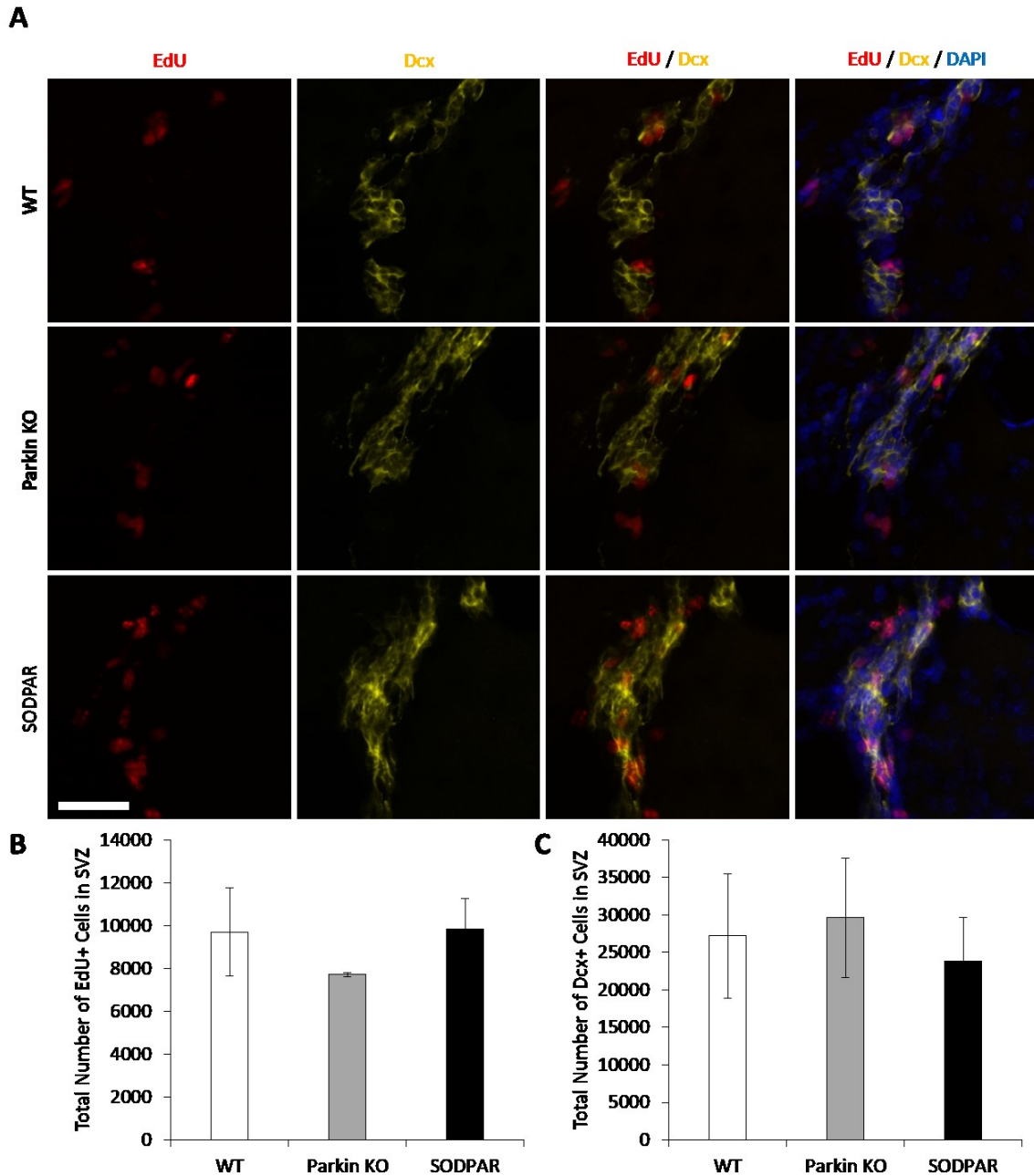
The possibility of an absence of parkin affecting cellular proliferation in the adult SVZ was then examined by using EdU to quantify the number of proliferating cells in the SVZ (Figure 10). There were no significant differences between the WT, parkin KO, and SODPAR mice with respect to the total number of EdU<sup>+</sup> cells in the SVZ (Figure 10B and Table S6), suggesting that parkin is not required for cellular proliferation in the adult SVZ.

The impact of a loss of parkin on cells derived from the neural precursor cell population in the adult SVZ was then studied by using Dcx as a marker for Type A cells (Figure 10). There were no significant differences between the WT, parkin KO, and SODPAR mice with respect to the





**Figure 9: Loss of parkin does not affect the total number of neural precursor cells in the adult SVZ.** (A) Representative confocal images of the SVZ from 6 month old WT, parkin KO, and SODPAR mice stained against Sox2, Nestin, GFAP, and DAPI. (B) Quantification of the Sox2<sup>+</sup>, Sox2<sup>+</sup>/Nestin<sup>+</sup>, Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup>, and Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cell populations in the SVZ. Arrowheads label activated Type B1 cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup>/DAPI<sup>+</sup>). Insets provide a zoomed-in view of the images. Quantitative data is represented as mean  $\pm$  SD (n=3 per genotype, one-way ANOVA and Tukey's). Scale bars = 50  $\mu$ m.

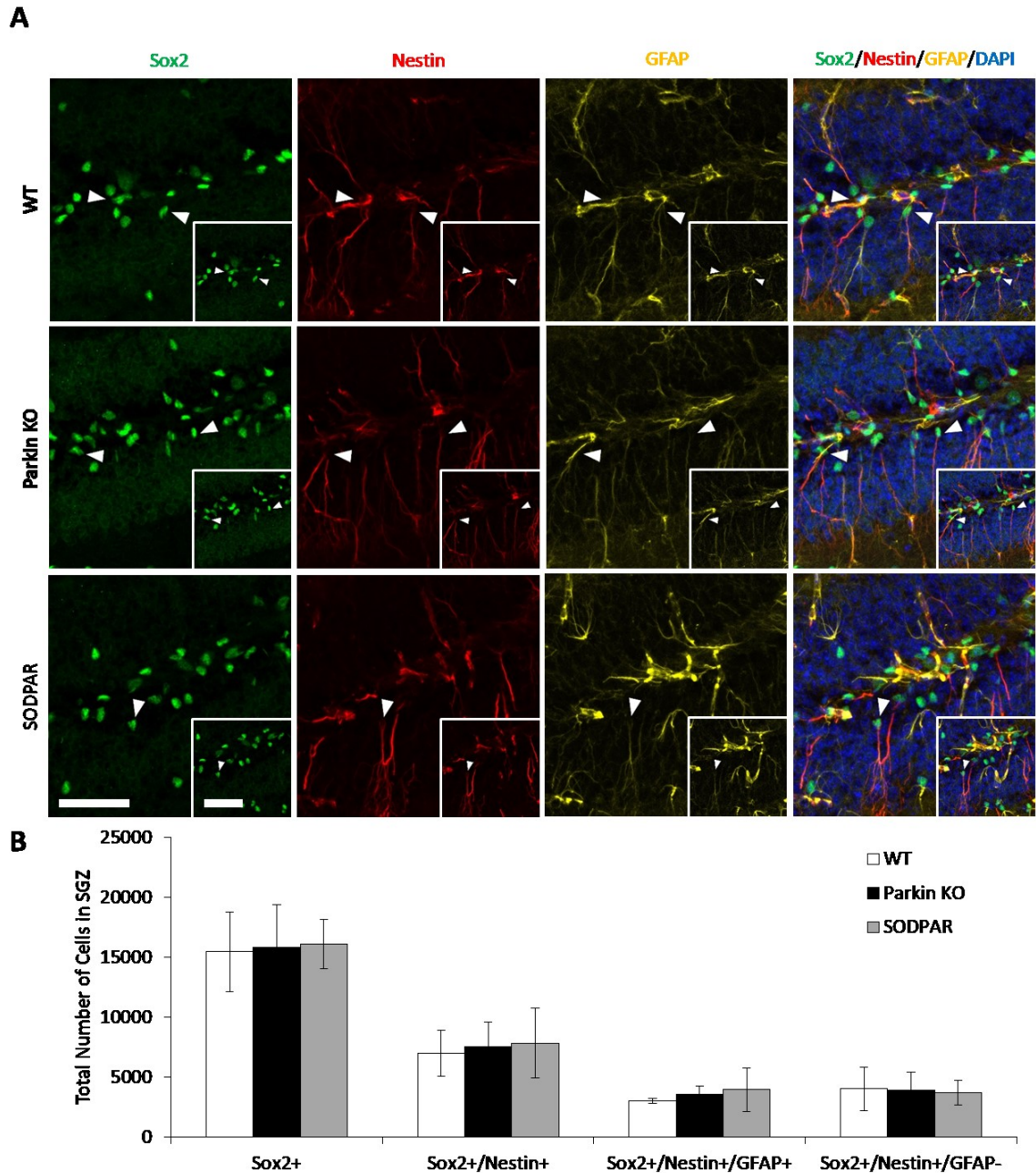


**Figure 10: Loss of parkin does not affect cell proliferation or the total number of Type A cells in the adult SVZ.** (A) Representative confocal images of the SVZ from 6 month old WT, parkin KO, and SODPAR mice stained against EdU, Dcx, and DAPI. (B) Quantification of the total number of EdU<sup>+</sup> cells in the SVZ. (C) Quantification of the total number of Dcx<sup>+</sup> cells in the SVZ. Quantitative data is represented as mean  $\pm$  SD (n=3 per genotype, one-way ANOVA and Tukey's test). Scale bar = 50  $\mu$ m.

total number of Dcx<sup>+</sup> (Type A) cells in the SVZ (Figure 10B and Table S6). This would imply that parkin is not necessary for the production of newborn neurons from the adult SVZ.

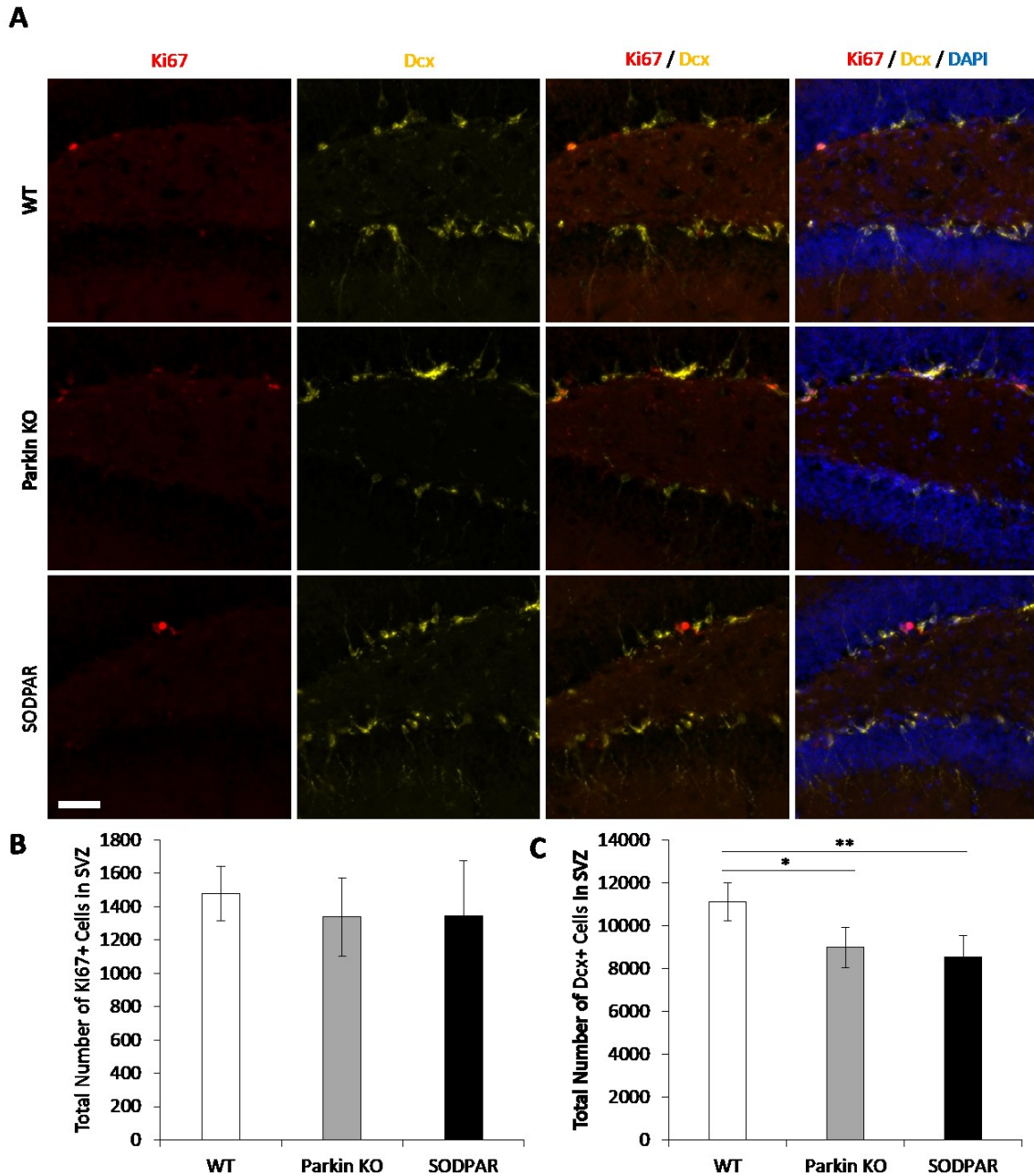
### **3.4. Role of Parkin in SGZ Adult Neurogenesis**

Given the existence of niche specific differences between the SVZ and SGZ (Bond et al., 2015; Ming and Song, 2011), we decided to also investigate the role of parkin in SGZ adult neurogenesis. An analysis of the neural precursor cell population using markers for Sox2, nestin, and GFAP (Figure 11) revealed no significant differences between the WT, parkin KO, and SODPAR mice with respect to the total number of neural precursor cells (Sox2<sup>+</sup> cells), nestin expressing neural precursor cells (Sox2<sup>+</sup>/Nestin<sup>+</sup> cells), Type I cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup> cells), or Type IIa cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cells) in the SGZ (Figure 11B and Table S7). The impact of an absence of parkin on cellular proliferation and cells derived from the neural precursor cell population was examined by staining for Ki67 and Dcx (Figure 12). There was also no difference in the total number of Ki67<sup>+</sup> cells in the SGZ between the WT, parkin KO, and SODPAR mice (Figure 12B and Table S8), suggesting that parkin is not necessary for cellular proliferation in the adult SGZ. However, the parkin KO and SODPAR mice were found to have significantly fewer Dcx<sup>+</sup> cells in the SGZ (~19.25% fewer for the parkin KO mice and ~23.17% fewer for the SODPAR mice) compared to the WT control mice (Figure 12C and Table S8). The decrease in the total number of Dcx<sup>+</sup> cells in the SGZ would imply a decrease in the total number of newborn neurons being produced. There was no significant difference between the parkin KO and SODPAR mice with respect to the total number of Dcx<sup>+</sup> cells in the SGZ (Figure 12C and Table S8).



**Figure 11: Loss of parkin does not affect the total number of neural precursor cells in the adult SGZ.** (A) Representative confocal images of the SGZ from 6 month old WT, parkin KO, and SODPAR mice stained against Sox2, Nestin, GFAP, and DAPI. (B) Quantification of the Sox2<sup>+</sup>, Sox2<sup>+</sup>/Nestin<sup>+</sup>, Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup>, and Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cell populations in the SGZ. Arrowheads label Type I cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup>/DAPI<sup>+</sup>). Insets provide a zoomed-in view of the images. Quantitative data is represented as mean  $\pm$  SD (n=3 per genotype, one-way ANOVA and Tukey's test). Scale bars = 50  $\mu$ m.





**Figure 12: Loss of parkin causes a decrease in the total number of newborn neurons in the adult SGZ.** (A) Representative fluorescent images of the SGZ from 6 month old WT, parkin KO, and SODPAR mice stained against Ki67, Dcx, and DAPI. (B) Quantification of the total number of Ki67<sup>+</sup> cells in the SGZ. (C) Quantification of the total number of Dcx<sup>+</sup> cells in the SGZ. Quantitative data is represented as mean  $\pm$  SD (n=3-4 per genotype, \*p<0.05, \*\*p<0.01, one-way ANOVA and Tukey's test). Scale bar = 50  $\mu$ m.

## DISCUSSION

### 4.1. Summary of Results

Given the central role of mitochondria in regulating NSC fate decisions, one would expect PD associated mitochondrial dysfunction to cause defects in adult neurogenesis (Khacho et al., 2019). The goal of this thesis was to assess the impact of a loss of PINK1 or parkin on adult neurogenesis. The results of this thesis support a number of conclusions:

- 1) PINK1 is required for the maintenance of the activated Type B1 (NSC) population in the adult SVZ.
- 2) PINK1 is required for cellular proliferation in the SGZ.
- 3) PINK1 is required for the maintenance of newborn neurons in the SGZ.
- 4) Parkin is required for the maintenance of newborn neurons in the SGZ.
- 5) A hemizygous KO of SOD2 is an insufficient stressor to exacerbate defects in adult neurogenesis in a parkin KO mouse model.

**Collectively, these findings support the hypothesis that a loss of either PINK1 or parkin would impair adult neurogenesis.** The following sections of this thesis discuss the major findings from this study and their implications.

## 4.2. Role of PINK1 in SVZ Adult Neurogenesis

Our investigation into the role of PINK1 in adult neurogenesis began with determining the impact an absence of PINK1 would have on the neural precursor cell population in the SVZ (Figure 5). Through immunohistochemistry, 6 month old PINK1 KO mice were found to have ~22.77% fewer activated Type B1 cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup> cells) in the SVZ compared to age matched WT controls (Figure 5B and Table S1). EdU labelling was conducted to test the possibility that a loss of PINK1 impairs cellular proliferation in the SVZ (Figure 6). However, no significant difference in the total number of EdU<sup>+</sup> cells in the SVZ was found between the WT and PINK1 KO mice (Figure 6B and Table S2), suggesting that the absence of PINK1 does not affect cellular proliferation in the SVZ. The observed decline in the activated Type B1 cell population could also have been the result of increased cell death or a defect in NSC activation. Numerous studies have demonstrated PINK1 to promote cell survival under various conditions by preventing apoptosis (Arena et al., 2013; Deng et al., 2005; Gandhi et al., 2009; Haque et al., 2008; Marongiu et al., 2009; Petit et al., 2005; Pridgeon et al., 2007; Wood-Kaczmar et al., 2008). A defect in NSC activation would lead to an increase in the total number of quiescent Type B1 cells at the expense of the activated Type B1 cell population (Daynac et al., 2016).

No significant differences were found between the WT and PINK1 KO mice with respect to the total number of neural precursor cells (Sox2<sup>+</sup> cells), nestin expressing neural precursor cells (Sox2<sup>+</sup>/Nestin<sup>+</sup> cells), or Type C cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cells) in the SVZ (Figure 5B and Table S1). Given that the activated Type B1 cell population is a part of the overall neural precursor cell population, a decline in the total number of activated Type B1 cells should have also affected the total number of neural precursor cells and/or other neural precursor subpopulations (Bond et al., 2015). It is possible that changes in these other cell populations were not detected due to the

presence of high statistical variance. This issue could be resolved by increasing the sample size used to compare the WT and PINK1 KO mice.

After examining the neural precursor cell population and cellular proliferation, we decided to investigate the impact an absence of PINK1 would have on the Type A cell (neuroblast) population in the SVZ (Figure 6). No significant difference was found between WT and PINK1 KO mice with respect to the total number of Dcx<sup>+</sup> cells in the SVZ (Figure 6C and Table S2). This result suggests that the loss of PINK1 does not affect the Type A cell population in the adult SVZ (at least until 6 months of age). Given that there was no significant difference in the total number of Type A cells in the SVZ between the WT and PINK1 KO mice, the observed decrease in the activated Type B1 cell population would likely have occurred relatively recently. In this case, examining additional time-points would allow for the observation of changes in cell populations derived from the activated Type B1 cell population.

#### **4.3. Role of PINK1 in SGZ Adult Neurogenesis**

The role of PINK1 in SGZ adult neurogenesis was also investigated by examining the impact an absence of PINK1 would have on the neural precursor cell population, cellular proliferation, and neural precursor derived cells. The absence of PINK1 was not found to affect the neural precursor cell population (Figure 7), with respect to the total number of neural precursor cells (Sox2<sup>+</sup> cells), nestin expressing neural precursor cells (Sox2<sup>+</sup>/Nestin<sup>+</sup> cells), Type I cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup> cells), or Type IIa cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cells) in the SGZ (Figure 7B and Table S3). Analysis of cellular proliferation in the SGZ (Figure 8) revealed that the PINK1 KO mice had ~25.09% fewer Ki67<sup>+</sup> cells (Figure 8B and Table S4) than the WT mice, suggesting that the loss of PINK1 resulted in a cellular proliferation defect in the SGZ. Analysis of cell



populations derived from the neural precursor cell population in the SGZ (Figure 8) revealed that the PINK1 KO mice had ~15.28% fewer Dcx<sup>+</sup> cells (Figure 8C and Table S4) than the WT mice, suggesting that PINK1 is involved with the production of newborn neurons in the SGZ.

Similar results have been reported in a study by Beckervordersandforth et al. (2017), which examined the importance of mitochondrial function in regulating adult hippocampal neurogenesis. In their study, defects in proliferation, differentiation, maturation, and survival were found in the SGZ of adult conditional TFAM KO mice. These defects were discovered to be the result of mitochondrial dysfunction negatively affecting committed neuronal cell-types that primarily rely on OXPHOS more than NSCs that primarily rely on glycolysis (Beckervordersandforth et al., 2017). Given that mitochondrial dysfunction has been observed in adult hippocampal NSCs derived from PINK1 KO mice (Agnihotri et al., 2017), the possibility of mitochondrial dysfunction preferentially affecting committed neuronal cell populations (that rely on OXPHOS) in the SGZ of PINK1 KO mice should be investigated (Beckervordersandforth et al., 2017).

#### **4.4. Role of Parkin in SVZ Adult Neurogenesis**

After studying the impact of a loss of PINK1 on adult neurogenesis, we decided to investigate the impact a loss of parkin would have on adult neurogenesis. PINK1 and parkin are known to cooperate in several pathways related to mitochondrial quality control, but independent functions for these proteins have been identified (Exner et al., 2012; McWilliams and Muqit, 2017; Mouton-Liger et al., 2017; Park et al., 2018; Truban et al., 2017). Analysis of the neural precursor cell population (Figure 9) in the SVZ revealed no significant differences between 6 month old WT, parkin KO, and SODPAR mice with respect to the total number of neural precursor cells (Sox2<sup>+</sup> cells), nestin expressing neural precursor cells (Sox2<sup>+</sup>/Nestin<sup>+</sup> cells), activated Type B1 cells

(Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup> cells), or Type C cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cells) in the SVZ (Figure 9B and Table S5). No significant differences in cellular proliferation (EdU<sup>+</sup> cells) or the total number of Type A cells (Dcx<sup>+</sup> cells) in the SVZ were found between the WT, parkin KO, and SODPAR mice (Figure 10 and Table S6). Based on these findings, the loss of parkin (even when combined with a reduction in SOD2) does not seem to affect the neural precursor cell population, cellular proliferation, or the production of newborn neurons in the SVZ (at least up to 6 months of age).

#### **4.5. Role of Parkin in SGZ Adult Neurogenesis**

The final part of this thesis involved studying the impact of a loss of parkin on SGZ adult neurogenesis. Examination of the neural precursor cell population in the SGZ revealed no significant differences between WT, parkin KO, and SODPAR mice (Figure 11), with respect to the total number of neural precursor cells (Sox2<sup>+</sup> cells), nestin expressing neural precursor cells (Sox2<sup>+</sup>/Nestin<sup>+</sup> cells), Type I cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>+</sup> cells), or Type IIa cells (Sox2<sup>+</sup>/Nestin<sup>+</sup>/GFAP<sup>-</sup> cells) in the SGZ (Figure 11B and Table S7). There was also no significant difference in cellular proliferation in the SGZ found between WT, parkin KO, and SODPAR mice (Figure 12B and Table S8). However, the parkin KO and SODPAR mice were found to have significantly fewer (~19.25% and ~23.17% fewer, respectively) Dcx<sup>+</sup> cells in the SGZ, compared to the WT mice (Figure 12C and Table S8). This would imply a decline in the production of newborn neurons, which could be the result of a defect in neuronal differentiation and/or survival in the SGZ. Similar to the PINK1 KO data, the decline in newborn neurons could be the result of mitochondrial dysfunction (caused by a loss of Parkin) impairing differentiation and survival in committed neuronal cell populations that rely primarily on OXPHOS (Beckervordersandforth et al., 2017).

#### **4.6. No Observable Differences between Parkin KO and SODPAR Mice**

While investigating the role of parkin in adult neurogenesis, no significant differences in SVZ or SGZ cell populations were observed between the parkin KO and SODPAR mice. The SODPAR mice were initially expected to display more pronounced changes in adult neurogenesis than the parkin KO mice, due to the combination of an absence of parkin with a reduction in the mitochondrial antioxidant enzyme SOD2 (Lebovitz et al., 1996; Weisiger and Fridovich, 1973; Zelko et al., 2002). However, the results of this thesis do not support the notation of a hemizygous KO of SOD2 as being a sufficient cellular stressor to exacerbate defects in adult neurogenesis caused by a loss of parkin.

#### **4.7. Future Directions**

In this thesis, adult neurogenesis in the SVZ and SGZ was examined at a single time-point (6 months of age) using immunohistochemistry to label a limited number of different cell populations. While this approach has provided some preliminary data on the importance of PINK1 and parkin in adult neurogenesis, a complete characterization of adult neurogenesis in our PD mouse models is still required. This would involve using additional immunohistochemical markers to refine the analysis of specific subpopulations of cells within the SVZ and SGZ. For example, markers for GFAP, prominin-1 (CD133), and the epidermal growth factor receptor (EGFR) can be used to differentiate quiescent NSCs (GFAP<sup>+</sup>/CD133<sup>+</sup>/EGFR<sup>-</sup> cells) from activated NSCs (GFAP<sup>+</sup>/CD133<sup>+</sup>/EGFR<sup>+</sup> cells) in the adult SVZ (Codega et al., 2014). Multiple time-points would need to be examined since PD is a progressive neurodegenerative disease (Exner et al., 2012), meaning that defects in adult neurogenesis may only become salient at an advanced age (Marxreiter et al., 2013b). Cell intrinsic and extrinsic regulation of NSC self-renewal,

differentiation, proliferation, and survival can also be assessed *in vitro* by studying neurospheres (Pastrana et al., 2011).

Several studies have shown PINK1 and parkin to be necessary for neuronal survival and maturation (Agnihotri et al., 2017; Dagda et al., 2014; Giguère et al., 2018; Wood-Kaczmar et al., 2008). Defects in survival have been reported for NSC derived human dopaminergic neurons with a knockdown in PINK1 and primary cortical neurons from PINK1 KO mice (Wood-Kaczmar et al., 2008). Another study, using primary cortical and midbrain neurons from PINK1 KO mice, found PINK1 to be involved with the regulation of dendritic length and complexity (Dagda et al., 2014). In the context of adult hippocampal neurogenesis, Dcx<sup>+</sup> newborn neurons in the SGZ of 10-12 week old PINK1 KO mice were discovered to have dendrites that were structurally less complex than those from WT control mice (Agnihotri et al., 2017). In a study by Giguère et al. (2018), cultured dopaminergic neurons from the SN of newborn parkin KO mouse pups (P0-P2) were found to develop defects in survival and axonal arborization over time. In this thesis, we did not assess long-term survival or activity of neurons being produced in the adult SVZ or SGZ from our PD mouse models. Lineage tracing experiments will need to be conducted in order to answer questions related to neuronal differentiation, survival, and functionality *in vivo* (Enikolopov et al., 2015).

Given the lack of robust changes in adult neurogenesis observed in the 6 month old PD mouse models used for this project, it may be prudent to use a different PD mouse model. For example, the parkin-mutator mouse model [which lacks parkin and has a mutated version of the mitochondrial DNA polymerase  $\gamma$  (POLG) with impaired proofreading function] has been reported to display progressive dopaminergic neurodegeneration (Goldberg et al., 2003; Kujoth et al., 2005; Pickrell et al., 2015). Evidence of aberrant changes to neurogenesis have been reported in the

progeroid POLG mutator mouse model (Ahlqvist et al., 2012). Neurospheres derived from embryonic POLG mutator mice have shown impaired self-renewal. In adult POLG mutator mice over 40 weeks of age, a decrease in the total number of nestin<sup>+</sup> neural precursor cells in the SVZ has been observed, with no changes in the total number of proliferating cells in the SVZ or calbindin<sup>+</sup> periglomerular interneurons in the OBs (Ahlqvist et al., 2012). The mitochondrial dysfunction associated with an absence of parkin combined with a defect in POLG activity (Pickrell et al., 2015) could potentially be severe enough to cause aberrant changes to adult neurogenesis (Beckervordersandforth et al., 2017; Khacho et al., 2016). Having a PD mouse model that displays robust changes in adult neurogenesis (especially at an earlier age of onset) would help to streamline research on the impact of PD associated mitochondrial dysfunction on adult neurogenesis.

After a detailed characterization of adult neurogenesis in a suitable PD mouse model, the next phase of this project would be to determine if observed changes in adult neurogenesis are the result of mitochondrial dysfunction. This would involve three key steps: (1) assessing mitochondrial integrity, (2) identifying molecular pathways responsible for aberrant changes to adult neurogenesis, and (3) performing phenotypic rescue experiments.

There are several parameters that can be examined in order to assess mitochondrial integrity within a suitable PD mouse model. Measuring the lengths of individual mitochondria in cells, through immunohistochemical staining of Tom20 (translocase of the outer membrane subunit 20), can be done to assess mitochondrial dynamics (Khacho et al., 2016). Parameters such as mitochondrial membrane potential ( $\Delta\Psi_m$ ), ATP production, cellular and mitochondrial ROS levels, oxygen consumption rate (OCR), and extracellular acidification rate (ECAR) can be examined in order to assess mitochondrial function and cellular metabolism (Agnihotri et al., 2017;

Khacho et al., 2016). Mitophagy can also be examined given the potential involvement of dysfunctional mitophagy in PD pathology (Cummins and Götz, 2018; Pickrell and Youle, 2015) and the mounting evidence supporting an involvement of autophagy in adult neurogenesis (Casares-Crespo et al., 2018). It is expected that there would be signs of mitochondrial dysfunction and altered cellular metabolism in the chosen PD mouse model, given the intimate relationship between PD pathology and mitochondrial dysfunction (Exner et al., 2012). In the study by Agnihotri et al. (2017), analysis of mitochondrial potential, OCR, and ECAR found evidence of mitochondrial dysfunction and a greater reliance on glycolysis for energy production in hippocampal NSCs derived from 10-12 week old PINK1 KO mice. A careful analysis of mitochondrial integrity would be necessary in order to be able to later identify key molecular pathways and plan appropriate phenotypic rescue experiments.

The identification of molecular pathways responsible for aberrant changes to adult neurogenesis can be achieved by using RNA-sequencing (RNA-seq) to identify potential genes of interest. In the study by Khacho et al. (2016), RNA-seq was used to study the mechanism behind the regulation of embryonic neurogenesis through mitochondrial dynamics. Over-represented transcription factors revealed through RNA-seq were analyzed in order to identify changes in groups of genes, involved with a particular cellular function (Khacho et al., 2016). A similar approach could be applied to studying the impact of PD associated mitochondrial dysfunction on adult neurogenesis. Single-cell RNA-seq, which has been successfully used to study the progression of neurogenesis in the adult SGZ (Shin et al., 2015) and SVZ (Zywitza et al., 2018), can be used to identify changes in specific cell populations.

Lastly, phenotypic rescue experiments will need to be conducted in order to demonstrate the possibility of rescuing adult neurogenesis in a chosen PD mouse model through the restoration

of mitochondrial integrity. Transgenic and pharmacological approaches can be used to restore mitochondrial integrity both *in vitro* and *in vivo* (Khacho et al., 2016; Sorrentino et al., 2018). Transgenic rescue experiments will involve modulating the expression of specific genes (levels of specific proteins) to improve mitochondrial dynamics and function. For example, the PD model mice could be crossed with mice overexpressing Opa1 (Opa1<sup>tg</sup> mice), which are reported to have improved OXPHOS efficiency as a result of mitochondrial elongation and improved mitochondrial cristae structure organization (Civiletto et al., 2015; Varanita et al., 2015). Pharmacological rescue experiments will involve the use of small molecule compounds to improve mitochondrial dynamics and function. Potential compounds that can be tested include mdivi-1 (Mitochondrial Division Inhibitor 1), nicotinamide riboside (NR), and piracetam (Beckervordersandforth et al., 2017; Cassidy-Stone et al., 2008; Cui et al., 2010; Zhang et al., 2016). Mdivi-1 promotes mitochondrial fusion by inhibiting the mitochondrial fission protein Drp1 (Cassidy-Stone et al., 2008). This compound was found to ameliorate aberrant changes to mitochondrial dynamics and function in PINK1 mutant B27 cells (Cui et al., 2010). NR supplementation in aged mice has been reported to revitalize muscle, neural, and melanocyte stem cell populations (Zhang et al., 2016). Piracetam treatment of aged mice was found to improve adult hippocampal neurogenesis by enhancing neuronal differentiation and maturation (Beckervordersandforth et al., 2017). The efficacy of all phenotypic rescue experiments can be assessed using metrics previously mentioned in this thesis.

## CONCLUSION

The purpose of this thesis was to investigate the impact a loss of PINK1 or parkin would have on adult neurogenesis in the SVZ and SGZ neurogenic niches. In the adult SVZ, PINK1 was found to be required for the maintenance of the activated Type B1 cell population. In the adult SGZ, PINK1 was found to be involved with cellular proliferation and the production of newborn neurons. The loss of parkin was not found to affect neurogenesis in the adult SVZ, but did cause a decline in the production of newborn neurons in the SGZ. These findings support our hypothesis that a loss of either PINK1 or parkin would impair adult neurogenesis. Future studies should focus on completing the characterization of adult neurogenesis in these PD mouse models and investigating the potential involvement of mitochondrial dysfunction. In order to streamline this research, a different mouse model of PD that displays robust changes in adult neurogenesis could be studied. Understanding the effect of PD on endogenous neural regeneration is essential for the development of effective therapeutic treatments for PD patients that are based on the use of NSCs to replace lost neurons.



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## APPENDICES

### Appendix I: Supplemental Data

| Genotype         | Sox2+ | Sox2+/Nestin+ | Sox2+/Nestin+/GFAP+ | Sox2+/Nestin+/GFAP- |
|------------------|-------|---------------|---------------------|---------------------|
| WT               | 55242 | 49590         | 26838               | 22752               |
|                  | 76572 | 72846         | 29952               | 42894               |
|                  | 63126 | 60408         | 25560               | 34848               |
| Average WT       | 64980 | 60948         | 27450               | 33498               |
| PINK1 KO         | 65226 | 63189         | 22596               | 40593               |
|                  | 55206 | 51390         | 19710               | 31680               |
|                  | 52326 | 35748         | 21294               | 17604               |
| Average PINK1 KO | 57586 | 50109         | 21200               | 29959               |

**Table S1: Cell counts involved with comparing the SVZ neural progenitor cell population between WT and PINK1 KO mice.**

| <b>Genotype</b>  | <b>EdU+</b> | <b>Dcx+</b> |
|------------------|-------------|-------------|
| WT               | 7830        | 42408       |
|                  | 8424        | 38628       |
|                  | 7470        | 43740       |
| Average WT       | 7908        | 41592       |
| PINK1 KO         | 8550        | 40626       |
|                  | 8946        | 39276       |
|                  | 10170       | 37800       |
| Average PINK1 KO | 9222        | 39234       |

**Table S2: Cell counts involved with comparing the total number of proliferating cells and Type A cells in the SVZ between WT and PINK1 KO mice.**

| Genotype         | Sox2+ | Sox2+/Nestin+ | Sox2+/Nestin+/GFAP+ | Sox2+/Nestin+/GFAP- |
|------------------|-------|---------------|---------------------|---------------------|
| WT               | 12402 | 5787          | 2601                | 3186                |
|                  | 16299 | 7173          | 3807                | 3366                |
|                  | 13905 | 5535          | 2097                | 3438                |
|                  | 15507 | 7452          | 3276                | 4176                |
| Average WT       | 14528 | 6487          | 2945                | 3542                |
| PINK1 KO         | 14391 | 7515          | 3951                | 3564                |
|                  | 15507 | 7326          | 4383                | 2943                |
|                  | 14022 | 6039          | 2979                | 3060                |
|                  | 14103 | 6426          | 3708                | 2718                |
| Average PINK1 KO | 14506 | 6827          | 3755                | 3071                |

**Table S3: Cell counts involved with comparing the SGZ neural progenitor cell population between WT and PINK1 KO mice.**

| <b>Genotype</b>  | <b>Ki67+</b> | <b>Dcx+</b> |
|------------------|--------------|-------------|
| WT               | 1707         | 12878       |
|                  | 2169         | 14004       |
|                  | 1521         | 12654       |
|                  | 1611         | 11385       |
| Average WT       | 1752         | 12730       |
| PINK1 KO         | 1491         | 9702        |
|                  | 1386         | 11007       |
|                  | 1185         | 11061       |
|                  | 1188         | 11370       |
| Average PINK1 KO | 1313         | 10785       |

**Table S4: Cell counts involved with comparing the total number of proliferating cells and newborn neurons in the SGZ between WT and PINK1 KO mice.**

| Genotype        | Sox2+ | Sox2+/Nestin+ | Sox2+/Nestin+/GFAP+ | Sox2+/Nestin+/GFAP- |
|-----------------|-------|---------------|---------------------|---------------------|
| WT              | 56502 | 51516         | 19530               | 31986               |
|                 | 54810 | 48852         | 23580               | 25272               |
|                 | 67554 | 47142         | 25668               | 21474               |
| Average WT      | 59622 | 49170         | 22926               | 26244               |
| Parkin KO       | 72702 | 50724         | 27324               | 29268               |
|                 | 63486 | 59364         | 27072               | 32292               |
|                 | 52326 | 49356         | 26352               | 23004               |
| Average PINK KO | 62838 | 53148         | 26916               | 28188               |
| SODPAR          | 66276 | 62874         | 29574               | 33300               |
|                 | 53766 | 51246         | 16596               | 34650               |
|                 | 60354 | 57510         | 23058               | 34452               |
| Average SODPAR  | 60132 | 57210         | 23076               | 34134               |

**Table S5: Quantitative data involved with comparing the SVZ neural progenitor cell population between WT, Parkin KO, and SODPAR mice.**



| <b>Genotype</b>  | <b>EdU+</b> | <b>Dcx+</b> |
|------------------|-------------|-------------|
| WT               | 10584       | 26496       |
|                  | 7362        | 19242       |
|                  | 11160       | 35802       |
| Average WT       | 9702        | 27180       |
| PINK1 KO         | 7830        | 32508       |
|                  | 7650        | 35712       |
|                  | 7668        | 20646       |
| Average PINK1 KO | 7716        | 29622       |
| SODPAR           | 10857       | 30093       |
|                  | 8172        | 22860       |
|                  | 10458       | 18396       |
| Average SODPAR   | 9829        | 23783       |

**Table S6: Cell counts involved with comparing the total number of proliferating cells and Type A cells in the SVZ between WT and PINK1 KO mice.**

| Genotype          | Sox2+ | Sox2+/Nestin+ | Sox2+/Nestin+/GFAP+ | Sox2+/Nestin+/GFAP- |
|-------------------|-------|---------------|---------------------|---------------------|
| WT                | 18468 | 9162          | 3159                | 6003                |
|                   | 16056 | 6390          | 2745                | 3645                |
|                   | 11898 | 5463          | 3060                | 2403                |
| Average WT        | 15474 | 7005          | 2988                | 4017                |
| Parkin KO         | 17478 | 8595          | 3726                | 4869                |
|                   | 18324 | 8838          | 4158                | 4680                |
|                   | 11754 | 5085          | 2880                | 2205                |
| Average Parkin KO | 15852 | 7506          | 3588                | 3918                |
| SODPAR            | 14274 | 5958          | 2322                | 3636                |
|                   | 15651 | 6336          | 3600                | 2736                |
|                   | 18330 | 11200         | 5900                | 4770                |
| Average SODPAR    | 16085 | 7831          | 3941                | 3714                |

**Table S7: Quantitative data involved with comparing the SGZ neural progenitor cell population between WT, Parkin KO, and SODPAR mice.**

| Genotype         | Ki67+ | Dcx+  |
|------------------|-------|-------|
| WT               | 1440  | 11061 |
|                  | 1539  | 12384 |
|                  | 1656  | 10413 |
|                  | 1269  | 10620 |
| Average WT       | 1476  | 11120 |
| PINK1 KO         | 1368  | 9630  |
|                  | 1557  | 9414  |
|                  | 1089  | 7893  |
| Average PINK1 KO | 1338  | 8979  |
| SODPAR           | 1764  | 9225  |
|                  | 1395  | 9396  |
|                  | 972   | 8253  |
|                  | 1251  | 7299  |
| Average SODPAR   | 1346  | 8543  |

**Table S8: Cell counts involved with comparing the total number of proliferating cells and newborn neurons in the SGZ between WT, Parkin KO, and SODPAR mice.**

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To Whom it May Concern,

My name is Joseph Bastasic and I am an MSc student at the University of Ottawa (Canada). I was wondering if it would be possible to obtain permission to use Figure 2 from the following paper in my thesis / dissertation (both in print and electronically)? I am not an author of this paper. The current title of my MSc thesis is "Studying the Impact of Parkinson's Disease on Mammalian Adult Neurogenesis."

Thank you,

Joseph Bastasic

Paper of Interest:

PINK1, Parkin, and Mitochondrial Quality Control: What can we Learn about Parkinson's Disease Pathobiology?

J Parkinsons Dis. 2017;7(1):13-29. doi: 10.3233/JPD-160989.

Truban D1, Hou X1, Caulfield TR1,2, Fiesel FC1,2, Springer W1,2.

Author information

1

Department of Neuroscience, Mayo Clinic, Jacksonville, FL, USA.

2

Mayo Clinic Graduate School of Biomedical Sciences, Jacksonville, FL, USA.

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Carry Koolbergen <C.Koolbergen@iospress.nl>

Fri, Mar 22, 2019 at 8:22  
AM

To: Joseph Bastasic

J Parkinsons Dis. 2017;7(1):13-29. doi: 10.3233/JPD-160989.

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Yours sincerely

***Carry Koolbergen (Mrs.)***

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1 message

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**Joseph Bastasic**

Fri, Mar 22, 2019 at 1:20 PM

To: Truban.Dominika@mayo.edu

Dear Dr. Truban,

My name is Joseph Bastasic and I am an MSc student at the University of Ottawa (Canada). I was wondering if it would be possible to obtain permission to use Figure 2 from the following paper in my thesis / dissertation (both in print and electronically)? I have already contacted the publisher, but was advised to contact the original authors as well. The current title of my MSc thesis is "Studying the Impact of Parkinson's Disease on Mammalian Adult Neurogenesis."

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Thank you,

Joseph Bastasic

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**Joseph Bastasic**  
To: Hou.Xu@mayo.edu

Fri, Mar 22, 2019 at 1:21 PM

Dear Dr. Xu,

My name is Joseph Bastasic and I am an MSc student at the University of Ottawa (Canada). I was wondering if it would be possible to obtain permission to use Figure 2 from the following paper in my thesis / dissertation (both in print and electronically)? I have already contacted the publisher, but was advised to contact the original authors as well. The current title of my MSc thesis is "Studying the Impact of Parkinson's Disease on Mammalian Adult Neurogenesis."

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Thank you,

Joseph Bastasic

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## Request Permission to Reuse a Published Figure for a Thesis / Dissertation

3 messages

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**Joseph Bastasic**

Fri, Mar 22, 2019 at 1:23 PM

To: Caulfield.Thomas@mayo.edu

Dear Dr. Caulfield,

My name is Joseph Bastasic and I am an MSc student at the University of Ottawa (Canada). I was wondering if it would be possible to obtain permission to use Figure 2 from the following paper in my thesis / dissertation (both in print and electronically)? I have already contacted the publisher, but was advised to contact the original authors as well. The current title of my MSc thesis is "Studying the Impact of Parkinson's Disease on Mammalian Adult Neurogenesis."

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Thank you,

Joseph Bastasic

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**Caulfield, Thomas, Ph.D.** <Caulfield.Thomas@mayo.edu>

Fri, Mar 22, 2019 at 3:20 PM

To: Joseph Bastasic

I have no issue. Have you asked Dr. Springer?

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**Joseph Bastasic**

Sat, Mar 23, 2019 at 2:47 PM

To: "Caulfield, Thomas, Ph.D." <Caulfield.Thomas@mayo.edu>

Dear Dr. Caulfield,

I have asked Dr. Springer and he has informed me that he has no problems with me using the figure.

Thank you,

Joseph Bastasic



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## Request Permission to Reuse a Published Figure for a Thesis / Dissertation

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**Joseph Bastasic**

Fri, Mar 22, 2019 at 1:24 PM

To: Fiesel.Fabienne@mayo.edu

Dear Dr. Fiesel,

My name is Joseph Bastasic and I am an MSc student at the University of Ottawa (Canada). I was wondering if it would be possible to obtain permission to use Figure 2 from the following paper in my thesis / dissertation (both in print and electronically)? I have already contacted the publisher, but was advised to contact the original authors as well. The current title of my MSc thesis is "Studying the Impact of Parkinson's Disease on Mammalian Adult Neurogenesis."

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Thank you,

Joseph Bastasic

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**Request Permission to Reuse a Published Figure for a Thesis / Dissertation**

2 messages

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**Joseph Bastasic**

Fri, Mar 22, 2019 at 1:26 PM

To: Springer.Wolfdieter@mayo.edu

Dear Dr. Springer,

Dear Dr. Truban,

My name is Joseph Bastasic and I am an MSc student at the University of Ottawa (Canada). I was wondering if it would be possible to obtain permission to use Figure 2 from the following paper in my thesis / dissertation (both in print and electronically)? I have already contacted the publisher, but was advised to contact the original authors as well. The current title of my MSc thesis is "Studying the Impact of Parkinson's Disease on Mammalian Adult Neurogenesis."

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Thank you,

Joseph Bastasic

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**Springer, Wolfdieter, Ph.D.** <Springer.Wolfdieter@mayo.edu>  
To: Joseph Bastasic

Fri, Mar 22, 2019 at 4:10 PM

Hi Joseph,

Thanks for your interest.

Please feel free to use the figure.

Good luck with your thesis.

Regards,

Wolfdieter

**Wolfdieter Springer, Ph.D.** | Associate Professor | Mayo Clinic College of Medicine and Science | [Translational Cell Biology of Parkinson's Disease](#)

Office: 904-953-6129 | Secretary: 904-953-2439 | Lab: 904-953-6821 | Fax: 904-953-7117 |  
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