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## Genetic determinants at the interface of cancer and neurodegenerative disease

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### Abstract

It has been hypothesized that oncogenesis and neurodegeneration may share common mechanistic foundations. Recent evidence now reveals a number of genes in which alteration leads to either carcinogenesis or neurodegeneration, depending on cellular context. Pathways that have emerged as having critical roles in both cancer and neurodegenerative disease include those involving genes such as *PARK2*, *ATM*, *PTEN*, *PTPRD*, and *mTOR*. A number of mechanisms have been implicated, and commonly affected cellular processes include cell cycle regulation, DNA repair, and response to oxidative stress. For example, we have recently shown that the E3 ubiquitin ligase *PARK2* is mutated or deleted in many different human malignancies and helps drive loss on chromosome 6q25.2–27, a genomic region frequently deleted in cancers. Mutation in *PARK2* is also the most common cause of juvenile Parkinson's disease. Mutations in *PARK2* result in an upregulation of its substrate cyclin E, resulting in dysregulated entry into the cell cycle. In neurons, this process results in cell death, but in cycling cells, the result is a growth advantage. Thus, depending on whether the cell affected is a dividing cell or a post-mitotic neuron, responses to these alterations may differ, ultimately leading to varying disease phenotypes. Here, we review the substantial data implicating specific genes in both cancer and neurodegenerative disease.

### Keywords

tumor suppressor; neurodegeneration; cancer; *PARK2*

### Introduction

Although neurons are generally considered to be post-mitotic cells that have terminally differentiated and are non-replicating, specific components of the cell cycle machinery may be reactivated in some neurons in response to certain stimuli, such as growth factors (Park *et al.*, 1998), excitotoxicity (Giardina and Beart, 2002; Verdaguer *et al.*, 2002) and DNA damage (Kruman *et al.*, 2004). However, reactivation of the cell cycle in neurons generally eventuates in apoptosis. Neurons are not mitotically competent, because of the absence of

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### Conflict of interest

The authors declare no conflict of interest.

requisite proteins such as certain cyclin-dependent kinases (CDK) and an inadequate subcellular structure for cell division (Nospikel and Hanawalt, 2003; Ackman *et al.*, 2007), and activation of the core cell cycle machinery in these cells often results in an abortive cell cycle and cell death. Moreover, neurons are unable to use synthesis-related mechanisms of DNA repair such as mismatch repair or nucleotide excision repair, thereby rendering these cells more sensitive to DNA damage, which can trigger apoptosis (Staropoli, 2008). Although the eventual outcome of cell cycle activation or DNA damage in neurons may be apoptosis, normally cycling cells may instead respond with proliferation and possibly tumorigenesis. Ultimately, these dichotomous pathways may manifest as either cancer or neurodegenerative disorders, depending on the cell affected. Disorders such as Parkinson's disease (PD), Alzheimer's disease (AD), Huntington's disease, and ataxia-telangiectasia (AT) provide windows into several genetic determinants of cancer and neurodegenerative diseases. Genes in which dysregulation is capable of producing both outcomes include *PARK2*, *ATM*, *PTEN*, *mTOR*, *APP*, and *PTPRD*.

## **PARK2: cell cycle dysregulation**

Modulation of the cell cycle requires a fine balance between a number of activating, inhibitory, and checkpoint proteins which together control progression through the phases of the cell cycle (G1, S, G2, mitosis), quiescence and re-entry (Deshpande *et al.*, 2005). To achieve tight temporal control, the cyclin and CDK complexes that drive cell cycle progression are post-translationally regulated by ubiquitin-mediated degradation. The accumulation of CDK5 and cyclin E in the brains of PD patients first suggested that dysfunction in ubiquitination of cell cycle proteins might be related to the development of PD (Brion and Couck, 1995; Staropoli *et al.*, 2003).

PD is one of the most frequent neurodegenerative disorders, with a prevalence of nearly 2% in those over 65 years of age. The typical motor signs of PD—resting tremor, rigidity, and bradykinesia—are the manifestation of massive loss of dopaminergic neurons within the pars compacta of the substantia nigra (Lucking *et al.*, 2000). Mutation in the gene *PARK2* is the most frequent cause of autosomal recessive early-onset PD, accounting for nearly 50% of early-onset cases. In this form of PD, germline *PARK2* mutations cause loss of dopaminergic neurons within the substantia nigra (Fearnley and Lees, 1991; Kitada *et al.*, 1998; Abbas *et al.*, 1999; Lucking *et al.*, 2000; Shimura *et al.*, 2000). *PARK2* is an E3 ubiquitin ligase with two really interesting new gene (RING) finger domains, acting within a multiprotein Skp1-Cullin1-F-box ligase complex (Shimura *et al.*, 2000, 2001; Tanaka *et al.*, 2001). This complex binds to UBCH7 and UBCH8 and thereby promotes mono- and poly-ubiquitination of target proteins, followed by proteasome-mediated degradation (Shimura *et al.*, 2001; Corti *et al.*, 2005; Sriram *et al.*, 2005; Hampe *et al.*, 2006). In neuronal systems, substrates for *PARK2* include CDCrel-1 and 2a, synphilin-1, Pael-R, synaptotagmin XI, RanBP2, p38/AIMP2, FUSE-binding protein 1, Hsp70 and ataxin-2 (Huynh *et al.*, 2007; Moore *et al.*, 2008) (Figure 1). Which of these targets are the most physiologically significant for the disease state is unclear. A particularly interesting target protein of *PARK2*-mediated ubiquitination and degradation is cyclin E, the primary cyclin that drives S-phase progression. CDK2/cyclin E phosphorylates the tumor suppressor retinoblastoma, releasing the transcription factor E2F-1 from inhibition. In cycling cells, E2F-1 upregulates proteins facilitating progression through S phase, but in post-mitotic neurons, E2F-1 triggers apoptosis through p53 and Bax (Harbour *et al.*, 1999; Nguyen *et al.*, 2002; Staropoli *et al.*, 2003).

By facilitating ubiquitin proteasome-mediated degradation of cyclin E and thereby inhibiting pro-apoptotic signaling, *PARK2* is able to carry out a number of neuroprotective functions. *In vitro* evidence has shown that *PARK2* protects neurons from a number of insults,

including partial proteasome inhibition (Petrucci *et al.*, 2002; Yang *et al.*, 2007), nerve growth factor withdrawal (Darios *et al.*, 2003), and kainate excitotoxicity (Staropoli *et al.*, 2003). These stressors are all associated with cell cycle dysregulation. Proteasome inhibition leads to apoptosis through CDK2 and CDK6 activation (Rideout *et al.*, 2003). Withdrawal of nerve growth factor induces apoptosis which can be prevented with CDK inhibitors and dominant-negative CDK4 and CDK6 (Park *et al.*, 1997, 1998). Kainate excitotoxicity is associated with upregulation of cyclin D, cyclin E, CDK2, and E2F-1 (Giardina and Beart, 2002; Verdaguer *et al.*, 2002). The involvement of cyclin E in these pro-apoptotic pathways is substantial and the ubiquitination of cyclin E by PARK2 is one means by which this protein may exert its neuroprotective effects.

The precise mechanism by which mutations in PARK2 lead to PD remains unclear. However, it has been shown that the PARK2 mutations identified in early-onset PD result in deficient E3 ligase activity (Imai *et al.*, 2000; Shimura *et al.*, 2000; Zhang *et al.*, 2000), abrogate binding to putative substrates (Imai *et al.*, 2000), or otherwise cause loss of function (Sriram *et al.*, 2005), allowing accumulation of cyclin E (Verdaguer *et al.*, 2002) and other substrates. Overexpression of PARK2 protects neurons from kainate excitotoxicity-mediated apoptosis, and PARK2 knockdown through siRNA causes accumulation of cyclin E and sensitivity to kainate excitotoxicity in neurons (Staropoli *et al.*, 2003). Kainate excitotoxicity of dopaminergic neurons is believed to be akin to glutamate excitotoxicity, which has been implicated in neuronal loss seen in sporadic PD (Olanow and Tatton, 1999). The sensitivity to excitotoxicity from PARK2 knockdown appears to be strongest in dopaminergic neurons (Staropoli *et al.*, 2003). Therefore, inactivating mutations of PARK2 prevent ubiquitin proteasome-mediated degradation of cyclin E, rendering dopaminergic neurons in the midbrain sensitive to excitotoxicity and susceptible to apoptosis, leading to neuronal cell death and PD.

In parallel with PARK2's relationship with cyclin E, PARK2 has also been shown to regulate signaling through the Wnt/ $\beta$ -catenin pathway. *In vitro* evidence reveals that PARK2 regulates  $\beta$ -catenin levels by reducing the ability of Wnt to stabilize  $\beta$ -catenin. Excessive signaling through this pathway in neurons cultured with Wnt3a results in cell cycle re-entry followed by apoptosis. Neurons in the ventral midbrain overexpress  $\beta$ -catenin, and Wnt3a administration leads to dopaminergic neuronal death in *Park2* null mice, but not in *Park2* wild-type mice (Rawal *et al.*, 2009). Together, these data show that PARK2 protects dopaminergic neurons from excessive Wnt/ $\beta$ -catenin signaling.

In non-neuronal cycling cells, the roles of PARK2 in regulating cyclin E suggest that it could be an important inhibitor of cell cycle progression. Alterations in PARK2 expression have been shown in hepatocellular carcinoma cell lines (Mazieres *et al.*, 2005; Lee *et al.*, 2006). Recent work by our group has identified this gene as a tumor suppressor or suppressor of cancer cell growth, and functional data are consistent with a role in cell cycle control (Veeriah *et al.*, 2009b). Chromosome 6q25.2–27 is a well known genomic region that frequently undergoes loss in multiple human cancers (Cesari *et al.*, 2003; Weir *et al.*, 2007; Parsons *et al.*, 2008; TCGA, 2008; Toma *et al.*, 2008). Our array comparative genomic hybridization data showed that chromosomal losses of *PARK2* occur in approximately 25% of glioblastoma multiforme and colon cancer tumors. Interestingly, by comparing array comparative genomic hybridization profiles across tumor types, we showed that *PARK2* is most likely the primary gene driving loss at 6q25.2–27 in cancer (Veeriah *et al.*, 2009b). When we sequenced *PARK2* in a number of human cancers, we found that somatic mutations occurred in the same domains as the germline mutations that cause early-onset PD, clustering in the ubiquitin-like, RING finger, and in-between RING finger domains. Many alterations were heterozygous in nature, suggesting that *PARK2* may act in a haploinsufficient manner, like *FBXW7/hCDC4*, another E3 ubiquitin ligase targeting

cyclin E (Mao *et al.*, 2004). Expression of PARK2 in PARK2-deficient human cancer cell lines inhibited growth, but did not inhibit growth in cell lines with intact PARK2 expression. PARK2 cDNA harboring cancer-specific mutations were unable to inhibit growth. Similar results were obtained *in vivo* using glioblastoma xenografts. The PARK2 mutants showed reduced E3 ligase function, and were found to have a decreased ability to bind, ubiquitinate, and degrade cyclin E. Knockdown of PARK2 with siRNA resulted in accumulation of cyclin E, and an increased proportion of cells in S and G2/M phases. Immunofluorescence staining after PARK2 knockdown showed an increased frequency of multipolar spindles and abnormal mitoses, and an increased number of nuclei with atypia or micronuclei (Veeriah *et al.*, 2009b).

Together, these genetic and functional data show that PARK2 is a tumor suppressor, and that somatic mutations in PARK2 abrogate its ability to ubiquitinate cyclin E, promoting tumor growth (Figure 2). These data provide evidence for the hypothesis that a common factor—cyclin E-mediated cell cycle activation—drives both neurodegeneration and tumorigenesis in the setting of PARK2 mutation, depending on whether the mutation is somatic or germline. PARK2 mutation is known to cause autosomal recessive early-onset PD, but has not been definitively linked with cancer predisposition. Among general populations of PD patients, there is believed to be a marginal but significant increase in cancer risk (Moller *et al.*, 1995; Olsen *et al.*, 2005), but causes for this remain speculative, and it is unknown whether PARK2 may be responsible. PARK2 hypermethylation may also be contributory, and has been shown in hematologic malignancies (Agirre *et al.*, 2006). Of note, cyclin E levels have been noted to be increased in a number of neurodegenerative diseases (Husseman *et al.*, 2000) and in many human cancers (Donnellan and Chetty, 1999), lending further support to the possibility that cell cycle dysregulation may be a common link.

## **AT-mutated (ATM) and ATM-related protein: loss of cell cycle control and DNA repair**

AT is a neurodegenerative disorder with a predisposition for cancer and radiation sensitivity (Lee and McKinnon, 2007). AT is characterized by a progressive loss of muscle coordination over the first few years of life, in addition to cutaneous and ocular telangiectasias (Chun and Gatti, 2004; Nowak-Wegrzyn *et al.*, 2004). Patients develop immune deficiencies (decreased or absent IgA, IgE, and IgG), sterility, and cerebellar degeneration (Farina *et al.*, 1994). Nearly 40% of AT-mutated (ATM) homozygotes will develop cancer, usually childhood leukemia or lymphoma. Solid tumors are less common, and include gastric adenocarcinoma, breast carcinoma, ovarian germ cell tumor, gonadoblastoma, and medulloblastoma (Ball and Xiao, 2005; Gumy-Pause *et al.*, 2006; Mavrou *et al.*, 2008).

AT is caused by mutations in the gene *ATM*. Located on chromosome 11q23, more than 400 mutations have been described, encompassing all parts of the gene (Mavrou *et al.*, 2008). Most ATM mutations are null mutations, leading to complete inactivation of the gene and absence of the ATM protein product, causing disease with nearly 100% penetrance (Prokopcova *et al.*, 2007). Rare missense mutations with lesser penetrance have been reported (Milne, 2009). The ATM protein kinase is part of the phosphatidylinositol-3 kinase (PI3K) superfamily, and is integral to both cell cycle control and DNA repair pathways. In cases of double-strand DNA breaks, ATM auto-phosphorylates and activates a number of substrates. One target is the Rad50–Mre11–Nbs1 protein complex, which binds to and coordinates repair of double-strand breaks. In addition, ATM is a master controller of cell cycle checkpoints, facilitating either a halt to cellular proliferation or the induction of apoptosis (Bao *et al.*, 2001; Falck *et al.*, 2001; Mavrou *et al.*, 2008; Staropoli, 2008). ATM

exerts checkpoint control at the G1/S, S phase, and G2/M transitions. At the G1/S checkpoint, ATM phosphorylates p53, stabilizing the protein, and increasing its activity (Banin *et al.*, 1998; Canman *et al.*, 1998; Lavin and Kozlov, 2007). p53 then either inhibits the cell cycle by inducing expression of p21 and 14-3-3 $\alpha$ , or induces Puma, Noxa, and Bax, causing apoptosis (Xiong *et al.*, 1993; el-Deiry *et al.*, 1993; Yu *et al.*, 2003; Chipuk *et al.*, 2004; Meulmeester *et al.*, 2005). Similarly, ATM activation controls S phase, G2/M, and spindle checkpoints through activation of BRCA 1, FANCD2, CHK1, and CHK2 (Taniguchi *et al.*, 2002). Through these and a wide variety of nearly 30 additional substrates, ATM has a central role in halting cell cycle progression or inducing apoptosis (Lavin and Kozlov, 2007) (Figure 3). Mutated ATM is unable to respond to double-strand DNA breaks with activation of DNA repair, or inhibition of the cell cycle, thereby predisposing cells to carcinogenesis.

*ATM* has been characterized as a susceptibility gene for several cancers. Epidemiologic studies have shown that heterozygous carriers of *ATM* mutations are at approximately twofold higher risk of developing breast cancer (Inskip *et al.*, 1999; Thompson *et al.*, 2005; Renwick *et al.*, 2006), and even less penetrant missense mutations confer a significant increase in the risk of breast cancer (Gatti *et al.*, 1999). Patients with homozygous and heterozygous *ATM* mutations are at significantly increased risk of various non-Hodgkin's lymphomas (Morrell *et al.*, 1986; Swift *et al.*, 1986), and *ATM* deletions have been associated with up to 15% risk of developing non-Hodgkin's lymphomas and B-cell chronic lymphocytic leukemia (Fegan *et al.*, 1995).

In contrast to cancer risk, neurodegeneration resulting from *ATM* mutation is not as well understood. In AT, the precise mechanism for neurodegeneration has not been fully described. Germline disruption of *ATM* does not result in overt, immediate neurodegeneration. However, neural development is believed to be a process that is highly reliant on intact DNA repair systems. It has been hypothesized that ATM-deficient neurons, unable to repair double-strand breaks or undergo apoptosis, may incorporate DNA aberrations into the genome of neurons during development, triggering cell death at a later time (Orii *et al.*, 2006; Lee and McKinnon, 2007; Subba Rao, 2007). It is unknown why granule and Purkinje cells of the cerebellum are particularly susceptible to these lesions.

In contrast to ATM, which is activated after double-strand DNA breaks, ATM-related protein (ATR) is activated by ultraviolet light-induced DNA damage and stalled DNA forks (Cliby *et al.*, 1998). ATR promotes DNA repair in concert with the Rad9–Rad1–HUS1 and Rad17–RFC complexes (Rauen *et al.*, 2000; Burtelow *et al.*, 2001; Lindsey-Boltz *et al.*, 2001; Roos-Mattjus *et al.*, 2002). Similar to ATM, ATR exercises checkpoint control through Chk1 and Chk2, facilitates apoptosis through p53, and facilitates DNA repair through BRCA1 (Liang *et al.*, 2009). *ATR* mutations have been identified in endometrial carcinomas, colon gastric cancers, and lymphomas (Lewis *et al.*, 2005; Zigelboim *et al.*, 2009). When in the germline, *ATR* mutations cause Seckel Syndrome, defined by growth retardation and microcephaly. As in AT, it is believed that neural development is highly dependent on intact DNA damage repair pathways, and that mutations in *ATM* or *ATR* lead to impaired neural development and degeneration of neurons (Alderton *et al.*, 2004; O'Driscoll *et al.*, 2006; Auclair *et al.*, 2008).

## Amyloid precursor protein: mitochondrial dysfunction

The *APP* gene encodes the amyloid precursor protein (APP). APP undergoes extensive post-translational modification, including initial cleavage by  $\alpha$ -secretase and  $\beta$ -secretase, forming soluble APP (sAPP), and cleavage of the remaining 99 amino acid fragment by  $\gamma$ -secretase, producing amyloid- $\beta$  (A $\beta$ ) (Nunan and Small, 2000). The 42 amino acids form of A $\beta$  forms



amyloid plaques that accumulate in brain regions affected by AD (Tabira *et al.*, 2002). The diagnosis of AD requires the presence of extracellular deposits of A $\beta$  and intracellular neurofibrillary tangles composed of tau protein. Several forms of familial early-onset AD have been linked to mutations in APP around the A $\beta$  region, leading to increased production of A $\beta$ 42 (Anandatheerthavarada and Devi, 2007). The precise mechanism of neuronal cell death resulting from A $\beta$  is attributable to mitochondrial dysfunction, through a number of mechanisms. A $\beta$  inhibits key mitochondrial enzymes, notably cytochrome *c* oxidase, leading to the release of cytochrome *c* and resultant apoptosis. Furthermore, A $\beta$  generates reactive oxygen and nitrogen species, and fragments mitochondrial DNA, all of which increase sensitivity to oxidative stress from free radical accumulation (Parker, 1991; Beal, 2005; Querfurth and LaFerla, 2010). APP gene overexpression is believed to result in accumulation of both APP and A $\beta$  in the mitochondria, causing mitochondrial dysfunction, and eventually, neuronal death.

The Alzheimer's-type neuropathology occurring in patients with Down syndrome has been attributed to trisomy 21 and accompanying upregulation of the APP gene on chromosome 21. The coexistent increased risk of hematologic malignancy in Down syndrome patients was an early suggestion that APP might predispose to cancer. In fact, there is a 10–20-fold increased risk of acute lymphoblastic leukemia and acute myeloid leukemia in Down syndrome children (Xavier *et al.*, 2009). Although several genes, including APP, have been implicated in the risk of leukemia, APP is the most overexpressed gene in acute myeloid leukemia patients with complex karyotypes (Baldus *et al.*, 2004). In solid tumors, APP has also been reported to be overexpressed in oral cavity, esophageal, pancreatic, neuroendocrine, thyroid, and colorectal cancers (Hansel *et al.*, 2003; Ko *et al.*, 2004; Arvidsson *et al.*, 2008; Krause *et al.*, 2008). APP is believed to be a growth factor, which has been shown to increase epithelial cell proliferation and migration, although the precise mechanism remains to be worked out (Schmitz *et al.*, 2002). Several reports have suggested that this effect is attributable to the N-terminal cleavage product of APP, sAPP, which is formed after cleavage by  $\alpha$ -secretase (Ko *et al.*, 2004). After binding to an unknown receptor, sAPP is able to induce cellular proliferation, possibly through activation of the MAP kinase (Nishimura *et al.*, 2003; Gakhar-Koppole *et al.*, 2008), protein kinase C (Ishiguro *et al.*, 1998), or PI3K/Akt/mammalian target of rapamycin (mTOR) pathways (Cheng *et al.*, 2002). In fact, this is consistent with an overall, pro-growth, anti-apoptotic role for APP. In a situation of nerve growth factor withdrawal, A $\beta$  production is upregulated, leading to neuronal apoptosis (Matrone *et al.*, 2008). In this respect, APP activates both trophic (through sAPP) and apoptotic (through A $\beta$ ) pathways, and the predominance of each may be context dependent.

Beyond APP, mitochondrial dysfunction may also form a link between neurodegeneration and cancer through the actions of polo-like kinase 2 and  $\alpha$ -synuclein. Mitochondrial dysfunction has been shown to induce high levels of polo-like kinase 2 expression, leading to phosphorylation of both  $\alpha$ -synuclein, a hallmark of PD and Lewy body dementia, as well as PLK1, a promotor of cell proliferation that is overexpressed in several human cancers (Inglis *et al.*, 2009; Matsumoto *et al.*, 2009).

## PTEN, PTEN-induced kinase 1, and DJ-1: sensitivity to oxidative stress

The gene *phosphatase and tensin homolog (PTEN)* encodes a protein that has a critical role in the PI3K/Akt/mTOR pathway. The primary role of the phosphatase protein encoded by PTEN is to dephosphorylate the inositol ring in phosphatidylinositol (3,4,5)-trisphosphate (PIP3), producing the biphosphate PIP2. In so doing, PTEN opposes the action of the PI3Ks and inhibits activation of the PI3K/Akt/mTOR signaling pathway, which ultimately promotes cell growth, survival, and metabolism (Wong *et al.*, 2009). PTEN has recently

been shown to be inhibited by P-REX2a (Fine *et al.*, 2009). PTEN is a tumor suppressor, which has been found to be mutated in a large number of human cancers. When present in the germline, mutation of *PTEN* results in Cowden syndrome, as well as other PTEN-related hamartoma syndromes. Affected patients with Cowden syndrome develop benign hamartomas of the hair follicles (trichilemmomas), mucocutaneous surfaces, breasts, thyroid, and intestines (Eng, 2000). These patients also experience elevated risk of malignancies of the breast, thyroid, endometrium, and genitourinary tract. Somatic mutation or deletion of *PTEN* is a common event in high-grade glioblastoma (30–40% prevalence), melanoma (7–20%), prostate cancer (20–50%), and endometrial cancer (50%). In addition, *PTEN* mutations have been reported at lower prevalence in cancers of the bladder, lung, ovary, colon, and in lymphoma (Cairns *et al.*, 1997; Gronbaek *et al.*, 1998; Kim *et al.*, 1998; Kohno *et al.*, 1998; Sansal and Sellers, 2004).

PTEN itself has been hypothesized to have a direct role in neurodegeneration through mitochondria-dependent apoptosis in situations of oxidative stress. Although human data have not been reported, in rat hippocampal cells, oxidative stress leads to mitochondrial accumulation of PTEN, which is associated with Bax and cytochrome *c*, and activates caspase 3. Knockdown of PTEN inhibits caspase 3 activation and prevents neuronal apoptosis (Zhu *et al.*, 2006).

There is evidence relating PTEN signaling to PD in humans, through two related genes: *PTEN-induced kinase 1 (PINK1)* and *DJ-1*. Both genes have a role in neuronal protection from mitochondrial damage in situations of oxidative stress, which are believed to be an important cause of neurodegenerative diseases such as PD. *PINK1*, which is transcriptionally activated by PTEN, has been associated with early-onset PD. PTEN deletion leads to downregulation of PINK1 (Inzelberg and Jankovic, 2007). A key role of PINK1 is to phosphorylate TRAP1, a mitochondrial molecular chaperone with anti-apoptotic function, preventing release of mitochondrial cytochrome *c* in cases of oxidative stress (Pridgeon *et al.*, 2007). In dopaminergic neurons, inhibition of PINK1 leads to impaired mitochondrial function, as evidenced by loss of mitochondrial membrane potential and decreased mitochondrial ATP synthesis (Gegg *et al.*, 2009). Through this mechanism, PINK1 deficiency causes sensitivity to oxidative stress, followed by neuronal death (Gispert *et al.*, 2009). PINK1 also forms an E3 ligase complex with PARK2 (Xiong *et al.*, 2009), and has recently been reported to recruit PARK2 to the mitochondria, where PARK2 has a role in facilitating mitochondrial autophagy. Through these mechanisms, PINK1 has an important neuroprotective role, loss of which causes neurodegeneration in PD (Vives-Bauza *et al.*, 2009). Mutations in *PINK1* have been reported in several kindreds with familial PD (Valente *et al.*, 2004). Thus, loss of PTEN, commonly an oncogenic event, is also able to predispose to neurodegeneration through PINK1. It will be of interest to determine whether *PINK1* is mutated in human cancers.

Dysregulation of PTEN and PD may also be related through *DJ-1*, a candidate oncogene that was originally identified as *PARK7*. *In vitro*, DJ-1 inhibits PTEN's negative regulation of the PI3K/Akt/mTOR pathway, which has neuroprotective and pro-survival properties in situations of oxidative stress (Delgado-Esteban *et al.*, 2007). Inhibition of DJ-1 with siRNA leads to cellular sensitivity to oxidative stress in *Drosophila* and mice brains (Kim *et al.*, 2005). DJ-1 itself may be a sensor of reactive oxygen species (Shendelman *et al.*, 2004). A small percentage of early-onset PD cases have been linked to loss-of-function mutations in *DJ-1* (Bonifati *et al.*, 2003). DJ-1 is also overexpressed in breast and lung cancers (Kim and Mak, 2006), consistent with its oncogenic role as an inhibitor of PTEN. Therefore, DJ-1 is both potentially oncogenic and neuroprotective. Together, DJ-1 and PINK1 show that PTEN, a tumor suppressor, is a 'double-edged sword' in the setting of central nervous system function—PTEN can mediate both neuroprotection and neurodegeneration. PTEN

signaling is necessary for protection of neuronal cells from oxidative stress (through PINK1), but high levels of PTEN signaling (when DJ-1 function is decreased) cause hypersensitivity to oxidative stress through inhibition of the PI3K/Akt/mTOR pathway.

### PTEN and Akt: regulators of tau and A $\beta$

In addition to its signaling role in oxidative stress, evidence has also linked PTEN to neurodegeneration in AD. Initially, Akt was believed to have pro-survival properties in neurons. In cell lines and mouse models, PI3K/Akt/mTOR pathway activation had been found to protect neurons from A $\beta$ -induced neurotoxicity (Stein and Johnson, 2002; Wei *et al.*, 2002). This was in line with the general function of the Akt pathway in promoting cell survival. This neuroprotective effect was believed to be mediated by glycogen synthase kinase 3. Activated Akt inhibits glycogen synthase kinase 3, preventing it from phosphorylating tau protein. Abnormally hyperphosphorylated tau is the primary component of the intraneuronal neurofibrillary tangles that, in addition to A $\beta$ , help define AD pathologically (Lovestone and Reynolds, 1997). However, more recent evidence has contradicted the initial premise of Akt as a pro-survival signal in this setting. Instead of neuroprotection, Akt now appears to be associated with neurodegeneration in AD. Consistent evidence from several human studies indicates that AD brains contain higher levels of phosphorylated Akt than control brains, and that levels of p-Akt are correlated with the severity of neural degeneration on the Braak histologic staging system (Braak *et al.*, 1996; Pei *et al.*, 2003; Rickle *et al.*, 2004, 2006). Further data have also shown significant loss of PTEN in the hippocampus of AD brains, indicating that PTEN loss and resultant constitutive Akt activation are present in AD (Griffin *et al.*, 2005). Indeed, it is now appreciated that PTEN loss and Akt activation are associated with progressive neuronal loss (Marino *et al.*, 2002; Chen *et al.*, 2003), and that glycogen synthase kinase 3 is unlikely to have a role (Kerr *et al.*, 2006).

There are currently two hypotheses for the role of PTEN and Akt in regulating phosphorylation of tau. The first is that Akt itself is a tau kinase, and activation of Akt predisposes toward accumulation of tau protein in neurons (Griffin *et al.*, 2005). The second is that PTEN acts on tau through the MAP kinase pathway. PTEN, a lipid phosphatase, is known to also lead to the inhibition of ERK1/2, kinases that phosphorylate tau (Kerr *et al.*, 2006). However, the *in vivo* significance of PTEN regulation of tau through the MAP kinase pathway remains unclear as this has only been shown *in vitro*. More recently, a separate role for Akt in regulating trafficking of APP has also been reported, and may hold implications for the pathogenesis of AD (Shineman *et al.*, 2009). Activation of Akt can result in feedback inhibition of the PI3K/Akt/mTOR pathway through insulin receptor substrate 1, inhibiting PI3K. Although the mechanisms are unknown, inhibition of PI3K has been shown to decrease intracellular accumulation of A $\beta$ . Therefore, PTEN and Akt have a role in the pathogenesis of AD. It remains unclear whether the primary pathway involves regulation of tau protein or APP, and more work will need to be done to clarify this. Nevertheless, these findings show that the regulatory roles of the PI3K/Akt/mTOR pathway include not only cell growth and survival, but also critical aspects of neuronal development and degeneration.

### mTOR and TSC: regulators of autophagy

The mTOR protein, a key component of the PI3K/Akt/mTOR signaling pathway, may also have a role in neurodegenerative disease, as a regulator of autophagy. mTOR provides an illustrative example of the potential importance of autophagy as a contributor to both cancer and neuronal degeneration.

Autophagy is the process of sequestration of cytoplasm and organelles, which are delivered to the lysosome in vesicles and degraded. This process permits the maintenance of essential



cellular functions in conditions of starvation, but also serves the role of eliminating damaged organelles or proteins, thereby protecting cells from death signals (Klionsky and Ohsumi, 1999; Levine and Yuan, 2005). Inhibition of autophagy is associated with neurodegeneration in otherwise normal neurons (Wang *et al.*, 2009). With respect to cancer, autophagy can be both oncogenic, promoting tumor cell survival, as well as tumor suppressive, reducing DNA damage and inflammation (Gozuacik and Kimchi, 2004, 2007; Tsuchihara *et al.*, 2009). The inherited neurodegenerative disorder Huntington's disease is believed to be in part because of a deficit in autophagy-mediated degradation of the mutant Huntingtin protein (Ravikumar *et al.*, 2008). Rapamycin, an mTOR inhibitor, reduces Huntingtin accumulation and cell death in models of Huntington's disease (Berger *et al.*, 2006; Ravikumar and Rubinsztein, 2006). This has been attributed to inhibition of autophagy by mTOR, and induction of autophagy with rapamycin, both of which have been shown in *Drosophila* (Wang *et al.*, 2009). PTEN and TSC, both tumor suppressors, have been shown to induce autophagy (Arico *et al.*, 2001; Feng *et al.*, 2005). Therefore, there is preliminary evidence to support a role for mTOR in neurodegeneration through inhibition of autophagy, but further investigation is required.

### Protein tyrosine phosphatase delta: axonal development

Protein tyrosine phosphatase delta (PTPRD) was recently identified by our group and others as a tumor suppressor, which is frequently mutated in glioblastoma, lung, colon, melanoma, and head and neck cancers (Weir *et al.*, 2007; Solomon *et al.*, 2008; Veeriah *et al.*, 2009a, b). Epigenetic silencing and reduced expression of PTPRD has also been identified in colon, breast, and glioblastoma tumors (Chan *et al.*, 2008; Veeriah *et al.*, 2009a). PTPRD is a protein tyrosine phosphatase that suppresses tumor growth by dephosphorylating the oncoprotein STAT3 (Chan *et al.*, 2008; Chan and Heguy, 2009; Veeriah *et al.*, 2009a). Interestingly, the PTPRD phosphatase was also recently identified in a genome-wide association study as a locus significantly associated with the restless legs syndrome. Restless legs syndrome is a neurological disorder with motor and sensory components, characterized by unpleasant sensations in the legs and an irresistible urge to move the legs. The mechanism of restless legs syndrome is unknown, although a familial neurodegenerative process is a possibility: 60% of cases are familial, and there is a pathologic evidence of dopamine dysfunction related to the substantia nigra (Connor *et al.*, 2003). Receptor tyrosine phosphatases are believed to have critical roles in neural development, underpinning functions such as neuronal differentiation and migration (den Hertog *et al.*, 1999). PTPRD in particular has been implicated in axonal growth and guidance in mammals, specifically in motor neurons (Bixby, 2000; Johnson and Van Vactor, 2003; Stepanek *et al.*, 2005). Furthermore, investigators have observed that germline *PTPRD* mutations in mice affect motor neuron development and learning (Uetani *et al.*, 2000, 2006).

### Concluding remarks

Certain genetic alterations are able to contribute to either cancer or neurodegeneration. The genes *PARK2*, *PTEN*, *mTOR*, *ATM*, *APP*, and *PTPRD* provide instructive examples of a number of mechanisms by which these dichotomous outcomes may occur. Strongest evidence supports dual roles for *PARK2* and *ATM*, in which the same mutation results in neuronal degeneration or cancer through similar molecular mechanisms, with outcome highly dependent on cellular context (that is germline vs somatic; neuron vs cycling cell). In the case of *PTEN*, *mTOR*, and related proteins, the risk of neurodegenerative disease shows that derangement of the PI3K/Akt/mTOR pathway has implications beyond carcinogenesis. In addition to its tumor suppressive role, *PTEN* appears to have central roles in neuronal survival through several pathways. The importance of autophagy as a potential common link between cancer and neurologic disease is suggested by mTOR, although further

investigation is needed. In the cases of APP and PTPRD, alterations in the same gene appear to lead to cancer or neuronal dysfunction through independent mechanisms. Indeed, the genes included in this review show the potential value of identifying shared risk factors. The early observation of increased cancer risk and Alzheimer's-type neuropathology in patients with trisomy 21 prompted investigation into the role of APP in both diseases. The identification of PTPRD as a tumor suppressor and STAT3 inhibitor will encourage further investigation into the mechanism of predisposition to restless legs syndrome. These findings provide significant insight and may pay clinical dividends by stimulating development of biomarkers or therapeutic agents for affected patients.

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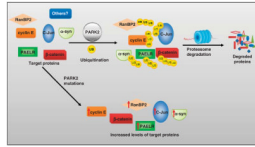
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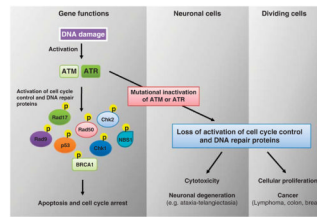


**Figure 1.**

Summary of PARK2 mechanism of action and selected known targets of ubiquitination. PARK2 is an E3 ubiquitin ligase that normally facilitates the ubiquitination and subsequent degradation of target proteins. Mutations in PARK2 result in a failure to ubiquitinate target proteins and results in increased levels of these targets. UB denotes a ubiquitin moiety.  $\alpha$ -syn, alpha-synuclein; C-Jun, c-Jun N-terminal kinase; PAELR, parkin-associated endothelin receptor-like receptor; RanBP2, RAN-binding protein 2.



**Figure 2.** Simplified model of PARK2 dysfunction in cancer and familial PD. In PD, mutational inactivation of PARK2 is sufficient to raise cyclin E levels, which helps bring about neurotoxicity. In cancer cells, PARK2 mutations occur in conjunction with other oncogenic alterations, resulting in increased tumor cell growth.



**Figure 3.** Model of differential effects of ATM and ATR mutation in neuronal vs dividing somatic cells. In neurons, ATM/ATR loss-of-function manifests as cell death and neurodegeneration. In normally dividing cells such as epithelial cells, the same mutations can result in the accumulation of additional mutations with each successive generation, eventually resulting in cancer. Yellow circles labeled with P denotes phosphorylation. Abbreviations: ATM, ataxia-telangiectasia mutated; ATR, ataxia telangiectasia and Rad3 related; BRCA1, breast cancer 1; NBS1, nijmegen breakage syndrome 1 (nibrin); Rad17, RAD17 homolog.