Phosphorylation of Parkin at serine 65 is essential for its activation in vivo

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Mutations in PINK1 and Parkin result in autosomal recessive Parkinson’s disease (PD). Cell culture and in vitro studies have elaborated the PINK1-dependent regulation of Parkin and defined how this dyad orchestrates the elimination of damaged mitochondria via mitophagy. PINK1 phosphorylates ubiquitin at serine 65 (Ser65) and Parkin at an equivalent Ser65 residue located within its N-terminal ubiquitin-like domain, resulting in activation; however, the physiological significance of Parkin Ser65 phosphorylation in vivo in mammals remains unknown. To address this, we generated a Parkin Ser65Ala (S65A) knock-in mouse model. We observe endogenous Parkin Ser65 phosphorylation and activation in mature primary neurons following mitochondrial depolarization and reveal this is disrupted in ParkinS65A/S65A neurons. Phenotypically, ParkinS65A/S65A mice exhibit selective motor dysfunction in the absence of any overt neurodegeneration or alterations in nigrostriatal mitophagy. The clinical relevance of our findings is substantiated by the discovery of homozygous PARKIN (PARK2) p.S65N mutations in two unrelated patients with PD. Moreover, biochemical and structural analysis demonstrates that the ParkinS65N/S65N mutant is pathogenic and cannot be activated by PINK1. Our findings highlight the central role of Parkin Ser65 phosphorylation in health and disease.

1. Introduction

Mutations in genes encoding PTEN-induced kinase 1 (PINK1) (human PARK6) and the ubiquitin E3 ligase Parkin (human PARK2) are causal for early onset Parkinson’s disease (PD). Cell culture and in vitro studies have elaborated the PINK1-dependent regulation of Parkin and defined how this dyad orchestrates the elimination of damaged mitochondria via mitophagy. PINK1 phosphorylates ubiquitin at serine 65 (Ser65) and Parkin at an equivalent Ser65 residue located within its N-terminal ubiquitin-like domain, resulting in activation; however, the physiological significance of Parkin Ser65 phosphorylation in vivo in mammals remains unknown. To address this, we generated a Parkin Ser65Ala (S65A) knock-in mouse model. We observe endogenous Parkin Ser65 phosphorylation and activation in mature primary neurons following mitochondrial depolarization and reveal this is disrupted in ParkinS65A/S65A neurons. Phenotypically, ParkinS65A/S65A mice exhibit selective motor dysfunction in the absence of any overt neurodegeneration or alterations in nigrostriatal mitophagy. The clinical relevance of our findings is substantiated by the discovery of homozygous PARKIN (PARK2) p.S65N mutations in two unrelated patients with PD. Moreover, biochemical and structural analysis demonstrates that the ParkinS65N/S65N mutant is pathogenic and cannot be activated by PINK1. Our findings highlight the central role of Parkin Ser65 phosphorylation in health and disease.

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Parkinson’s disease (PD) with clinically indistinguishable phenotypes [1,2]. Patients typically exhibit a motor syndrome associated with nigrostriatal pathology that can occur in the absence or the presence of Lewy body inclusions [3]. Under specific conditions of mitotoxic stress in cultured cells, PINK1 and Parkin converge in a common signal transduction pathway to eliminate damaged mitochondria via autophagy, known as mitophagy [4–6]. Over the last decade, this pathway has been intensively studied to understand the mechanisms by which these enzymes regulate mitochondrial homeostasis [4–6]. In cell culture, PINK1 is activated upon mitochondrial depolarization that can be induced using mitochondrial uncoupling agents, e.g. antymycin A/oligomycin (A/O). This results in the recruitment and activation of Parkin at the outer mitochondrial membrane (OMM) [4–6]. PINK1 directly phosphorylates Parkin at a highly conserved serine 65 (Ser65) residue within its N-terminal ubiquitin-like domain (Ubl), as well as the equivalent Ser65 residue of ubiquitin (Ub). Phosphorylation of both Parkin and ubiquitin is required for maximal activation of Parkin E3 ligase activity [7–11]. Upon activation, Parkin ubiquitylates multiple substrates at the OMM leading to both de novo assembly and elongation of existing ubiquitin chains that are, in turn, phosphorylated by PINK1. Together, this generates a feed-forward enhancement of Parkin activation and mitochondrial ubiquitylation that heralds the recruitment of selective autophagy adaptors necessary for the completion of mitophagy [12–15].

Our present understanding of PINK1-dependent Parkin activation is largely predicated on in vitro observations and cell culture studies, which often exploit the over-expression of exogenous Parkin and/or PINK1 at supra-physiological levels [4–6]. These include the previous demonstration that Parkin Ser65 phosphorylation may not be essential for its complete E3 ligase activity [8,12] or its depolarization-induced mitochondrial translocation [7,10]. Despite a concerted body of work in this area from many laboratories, the physiological significance of Parkin Ser65 phosphorylation by PINK1 in vivo remains largely enigmatic. Furthermore, additional substrates for PINK1 have been widely reported [16] but, to date, it is unknown whether activation of PINK1-dependent substrate phosphorylation is sufficient to recapitulate neurodegeneration in vivo. Models of germ-line Parkin knockout mice only exhibit mild phenotypes, with chronic mitotoxicity or extreme stress required to elicit PD-relevant neurological phenotypes [17–21]. To test the hypothesis that Parkin Ser65 phosphorylation is critical for its activation in vivo, we generated a knock-in mouse model in which the codon encoding Parkin Ser65 was altered by homologous recombination to alanine to prevent Parkin protein phosphorylation by PINK1 (figure 1a). Homozygous ParkinS65A/S65A mice were born at expected Mendelian frequencies and wild-type and mutant mice were indistinguishable in terms of gross measures of growth, weight and development (data not shown).

The expression and stability of the endogenous mutant ParkinS65A protein in ParkinS65A/S65A knock-in mice was comparable to wild-type mice across all brain regions (olfactory bulb, cortex, thalamus, striatum, hippocampus, ventral midbrain, cerebellum, brainstem and spinal cord) and extra-neural tissues (heart, spleen, lung and pancreas) (figure 1b and electronic supplementary material, figure S1). To assess how the S65A mutation affects Parkin ubiquitin E3 ligase activity, we undertook biochemical analysis of endogenous substrate ubiquitylation in cultured primary neurons. Given the availability of reliable reagents and building upon our previous work in this area [11,23], we focused our attention on the mitochondrial Fe/S domain-containing protein CISD1, a well-described Parkin substrate, in addition to monitoring endogenous PINK1-mediated Parkin Ser65 phosphorylation. We have previously observed that endogenous Parkin is expressed at low levels in mouse embryonic fibroblasts (MEFs) which limits the robust detection of endogenous Parkin signalling [23]. However, in primary cortical neuron cultures established from E16.5 mouse embryos cultured to maturity for 21 days in vitro (DIV), endogenous Parkin phosphorylation and substrate ubiquitylation are reliably detectable after combined anti-antymycin A and oligomycin stimulation (to trigger mitochondrial depolarization; hereafter referred to as A/O) [24]. Upon treatment of mature (21 DIV) cortical neurons with A/O for three hours (3 h), we observed complete loss of CISD1 ubiquitylation in ParkinS65A/S65A neurons compared to wild-type, as measured by anti-CISD1 immunoblotting (figure 1c). Immunoblot analysis using anti-phospho-Ser65 Parkin antibodies confirmed the loss of Parkin phosphorylation at Ser65 in mutant neurons (figure 1c). We also assessed endogenous ubiquitylation status of additional Parkin substrates including Mitofusin2, Miro2 and VDAC1; however, we were...
unable to detect robust signal in neurons in whole-cell lysates or following HALO-Ubiquilin1 UBA-domain tetramer (UBA\textsubscript{UBQLN1}) TUBE-pulldown experiments (electronic supplementary material, figure S2). This may be due to their low stoichiometry of ubiquitylation, demonstrated recently in human neurons by quantitative mass spectrometry [25]. We next asked whether loss of Parkin activity in Parkin\textsuperscript{S65A/S65A} neurons influenced the PINK1-dependent
phosphorylation of ubiquitin at Ser65 and its subsequent accumulation. We undertook comparative biochemical analyses of mature primary neuron cultures established from homozygous Parkin\(^{S65A/S65A}\), Pink1 knockout and Parkin knockout mice with their respective corresponding wild-type littermate controls. Consistent with previous studies in proliferating cell lines, we observed complete loss of Ser65-phosphorylated ubiquitin (phospho-ubiquitin) and CISD1 ubiquitylation in Pink1 knockout neurons, as judged by immunoblotting of HALO-UBA\(^{UBQLN1}\) pulldowns with anti-phospho-Ser65 ubiquitin and anti-CISD1 antibodies (figure 2). Strikingly, we did not observe phospho-ubiquitin accumulation in either Parkin\(^{S65A/S65A}\) or Parkin knockout neurons that were associated with loss of CISD1 substrate ubiquitylation (figure 2). These data support the Parkin-dependent feed-forward model of phospho-ubiquitin accumulation [12,15]. Similar findings were recently reported in CRISPR/Cas9-mediated S65A mutant human embryonic stem (ES) cell-derived neurons stimulated with A/O in which phospho-ubiquitin was not detectable by immunoblotting, although the authors were able to detect phospho-ubiquitin by mass spectrometry [25]. To confirm this finding in other primary mouse cell types, we exploited a tractable culture paradigm of mouse primary adult lung fibroblast cultures [26]. We stimulated adult primary fibroblast cultures from Parkin\(^{S65A/S65A}\) and Pink1 knockout mice with the protonophore carbonyl cyanide m-chlorophenyl hydrazone (CCCP) for 18 h, which dissipates mitochondrial membrane potential similar to A/O. As Parkin protein levels were lower in primary lung fibroblasts compared with neurons, we performed an additional mitochondrial enrichment step prior to ubiquitin capture by HALO-UBA\(^{UBQLN1}\) pulldown. Consistent with our results in neurons, we did not observe the accumulation of phospho-ubiquitin or CISD1 ubiquitylation in either Parkin\(^{S65A/S65A}\) or Pink1 knockout fibroblasts compared with wild-type cultures (electronic supplementary material, figure S3). Overall, our data indicate that phosphorylation of Parkin Ser65 by PINK1 is essential for both activation of its E3 ligase activity and the robust generation of phospho-ubiquitin in mature mammalian neurons.

2.2. Parkin\(^{S65A/S65A}\) knock-in mice exhibit selective motor impairments

Since our Parkin\(^{S65A/S65A}\) mice have been engineered with an inactivating point mutation in the endogenous Park2 locus and express comparable levels of Parkin protein, we speculated that our model may bypass epistatic compensation induced by the loss of total protein in traditional knockout models. We therefore undertook a comprehensive behavioural characterization of our Parkin\(^{S65A/S65A}\) mice to investigate if the loss of endogenous Parkin phosphorylation could influence striatal function in vivo. Overall, Parkin\(^{S65A/S65A}\) mice exhibited normal gross development and ageing in terms of neurological and behavioural function. We employed the raised balance beam as a more sensitive and powerful test of voluntary locomotor function, balance and coordinated limb use in our mice. Strikingly, we observed that Parkin\(^{S65A/S65A}\) mice at 12 and 18 months of age exhibited consistent impairments in all measures of balance beam performance compared with wild-type control mice (figure 3a).

Both the latency to turn towards the goal box when placed on the beam end (AGE × GENO: \(F_{1,32} = 11.41, p < 0.01\)), and the subsequent latency to cross the beam (AGE × GENO × SEX: \(F_{2,32} = 12.82, p < 0.01\)) were slower for Parkin\(^{S65A/S65A}\) mice compared with wild-type controls, with mutant males being slower to traverse the beam than their female counterparts (figure 3a). Furthermore, quantitation of foot-slips while traversing the balance beam demonstrated that the number of forelimb (GENO: \(F_{1,47} = 29.08, p < 0.01\)) or hindlimb (GENO: \(F_{1,47} = 38.52, p < 0.01\)) slips made by Parkin\(^{S65A/S65A}\) mice was greater than controls (figure 3a), but this phenotype was not exacerbated at 18 months. In addition to deficits in motor function, the impairments observed in Parkin\(^{S65A/S65A}\) mice to complete the task, particularly during the ‘beam turn’ aspect, could also indicate an underlying, yet subtle defect in cognitive planning (figure 3a). Rotarod testing at 12 and 18 months of age did not reveal any substantial differences between Parkin\(^{S65A/S65A}\) and wild-type mice (AGE × GENO: \(p = 0.058\)) (electronic supplementary material, figure S4).

Additionally, Parkin mutant mice did not exhibit any impairments in gait in comparison to wild-type mice in terms of stride length and stride width (electronic supplementary material, figure S4). Although the rotarod is routinely used to assess locomotor function in rodents, its lack of sensitivity and confounding variables are well recognized [27]. Overall, these data demonstrate that endogenous Parkin inactivation in vivo results in selective deficits in a sensitive test of voluntary motor function. Consistent with our results, deficits in fine motor coordination were reported in one previous characterization of Parkin knockout mice generated by targeted deletion of exon 3 [17]; however, in another independently generated exon 3 deleted knockout model, no motor deficits were reported although these mice

![Figure 2](image-url)
exhibited learning and memory deficits [28]. More recently, similar fine motor defects were found in Pink1 knockout mice in the absence of nigrostriatal degenerative pathology [29], further underscoring the importance of performing more sensitive behavioral testing in mouse models of PD. In our study, we were unable to determine the age-of-onset of the motor deficits, although it was reported that Pink1 knockout mice take approximately six months to exhibit detectable locomotor dysfunction [29].

Given the mitochondrial-centric functions ascribed to the PINK1–Parkin dyad, we next investigated if the selective motor phenotype in our Parkin<sup>S65A/S65A</sup> mice could be attributed to mitochondrial dysfunction. We assayed mitochondrial respiration in discrete adult brain regions from 3-month-old and 12-month-old wild-type and mutant mice using high-resolution (Oroboros Oxygraph-2k) respirometry [20]. In 3-month-old mice, we observed no difference in the respiratory control ratio (RCR) defined as State3<sub>ADP</sub>/State4 that reflects mitochondrial oxidative phosphorylation coupling efficiency independently of mitochondrial content [30,31] (electronic supplementary material, figure S5a). By contrast, we detected a highly selective and consistent difference in mitochondrial RCR between the striatum of 12-month-old Parkin<sup>S65A/S65A</sup> and wild-type mice but not in other brain regions including cortex (figure 3b and electronic supplementary material, figure S5b). This is consistent with previous reports of impaired mitochondrial respiration in select brain regions of aged Parkin knockout mice [20], and suggests that Parkin Ser65 phosphorylation contributes to mitochondrial integrity in this brain region.

2.3. Nigrostriatal integrity and basal mitophagy levels are normal in Parkin<sup>S65A/S65A</sup> knock-in mice

The observed locomotor and striatal mitochondrial dysfunction in Parkin<sup>S65A/S65A</sup> mice suggested that endogenous Parkin inactivation could also negatively impact nigrostriatal integrity in vivo. We next performed histological analysis of the substantia nigra of aged (approx. 18 months) Parkin<sup>S65A/S65A</sup> and wild-type mice to investigate if the impaired viability of nigrostriatal dopaminergic (DA) neurons might account for the selective motor defects in Parkin<sup>S65A/S65A</sup> mice. Inactivation of endogenous Parkin did not influence striatal anatomy or volume in aged mice (figure 4a–c). Nigrostriatal projections are highly complex, with a single DA neuron capable of innervating up to 2% of its terminal target field [5,32]. Although total DA neuron numbers were comparable between Parkin<sup>S65A/S65A</sup> mice and controls (data not shown), it is conceivable that differences in target-field arborization could account for the observed motor defect in our mutant animals. At a gross neuroanatomical level, conventional chromogenic tyrosine hydroxylase (TH)-immunohistochemistry revealed indistinguishable striatal innervation between genotypes (figure 4a); however, this approach does not permit a high-resolution analysis of the nigrostriatal projection. To determine whether Parkin inactivation could impact the ontogeny and arborization of DA neurons in vivo, we employed whole volume imaging of the entire nigrostriatal pathway within intact, optically cleared adult brains using dDISCO<sup>+</sup> [22,33,34]. This approach enabled utilization of confocal microscopy to assess the degree of innervation and overall connectivity between aged Parkin<sup>S65A/S65A</sup> and littermate control mice at high resolution. Using this approach, we successfully resolved DA projections in wild-type and Parkin<sup>S65A/S65A</sup> mice; however, we observed no differences between groups (figure 4b). Dysfunction in non-neuronal cells is also a reported feature of PD mouse models [35]. However, immunohistochemical labelling of microglia and astroglia by Iba1 and GFAP, respectively, revealed no overt differences between wild-type and Parkin<sup>S65A/S65A</sup> mice (data not shown). To further investigate nigrostriatal function, we
next profiled catecholamine neurotransmission in our mutant mice. We rapidly dissected striatal tissue from age-matched wild-type and Parkin$^{S65A/S65A}$ littermates and subjected these to HPLC analysis. We observed comparable levels of DA and DA turnover in wild-type and Parkin$^{S65A/S65A}$ striata (figure 4c), indicating that in our mouse model, genetic ablation of endogenous Parkin phosphorylation and activation is not sufficient to impact DA neurotransmission in vivo. Collectively, these data

Figure 4. Parkin$^{S65A/S65A}$ mice do not exhibit nigrostriatal degeneration or defective mitophagy. (a–c) Striatal innervation is indistinguishable between wild-type and Parkin$^{S65A/S65A}$ (KI) mice. (a) No differences in neuron number or striatal innervation were observed by anti-tyrosine hydroxylase (TH)-based immunohistochemistry analysis of midbrain and striatum between genotypes. (b) Striatal innervation analysis of TH-positive DA neurons within intact brains processed by iDISCO$^+$. Arborization of DA neurons is indistinguishable between wild-type and KI mice. (c) No differences were observed in striatal volume between genotypes. Error bars represent standard errors of the mean. Striatal dopamine levels are unaltered in Parkin$^{S65A/S65A}$ mice. HPLC analysis revealed no differences in dopamine (DA) and 3,4-dihydroxyphenylacetic acid (3,4-DOPAC) levels between wild-type and KI mice ($n=10$ per genotype). Data represent mean values $\pm$ s.e.m. n.s., not significant. (d) Basal mitophagy is unaltered by endogenous Parkin activation in vivo. Maximum z-projections of midbrain DA neurons from mito-QC wild-type and KI mice immunolabelled with antibodies to TH (blue) and LAMP1 (greyscale). Arrows point to mitochondria and arrowheads point to mitochondria associated with (autophagosome/mitolysosome as defined by co-localization of LAMP1 and mito-QC staining. Mitochondrial delivery to lysosomes (mitophagy) is associated with quenching of GFP signal of the mito-QC reporter and residual mCherry only signal intensity. Scale bar 5 $\mu$m. Asterisks indicates cells within insets. (e) Quantitation revealed no differences between mitophagy in DA cell bodies or axons. Results are expressed as mean values $\pm$ s.e.m.
demonstrate that endogenous Parkin inactivation results in a selective locomotor defect in the absence of structural nigrostrialal dysfunction in vivo. Importantly, our findings highlight the importance of Parkin activation under steady-state conditions in vivo.

Parkin has received most attention for its role in modulating mitochondrial quality control [5]. Maximal activation of Parkin E3 ligase activity leads to ubiquitylation of myriad substrates on the mitochondrial outer membrane, that engage autophagy receptors and drive the elimination of damaged mitochondria via mitophagy [4–6]. This widely accepted and reproducible model is largely based on in vitro findings, however recent advances in mouse genetics using the mito-QC and mt-Keima reporter models have revealed the physiological nature of basal mitophagy in vivo [22,26,37]. Furthermore, DA neurons have recently been shown to undergo high levels of mitophagy in vivo which occurs independently of PINK1 [38,39]. To investigate the regulation of basal mitophagy in the context of endogenous Parkin inactivation in mammals, we crossed Parkin<sup>S65A/S65A</sup> mice with the mito-QC mitophagy reporter model to generate Parkin<sup>S65A/S65A</sup>-mito-QC mice. An assessment of wild-type and S65A mito-QC animals revealed that basal mitophagy in nigrostriatal DA cell bodies and projections was indistinguishable between wild-type and mutant mice (figure 4d,e). These data reveal that nigrostriatal mitophagy is unaffected in a mouse model of endogenous Parkin inactivation exhibiting selective defects in motor and mitochondrial function.

2.4. **PARK2<sup>S65N</sup> mutations cause human Parkinson’s disease via direct disruption of the PINK1–Parkin axis**

Human patients with PARK2 mutations typically present with early onset PD displaying slow progression and sustained response to L-DOPA. Mutations in several key regulatory residues of Parkin have previously been identified, including Cys<sup>431</sup>Phe which disrupts the catalytic acceptor cysteine within the RING2 domain [40]. However, to date, no mutations affecting the Ser<sup>65</sup> phosphorylation site have been reported. Here we report the first clinical and genetic evidence of PD associated with homozygous mutations at p.S65N, the critical node of the PINK1–Parkin pathway.

2.5. Case series

2.5.1. Case 1

We report a 71-year-old Finnish male, diagnosed with early onset PD at the age of 40 years with no reported family history of Parkinson’s. His symptomatic presentation included rigidity of the lower limbs that was initially more marked on the left-hand side, and he exhibited shortness of steps. He has continued to experience rigidity throughout his disease course, without the development of tremor. Recently, the patient has suffered from a mild gait disturbance with occasional freezing and postural instability. Overall, the progression of his illness has been exceptionally slow with a sustained response to medication that currently comprises: levodopa (300–400 mg d<sup>−1</sup>), pramipexole (2.1 mg d<sup>−1</sup>) and selegiline (10 mg d<sup>−1</sup>). On examination during the years 2016–2017, he was categorized at stage 2.5 of the modified Hoehn and Yahr Scale, with a United Parkinson’s Disease Rating Scale (UPDRS) score of 41/199 (electronic supplementary material, table S1). Dopamine transporter (DaT) single-photon emission computerized tomography (SPECT) of the brain demonstrated reduced density of DA synaptic terminals in the caudate and putamen consistent with degenerative PD (figure S5).

Targeted next-generation sequencing (NGS) revealed that the patient carried a novel homozygous c.194G &gt; A variant in exon 3 of the PARK2 gene causing an amino acid change p.Ser<sup>65</sup>Asn (S65N) in the PARKIN protein (figure S5b). The variant is very rare: only two heterozygous carriers among 122 271 subjects were found in the Genome Aggregation Database (gnomAD) with an allelic frequency of 8.2 × 10<sup>−6</sup>. In the Exome Aggregation Consortium (ExAC) database, two heterozygotes were found among 60 691 subjects (allele frequency 1.6 × 10<sup>−5</sup>). Furthermore, the variant site is highly conserved in vertebrates (electronic supplementary material, figure S6a), and in silico analysis of the variant by the method of Combined Annotation Dependent Depletion (CADD) [42] predicted that the mutation is deleterious with a CADD C-score of 25.5. We analysed coding variants in 82 selected PD-associated loci (electronic supplementary material, table S2) with a CADD C-score of greater than 20 and population carrier frequency less than 1%, but did not find any other likely pathogenic variant in S65N-M70.

2.5.2. Case 2

A 60 year-old Caucasian female diagnosed with PD at the age of 54 was identified from the Parkinson’s Progression Markers Initiative (PPMI). Her initial clinical features were bradykinesia and gait difficulty on the right side. She exhibited characteristic but mild motor symptoms for PD and no atypical features have been observed. Twelve months following her diagnosis, she was commenced on pramipexole resulting in a positive and sustained response (current dose 2.25 mg of pramipexole/day). At her latest examination, the patient was categorized at Stage 2 of the Hoehn and Yahr Scale, and she has also been examined using the Unified Parkinson’s Disease Rating Scale (MDS-UPDRS) for 5 years (scores from latest examination are provided in electronic supplementary material, table S1).

The patient has also been followed up by DaT imaging for four years, which has demonstrated reduced density of DA synaptic terminals in the caudate and putamen consistent with DA denervation (striatal binding ratio (SBR) calculations from the latest session are provided in electronic supplementary material, table S1).

Genetic analysis of the individual revealed a homozygous Parkin p.S65N mutation. Analysis of 82 PD-associated loci revealed three other gene variants (in POLG, MCLR and Glucocerebrosidase (GBA) (electronic supplementary material, table S3) that passed our filtering criteria (CADD C-score greater than 20, carrier frequency less than 1%). A heterozygous recessive variant (p.G268A) in POLG has been linked to autosomal recessive/sporadic progressive external ophthalmoplegia (PEO) in compound heterozygous or homozygous form [43,44], but also described as single-heterozygous in a child with a syndrome including Parkinsonism born from consanguineous parents (probable autosomal recessive mode of inheritance) [45]. She also carried another POLG variant, a rare frameshift deletion (exon2: c.153_158del:p.Gln54_Gln55del) in a tandem repeat region of POLG; however, this is likely a benign variant, given a CADD C-score of 6.2. Overall, we did
not consider the heterozygous p.G268A POLG mutation as disease-causing in the patient. A rare heterozygous variant (p.R142H) was detected in the MC1R gene. This gene was initially found to be associated with PD, but subsequent studies with large patient cohorts have not supported this finding [46–49]. Furthermore, the p.R142H variant has to date only been associated with red hair and not PD [46]. Thus, we did not consider p.R142H being a disease-causing variant in this patient. By contrast, a heterozygous p.N409S variant in GBA was detected, which is a recognized susceptibility factor for PD [50] although the variant does not always lead to PD [51]. Therefore, we conclude that the PARKIN p.S65N mutation is likely to be the major disease-causing variant in the patient, although we cannot exclude that the GBA p.N409S variant may contribute to pre-disposition and/or the clinical phenotype of the patient.

2.5.3. Functional analysis of the PARKIN\textsuperscript{S65N/S65N} mutation

We initially assessed the pathogenicity of the Parkin\textsuperscript{S65N/S65N} mutation by assaying PINK1–Parkin signalling in Flp-In

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Figure 5. (Caption opposite.)
We next investigated the effect of the endogenous PARKIN$^{S65N/S65N}$ mutation on basal and depolarization-induced mitophagy. We first generated a stable mitophagy reporter cell line via retroviral transduction of mito-QC [39, 52] in both control and PARKIN$^{S65N/S65N}$ patient fibroblast lines. To induce substantial levels of mitophagy in culture, patient and control cells expressing mito-QC were stimulated with A/O for 24 h. Upon A/O stimulation, we observed no difference in mitophagy between control and PARKIN$^{S65N/S65N}$ mito-QC cells (electronic supplementary material, figure S8). These data are consistent with previous reports demonstrating that endogenous Parkin is dispensable for basal and depolarization-induced mitophagy in patient-derived primary fibroblasts [52].

2.5.4. Structural analysis of the Parkin$^{S65N}$ mutant protein

To understand precisely how the pathogenic S65N mutation affects Parkin activity, we crystallized and solved the structure of the novel human Parkin PD mutant (UBLR01RBR, ∆84–143) at 2.9 Å. Comparative analyses of wild-type and Parkin$^{S65N}$ x-ray crystal structures did not reveal any conformational differences between the wild-type and mutant protein (figure 5e and electronic supplementary material, figure S6c), indicating that the S65N mutation does not significantly perturb Parkin structure. However, as the S65N mutation prevents incorporation of a phosphate group at this position, the absence of a negative charge at the UBL enables cleavage of the ParkinS65N structure in the presence of the putative substrates, thereby resulting in the loss of Parkin activity.

3. Discussion

Combining a novel mouse knock-in model and unique human clinical case studies, we present the most compelling evidence to date demonstrating the physiological and clinical significance of PINK1-dependent Parkin Ser65 phosphorylation. Furthermore, despite over 20 putative substrates reported in the literature [57, 58], our research indicates that inactivation of this PINK1 phosphorylation site on Parkin alone is sufficient for humans to develop early onset Parkinson’s disease (PD).
Multiple lines of evidence suggest that levels of dopamine in mice [29] in the absence of nigrostriatal pathology. Our analysis revealed a mild, age-dependent defect in mitochondrial monoamine transporter (VMAT2) and higher levels of expression of both the dopamine transporter (DAT) and vesicular monoamine transporter (VMAT2) and higher levels of extracellular dopamine in the striatum [17,18]. Mild mitochondrial defects have also been reported in 24-month-old Parkin knockout mice that are not observed in younger mice (9 months of age) [20]. These effects were restricted to the striatum, and not detected in other brain regions including the midbrain or cortex [20]. Using a similar approach, our analysis revealed a mild, age-dependent defect in mitochondrial respiration in the striatum of Parkin knock-in mice (figure 3b). Interestingly, this was not associated with any change in basal nigrostriatal mitophagy in Parkin knock-in mice (figure 4d,e). Our current findings are also consistent with our recent demonstration of PINK1-independent mitophagy in vivo [39]. Recent analysis of Drosophila melanogaster models expressing fluorescent mitophagy reporters has also revealed that basal mitophagy proceeds independently of both PINK1 and Parkin in vivo [38]. Nevertheless, because cell culture studies in vitro provide a compelling case for Parkin activation in stress-evoked mitochondrial quality control pathways [4–6], it will be vital to investigate if nigrostriatal mitophagy is specifically affected in models of constitutive mitotoxicity reporting PD-relevant pathology, e.g. Poly mutator mouse crossed with Parkin knockout mice [21,62]. Ultimately, our findings highlight the importance of uncovering the mitophagy-independent pathways by which endogenous Parkin sustains striatal function and mitosis during ageing. Our data also adds to the growing body of evidence that suggests multiple mitophagy pathways operate to sustain mitochondrial quality control during specific contexts i.e. under basal conditions compared to extreme or chronic stress.

At the molecular level, the feed-forward mechanism of Parkin activation stipulates that (i) PINK1-dependent generation of phospho-ubiquitin stimulates Parkin recruitment to damaged mitochondria, (ii) this primes Parkin for phosphorylation by PINK1 and thus maximal activation, (iii) leading to further phospho-ubiquitin accumulation [4–6]. Evidence for this model includes the demonstration that the Parkin His302Ala (H302A) mutant, that cannot bind phospho-ubiquitin but is catalytically competent, exhibits reduced mitochondrial recruitment, Parkin Ser65 phosphorylation and ubiquitylation of substrates in HeLa cells [11,41]. However, HeLa studies also suggest that the initial amount of phospho-ubiquitin generated by PINK1 (independent of Parkin activity) is likely to be low because over-expression of the catalytically inactive Parkin Cys431Ser mutant does not result in significantly detectable phospho-ubiquitin accumulation [12,15]. Consistent with this latter observation, we did not observe any phospho-ubiquitin accumulation in mature primary cortical neurons (figure 2) or adult primary lung fibroblasts (electronic supplementary material, figure S3) subjected to mitochondrial depolarization from ParkinS65A/S65A and Parkin knockout mice. This is consistent with recent analysis of CRISPR/Cas9-mediated S65A mutant human ES cell-derived neurons stimulated with A/O [25]. By contrast, we did detect phospho-ubiquitin accumulation in ParkinS65N mutant patient-derived fibroblasts and HeLa cells (figure 5c and electronic supplementary material, figure S6b), albeit at lower levels than wild-type cells, suggesting potential redundancy of Parkin in these cell types with both Parkin-dependent and Parkin-independent formation of phospho-ubiquitin. The MUL1 E3 ligase has recently been reported to operate in a parallel pathway to Parkin in non-neuronal cells, and could account for the phospho-ubiquitin we observe in our human cell systems [63], although further work is required to substantiate this.

We and others have previously demonstrated that phospho-ubiquitin can partially activate recombinant non-phosphorylatable Parkin S65A protein in vitro [8,12]. Despite detectable accumulation of phospho-ubiquitin in fibroblasts, we observed complete loss of E3 activity in PARLINS65N/S65N mutant cells. The interaction affinity between the non-phosphorylated Parkin-phospho-ubiquitin complex with its charged E2 ~ Ub is approximately 20-fold lower than that for the Phospho-Ser65-Parkin and phospho-ubiquitin complex [64], which may partly explain the lack of activation of endogenous ParkinS65N (and similarly ParkinS65A) protein. Our results therefore highlight the importance of studying signalling pathways at endogenous levels in physiologically relevant systems. Moreover, our data may also be explained by recent structural analysis of Parkin activation mechanisms. Initial binding of phospho-ubiquitin triggers a conformational shift that exposes a donor ubiquitin-binding site and partial activation of Parkin catalytic activity [54]. The subsequent PINK1-dependent phosphorylation of Parkin Ser65 ultimately drives Parkin activation by a series of structural alterations. In particular, displacement of the phospho-Ubl domain maintains interaction of the ubiquitin-charged E2 to the RING1 domain, and the phospho-Ubl subsequently binds to a basic phosphate-binding site on RING0 (flanked by residues Lys161 and Lys211 as well as Arg163) [53,55,56]. The binding of phospho-Ubl to RING0 leads to the release of the catalytic RING2 domain thereby exposing C431 to promote full Parkin activation and enhancing interactions with E2 [53,55,56]. Collectively, our endogenous neuronal results combined with recent structural insights highlight the pre-eminent status of Parkin Ser65 phosphorylation in modulating its catalytic activation.

The clinical importance of endogenous PINK1-mediated Parkin phosphorylation is substantiated by our discovery of two unrelated PD patients harbouring novel mutations at Parkin Ser65. Numerically, mutations in Parkin are associated with early onset PD, accounting for approximately 40% of cases with age of onset below 45 years; however, patients with pathogenic Parkin inactivating mutations have been
reported with mid-age-of-onset that would be consistent with the second case [65]. In line with our mouse data, we found that basal and depolarization-induced mitophagy in S65N patient-derived primary fibroblasts was not diminished, despite a loss of Parkin E3 ligase activity (electronic supplementary material, figure S8). In the future, it will be exciting to address whether this is the case in a more neural context, by generating dopamine neurons derived from human pluripotent stem cells (hPSCs).

Although PINK1–Parkin signalling constitutes a clear pathway that modulates depolarization-induced mitophagy in vitro, basal mitophagy is unaffected in both PINK1 knockout and Parkin S65A knock-in mice. Though the clinical significance of PINK1–Parkin signalling is incontrovertible, the contribution of this pathway to mitophagy in vivo remains unclear, as does the contribution of dysregulated mitophagy to PD [66]. We predict that distinct mitophagy pathways orchestrate mitochondrial homeostasis under steady-state and stress-response scenarios. 

In summary, this study is the first to establish both the physiological and clinical significance of PINK1-mediated phosphorylation of Parkin at serine 65. Our findings shed much-needed light on endogenous Parkin function and should provoke a reassessment of how it orchestrates cell-specific mitosis in vivo.

4. Material and methods

4.1. Generation and validation of Parkin\(^{S65A/S65A}\) knock-in mice

Parkin\(^{S65A/S65A}\) mice were generated by TaconicArtemis GmbH, using a targeting strategy to introduce a constitutive knock-in of a point mutation (KI-PM) in the Park2 gene by homologous recombination in mouse ES cells. The targeting strategy was based on NCBI transcript NM_016694.3. Exon 1 contains the translation initiation codon, and the S65A mutation was introduced into exon 3. A positive selection marker (puromycin resistance, PuroR) flanked by FRT sites was inserted into intron 2. The targeting vector was generated using BAC clones from the C57BL/6J RPCIB-731 BAC library and transfected into the TaconicArtemis C57BL/6N Tac ES cell line. Homologous recombinant clones were isolated using positive and negative (thymidine kinase, TK) selection, and the constitutive KI-PM allele was obtained after Flp-mediated removal of the selection marker. This KI-PM allele was predicted to express the mutated Park2 S65A protein product. The remaining recombination site will be located in a non-conserved region of the genome. The knock-in mice were generated and maintained on an inbred C57BL/6J background. Genotyping was performed by endpoint PCR using genomic DNA isolated from tails using the following primer sets at an annealing temperature of 60°C: Primer 1 (5’GACACAGATAGGACACAGAAG 3’) and Primer 2 (5’GACCATTTACCTCAGAGTGC 3’) that enabled detection of the wild-type (290 bp) and S65A knock-in (365 bp) alleles. The mito-QC mouse model used in this study was generated as previously described on a C57BL/6N background strain [22] and crossed with Parkin S65A knock-in heterozygote animals to produce homozygous knock-in animals and wild-type littermate controls with endogenous mito-QC reporter.

4.2. Materials and reagents

HaloLink resin was purchased from Promega. All mutagenesis was carried out using the QuikChange site-directed mutagenesis method (Stratagene) with KOD polymerase (Novagen). All DNA constructs were verified by the MRC Protein Phosphorylation and Ubiquitylation Unit (PPU) DNA Sequencing Service, School of Life Sciences, University of Dundee, using DYEnamic ET terminator chemistry (Amer sham Biosciences) on Applied Biosystems automated DNA sequencers. DNA for bacterial protein expression was transformed into Esherichia coli BL21 DE3 RIL (codon plus) cells (Stratagene). Stock solutions of carbonyl cyanide m-chlorophenyl hydrazone (CCCP; Sigma), antimycin A (Sigma) and oligomycin (Sigma) were used for experiments in cells. Unless otherwise specified, general reagents and chemicals were from Sigma-Aldrich (Merck) and cell culture reagents were from Gibco/Invitrogen (Thermo Fisher Scientific). All cDNA plasmids, antibodies and recombinant proteins generated in house for this study are available on request through our dedicated reagents website: https://mrcppureagents.dundee.ac.uk/

4.3. Mouse motor and behavioural studies

In total, 51 PARK2 S65A mice were used for behavioural experiments in groups which consisted of 25 wild-type (14 males and 11 females) and 26 Park2\(^{S65A/S65A}\) mice (11 males and 15 females). At 18 months 35 mice remained, 16 wild-type (10 males and 6 females) and 19 Park2\(^{S65A/S65A}\) mice (9 males and 10 females). Mice were housed in sex-matched littermate groups of between two and five animals per cage with lights adjusted to a 12 L : 12 D cycle (lights on at 06.30) and with a constant ambient room temperature of 21 ± 1°C. Animals had ad libitum access to food and water throughout. The mice underwent behavioural testing at 12 months and 18 months of age and all experiments were conducted in accordance with the 2013 European Union Directive 2010/63/EU and the UK Animals (Scientific Procedures) Act of 1986 and local ethical review at the University of Cardiff.

The motor test battery has been described previously elsewhere [67], but briefly mice were tested for simple neurological deficits using: clumping and reaching assays; accelerating rotarod and balance beam test to measure motor coordination and balance; 30 min and 24 h open field activity; footprint analysis to measure changes in gait; and inverted grid task to measure grip strength. For the rotarod test (Ugo Basile, Varese, Italy), mice are placed on a rotating beam which accelerates. Initial training consisted of training the mice at different speeds for 2 min (4, 8 and 12 r.p.m.). Data were collected from five sessions at the 12-month time point and two sessions at the 18-month time point whereby the mice were placed on the rod that accelerated from 4 to 40 r.p.m. over 5 min. The latency of the mice to fall from the beam was recorded and used as a measure of motor coordination. For the balance beam test (see above reference for dimensions), each mouse was trained to run the beam prior to the test session. This consisted of starting the mice in the goal box at the top of the inclined beam and over repeated exposures moving the starting point on the beam to the lower end (start point) such that the mice ran further as the training progressed. Training was complete when the...
mouse was placed on the lower end of the beam (facing away from the beam) and the mouse turned and ran the length of the beam unprompted. Foot-slips were recorded when a foot slipped from the beam onto the narrow ledge that ran either side of the length of the beam. Each mouse provided data (fore and hind limb foot-slips, latency to turn and cross the beam) from two runs for analysis. Gait analysis was run using a footprint test whereby the feet of the mice were painted with red (front feet) and blue (rear feet) non-toxic water-based paint, and the mice were permitted to run a 1-m terminal course that was fitted with paper on the floor such that they left coloured paw prints. The paw print patterns permit the measurement of variation in gait: stride length; base width (distance between left and right front/hind limbs); fore/hind paw overlap (in normal locomotion the hind paw placement overlaps closely with the location where the fore paw had previously landed; gait impairment is manifest by an increase in the magnitude and variability of the separation. For the motor activity testing using an automated system (Med Associates Inc, Vermont, USA), mice were placed in an open field arena for 32 h with free access to food and water throughout. Data were collected automatically with activity being measured as the number of infrared beam breaks. Activity was measured as the initial 30 min period (transfer activity) and a 24 h period (15.00 to 15.00) to capture a circadian cycle. In addition, several simple behavioural assessments were run: claspings and reaching reflexes where the mice is suspended by the tail and lowered to the benchtop with clapping and reaching measured through observation and recorded as present or absent; negative geotaxis, measuring the natural inclination of the mouse to face upwards when placed head down on a vertical grid, with the mouse being allowed 30 s to correct its orientation to the upright position; and horizontal grid grip strength, whereby the mouse is placed on a flat grid surface which is then rotated 180° along the horizontal axis such that the mouse is clinging to the underside of the grid, the maximum time for the mouse to remain upturned being 60 s without falling.

4.3.1. Statistical analyses of mice behavioural studies

Parametric split-plot analyses of variance using age as the within groups factor and genotype and sex as between-group factors were used where applicable as three-way ANOVAs. All statistical analyses were conducted on GENSTAT 17 (VSN International, Hemel Hempstead, UK). Missing values were corrected with an inbuilt linear interpolation routine. For non-parametric data, $\chi^2$ was used to determine significance. Significance level was taken at 95% confidence.

4.4. Immunohistochemistry, iDISCO$^+$ and microscopy

Transcardial perfusion was performed under terminal general anaesthesia to obtain tissues for histological analyses. Histology, immunohistochemistry, immunocytochemistry and confocal microscopy were performed as previously described [22,39,68,69], with minor modifications. Following terminal anaesthesia via intraperitoneal administration of Euthatal, adult animals were trans-cardially perfused with phosphate-buffered saline (PBS) to remove excess blood. Tissues were rapidly harvested and processed by immersion fixation in freshly prepared 3.7% PFA at pH 7.0 in 0.2 M HEPES. For mito-QC animals, transverse brain sections (200 mm) were acquired using a vibratome (Leica). For chromogenic immunohistochemistry and stereological analyses, coronal brain sections (40 mm) were cut on a slide microscope equipped with a freezing stage (Leitz) and processed for free-floating immunohistochemistry. The following primary antibodies were used: rat monoclonal anti-lysosomal associated membrane protein 1 (LAMP1) (1D4B) (Cat#: sc-19992 RRID: AB_2134495; Santa Cruz Biotechnology, Inc.); rabbit, sheep and mouse anti-Tyrosine Hydroxylase (rabbit: Cat#: AB152; RRID: AB_390204; sheep: Cat#: AB1542; RRID: AB_90757; mouse: Cat#: MAB318; RRID: AB_2201528; Millipore); rabbit polyclonal anti-Ionized calcium binding adaptor molecule 1 (Iba1) (Cat#: 019-19741; RRID: AB_839504 - Wako), chicken anti-GFP (Cat# GFP-1020, RRID:AB_10000240; Aves Labs; Cat# ab13970, RRID:AB_300798; Abcam). Alexa-Fluor conjugated secondary antibodies were obtained from Life Technologies (Molecular Probes/Thermo Fisher Scientific) as described previously [39]. VECTASHIELD Antifade Mounting Medium H-1000 was used to mount tissue sections on slides (Leica Surgipath). For cell counts and tinctorial histochemistry, Cresyl fast violet (Nissl) stain was obtained from Sigma-Aldrich (C5042-10G). For whole-mount imaging of the nigrostriatal pathway in intact mouse brains, specimens were processed, stained using rabbit-TH (AB152) and optically cleared using the detailed protocol specified for iDISCO$^+$ [33] (https://idisco.info). Following the acquisition of images from intact whole brains (dorsal and ventral surfaces), cleared brain specimens were hemisected along the midline and subsequently bisected to facilitate deeper imaging in the sagittal and coronal planes, respectively. Images were acquired using a Zeiss LSM 710 laser scanning microscope (Plan-Neofluar 340 objective, NA 1.30; Plan Apochromat 365 objective NA 1.4; Plan Apochromat 320 objective, NA 0.8), or a Zeiss LSM880 Airyscan confocal scanning microscope (ZEISS; Plan Apochromat 363 objective, NA 1.4) and processed using ZEISS ZEN software/Adobe PHOTOSHOP or IMARIS (Bitplane) for 3D isosurface rendering. Images were digitally altered within linear parameters, with minimal adjustments to levels and linear contrast applied to all images.

4.5. Quantification and statistical analysis

Semi-automated quantitation images were processed with VOLUMETRY 6.3 image analysis software (PerkinElmer) using algorithms developed to analyse object overlap and count individual structures. For all analyses, we obtained images using uniform random sampling by an experimenter blind to all conditions. All images in each experimental group were processed as a batch using identical protocols. All images were prefiltered to suppress noise (3 $\times$ 3 median filter). The same strategy was used to quantify all non-immunolabelled mito-QC labelled images using auto-thresholding to identify objects (mean intensity + 3 standard deviations). Objects were filtered using a minimum size cutoff (0.16 mm$^2$) and touching objects were separated using a guide size (0.4 mm$^2$). Mitolysosomes were typically identified on the basis of thresholded red signal not overlapping with green (this condition was relaxed in the case of samples where dequenching of the mito-QC probe was observed).
Where dequenching or spectral-overlap was observed in some instances, we employed LAMP1 immunohistochemistry to verify the lysosomal nature of mitolysosomes and green channel/combined with LAMP1 immunostaining was used as a proxy for mitolysosomes. In the case of immunolabels used to identify cells of interest in brain sections (TH, Iba1), we employed an autothresholding criterion of mean intensity + 1.5 standard deviations. A minimum size of 0.16 mm² was required, and a ‘Fill Holes in Objects’ processing step was applied, and a ‘Cell Count’ object set at 100×.

Cell counts were conducted using two-dimensional stereology with an automated stage and stereology module ‘NEWCAST TM’ from VISIOPHARM integrator system software (Visiopharm) on an Olympus BX50 microscope (Olympus Optical Co. Ltd, Tokyo, Japan). For NeuN immunohistochemistry, cell counts were conducted on a 1:12 series throughout the entire striatum (left and right sides), with the counting objective set at 100× and the randomized sampling counting frame area at 285 µm² and corrected using the Abercrombie formula [70]. For the TH and Calbindin double labelling, cell counts were carried out on a 1:12 series through the substantia nigra with the counting objective set at 40×, and all visible cells were counted within this area with double-stained cells denoting A10 dopamine cells and cells only stained for TH denoted as A9 dopamine cells.

4.6. Mitochondrial respiration assays
Wild-type and Parkin S65A knock-in mice (10 per genotype) were killed by decapitation without prior anaesthesia. A fragment of the tail was retrieved for confirmation of the genotype, determined by PCR amplification, as previously described [71]. The brains were rapidly removed and the regions of interest (striatum, midbrain and cortex) dissected on ice and weighed. Post-nuclear supernatants were obtained by manual homogenization of brain samples in nine volumes of isolation buffer (300 mM sucrose, 1 mM EGTA, 5 mM Tris–HCl pH 7.4), using a glass Dounce homogenizer with a glass pestle, followed by centrifugation at 100,000 g, 4 °C, for 10 min. The post-nuclear supernatants were directly used for respiration and protein assays, as well as for the analysis of citrate synthase (CS) activity. The post-nuclear supernatants were analysed in a thermostatically controlled oxygraphic chamber at 25 °C with continuous stirring (Oxygraph-2k, Oroboros Instruments, Innsbruck, Austria) as previously described [20]. In brief, the samples were resuspended in 2 ml of mitochondrial respiration medium (100 mM KCl, 40 mM sucrose, 10 mM TES, 5 mM MgCl₂, 1 mM EGTA, 0.4% w/v fatty acid free-BSA (bovine serum albumin), pH 7.2) and the protein concentration was determined (Bradford protein assay, Bio-Rad). Each respiration assay was run with a constant amount of protein from one wild-type and one knock-in mouse (0.3 mg for striatum, 0.6 mg from midbrain and cortex). The results were expressed in nmol of O₂/min mg⁻¹ of total protein. The respiration rate was recorded sequentially: (i) basal respiration in the presence of complex I substrates (10 mM glutamate, 5 mM malate); (ii) state 3 respiration with addition of 1 mM ADP; (iii) state 4 respiration with 1 µg ml⁻¹ oligomycin; and (iv) maximal respiration rate was determined by progressive additions of 1.25 µM carbonyl cyanide m-chlorophenyl hydrazone (CCCP). The respiratory reserve capacity was calculated as maximal respiration – basal respiration. Respiratory control ratio or RCR was calculated as state 3/state 4.

4.7. Determination of citrate synthase activity
CS activity was determined using a colorimetric assay based on the reaction between 5,5'-dithiobis-(2-nitrobenzoic acid) (DTNB) and CoA-SH to form 5-thio-2-nitrobenzoic acid (TNB), which exhibits maximum absorbance at 412 nm, according to the manufacturer’s instructions (Sigma, CS0720). In brief, 20 µl of cold CellLytic M supplemented with protease inhibitors (protease inhibitor cocktail, Thermo Scientific 1861279) was added to 10 µl of post-nuclear supernatant. The sample was homogenized and centrifuged at 12,000 g for 10 min. The supernatant was collected, and protein concentration was determined by the Bradford method (BioRad). Fifteen to 20 µg of protein was added to a 200 µl reaction mixture containing 1× assay buffer, 300 µM acetyl CoA and 100 µM DTNB. The reaction was initiated by addition of oxaloacetate (OAA) to a final concentration of 0.5 mM. CS activity was evaluated by following the absorbance of the reaction mixture at 412 nm (SpectraMax M4) before and after addition of OAA every 10 s, for 2 min. Each sample was run in duplicate and CS activity was expressed as units/min mg⁻¹ of total protein.

4.8. Dopamine HPLC analysis
Dopamine and its metabolite 3,4-dihydroxyphenylacetic acid (DOPAC) concentrations were measured in the dorsal striatum by reverse phase high-performance liquid chromatography coupled with electrochemical detection (Coulochem III, Thermo Scientific) as described earlier [72]. Briefly, 18-month-old wild-type and ParkinS65A/S65A mice were killed by cervical dislocation. Brains were quickly removed, pre-commissural dorsal striatum was dissected on an ice-cold Petri dish and freshly homogenized in 0.4 M perchloric acid. Following centrifugation and filtration of the supernatant, dopamine and DOPAC were separated using a C18 reverse phase column (Thermo Scientific). The mobile phase consisted of 10% acetonitrile, 75 mM NaH₂PO₄·H₂O, 0.17 mM octanesulfonic acid, 2.5 mM triethylamine and 25 mM EDTA, adjusted to pH 3.0 with orthophosphoric acid, and was delivered at a flow rate of 0.6 ml min⁻¹. Protein levels were determined by Lowry assay from pellets of the homogenates and catecholamine concentrations are expressed per milligram protein.

4.9. Antibodies for biochemical studies
The following primary antibodies were used: total Parkin immunoblotting (sc2282, Santa Cruz), mouse Parkin immunoprecipitation (in-house, S328D, 5th bleed), β-tubulin (Sigma), β-actin (Sigma), Calbindin (49848Sigma), GAPDH (Santa Cruz), CisD1 (Proteintech), NeuN (MAB377, Millipore), PINK1 immunoblotting (BC100-494, Novus), PINK1 immunoprecipitation (in-house S085D, 3rd bleed), Mitofusin2 (MFN2) (in-house, S781D, 4th bleed), OPA-1 (16612607, BD Biosciences), RHOT2 (Miro2) (H00089941, Abnova), COX IV (#4850, Cell signalling technology), PDI (#2784, Cell signalling technology), Tyrosine Hydroxylase (ab112, Abcam), VDAC1 (ab15895, Abcam), Vinculin (#4650, Cell signalling technology). Horseradish-peroxidase (HRP)-conjugated
secondary antibodies (Sigma) were used. Anti-Parkin phospho-Ser65 rabbit monoclonal antibody was raised by Abcam in collaboration with the Michael J. Fox Foundation for Research. Anti-phospho-Ser65-ubiquitin rabbit polyclonal antibodies were generated by 21st Century Biochemicals Inc. (Marlborough, MA, USA) using two phosphorylated peptides, C-Ahx-YNIQKE[pS]TLHLVL-amide and Ac-YNIQKE[pS]TLHLVL-Ahx-C-amide, that correspond to amino acid residues 59–71 of ubiquitin. Antibodies were affinity purified using phosphorylated and non-phosphorylated versions of the peptide immunogen (electronic supplementary material, figure S9b). A fragment of human Miro1 fusion protein encompassing residues 1–592 with N-terminal His-amino acids, 1 mM sodium pyruvate, 100 Units/ml penicillin supplemented with 10% FBS (LSP #S-001-BR), 1 of 0.1 mM [73]. Cultures were induced to express protein by addition of 0.1 mM of doxycycline to the medium for 24 h. To depolarize or uncouple mitochondrial membrane potential, proliferating cells were treated with 10 µM antimycin (Sigma) and 1 µM oligomycin dissolved in DMSO. Primary mouse cortical neurons were isolated from the brains of wild-type or mutant embryos of either sex at E16.5. Embryonic cortices were collected in HBSS, and cells were dissociated by incubation with trypsin-EDTA (#25300-054, Gibco) at 37°C. Cells were then diluted in Neurobasal medium containing B27 supplement, Glutamax, penicillin/streptomycin and plated at a density of 6.0 × 10⁴ cells/well on 6-well plates coated with 0.1 mg ml⁻¹ poly-L-lysine (PLL; Sigma). Neurons were cultured at 37°C in a humidified incubator with 5% CO₂. Every 7 days, the medium was replaced with fresh medium containing B27. To depolarize or uncouple mitochondrial membrane potential in neurons, cultures were treated with 10 µM antimycin (Sigma) and 1 µM oligomycin dissolved in DMSO at 37°C.

Primary lung fibroblasts were derived from adult mice as previously described and maintained in DMEM (Dulbecco’s modified Eagle’s medium) supplemented with 10% FBS (fetal bovine serum), 2 mM L-glutamine, 1% (v/v) Triton X-100, 0.25 M sucrose, 150 mM NaCl, 2 mM sodium orthovanadate, 1 mM NaF, 10 mM sodium glycerophosphate, 1.15 mM sodium molybdate, 4 mM sodium tartrate dehydrate, 100 mM 2-chloroacetamide, 1 mM DTT and complete protease inhibitor cocktail (Roche). All inhibitors and DTT were added immediately prior to use. Tissue homogenization was performed using a probe sonicator at 4°C (Branson Instruments). Crude lysates were incubated at 4°C on wet ice for 30–45 min, before clarification by centrifugation at 14,000 r.p.m. for 30 min at 4°C. Supernatants used for subsequent steps were carefully removed and either used for downstream biochemical analyses or snap-frozen and stored at −80°C.

For analysis of endogenous Parkin protein expression in vivo, fresh brains were rapidly excised, placed in cold PBS and microdissected with ultratine microknives under stereomicroscopy. Upon isolation, each brain region was collected in a single 1.5 ml microcentrifuge tube and immediately plunged into dry ice. Tissue samples were stored at −80°C until ready for processing. To make protein extracts, all tissues (neural subregions and extra-neural tissues) were weighed and defrosted on wet ice in fivefold mass excess of freshly prepared, ice-cold lysis buffer containing: 50 mM Tris/HCl pH 7.5, 1 mM EDTA pH 8.0, 1 mM EGTA pH 8.0, 1% Triton X-100, 0.25 M sucrose, 150 mM NaCl, 2 mM sodium orthovanadate, 1 mM NaF, 10 mM sodium glycerophosphate, 1.15 mM sodium molybdate, 4 mM sodium tartrate dehydrate, 100 mM 2-chloroacetamide, 1 mM DTT and complete protease inhibitor cocktail (Roche). All inhibitors and DTT were added immediately prior to use. Tissue homogenization was performed using a probe sonicator at 4°C (Branson Instruments). Crude lysates were incubated at 4°C on wet ice for 30–45 min, before clarification by centrifugation at 14,000 r.p.m. for 30 min at 4°C. Supernatants used for subsequent steps were carefully removed and either used for downstream biochemical analyses or snap-frozen and stored at −80°C.

4.10. Tissue culture: proliferating and primary cells

Flp-In T-Rex HeLa stable cell lines were cultured in DMEM (Dulbecco’s modified Eagle’s medium) supplemented with 10% FBS (fetal bovine serum), 2 mM L-glutamine, 1% (v/v) Triton X-100, 0.25 M sucrose, 100 Units/ml penicillin supplemented with 10% FBS (fetal bovine serum), 2 mM L-glutamine, 1% (v/v) Triton X-100, 0.25 M sucrose, 150 mM NaCl, 2 mM sodium orthovanadate, 1 mM NaF, 10 mM sodium glycerophosphate, 1.15 mM sodium molybdate, 4 mM sodium tartrate dehydrate, 100 mM 2-chloroacetamide, 1 mM DTT and complete protease inhibitor cocktail (Roche). All inhibitors and DTT were added immediately prior to use. Tissue homogenization was performed using a probe sonicator at 4°C (Branson Instruments). Crude lysates were incubated at 4°C on wet ice for 30–45 min, before clarification by centrifugation at 14,000 r.p.m. for 30 min at 4°C. Supernatants used for subsequent steps were carefully removed and either used for downstream biochemical analyses or snap-frozen and stored at −80°C.
Cat # 11836170001). Lysates were centrifuged at 20,800g for 10 min at 4°C. Supernatants were collected, quantified by Bradford assay (Thermo Scientific) and subjected to immunoblot analysis.

4.12. Membrane fraction enrichment

Cells were collected in ice-cold PBS containing 200 mM chloroacetamide. They were then lysed in buffer containing 250 mM sucrose, 20 mM HEPES, 3 mM EDTA, 1% (w/v) 1 mM sodium orthovanadate, 10 mM sodium β-glycerophosphate, 50 mM NaF, 5 mM sodium pyrophosphate, pH 7.5 and protease inhibitor cocktail (Roche) supplemented with 100 mM chloroacetamide at 4°C. Cells were disrupted using a glass hand-held homogenizer (40 passes) and the lysates were clarified by centrifugation (800g at 4°C for 10 min). The supernatant was harvested and subjected to an additional centrifugation step at 16,600g for 10 min at 4°C. The supernatant arising from this step contained solubilized mitochondrial proteins.

4.13. Immunoblotting and immunoprecipitation

For immunoprecipitation of endogenous PINK1 from human skin fibroblasts, 150 µg of whole-cell lysate was incubated overnight at 4°C with 5 µg of protein G pre-bound to PINK1 antibody. The immunoprecipitations were washed four times with lysis buffer containing 150 mM NaCl, then twice with buffer containing 50 mM Tris–HCl pH 7.5, 0.1 mM EDTA, and eluted by resuspending in 20 µl of 1× SDS sample buffer. Denatured samples were subjected to SDS-PAGE (4–12% Bis-Tris gels) and were transferred on to 20% glycerol, the native dataset was collected at ID30A-1 beamline, European Synchrotron Radiation Facility (ESRF, Grenoble). Data were processed using Mosflm and Aimless in CCP4 [76], respectively. The final model obtained from Phaser was further constructed and refined using Coot (EMD-Research, London). ParkinS65N was crystallized at 4°C with 1% Triton X-100 and centrifuged at 13,000 r.p.m. for 10 min at 4°C. The supernatant arising from this step contained solubilized mitochondrial proteins.

4.15. Ubiquitin enrichment

His-Halo-Ubiquitin UBA-domain tetramer (HALO-UBA\(^{UBQLN1}\)) was expressed in E. coli BL21 cells, affinity purified on Ni-NTA-agarose and dialysed into 50 mM HEPES pH 7.5, 10% glycerol, 150 mM NaCl, 1 mM DTT [11]. For ubiquitin capture, 200–400 µg of whole-cell extract or 1 mg of membrane-enriched fraction was used for pull-down with HALO-UBA\(^{UBQLN1}\) [11]. HALO-UBA\(^{UBQLN1}\) was incubated with 200 µl of HaloLink resin (Promega) in binding buffer (50 mM Tris–HCl pH 7.5, 150 mM NaCl, 0.05% NP-40) overnight at 4°C under agitation [11]. HALO-TUBE beads (20 µl) were added to lysates and incubated at 4°C for 4 h under agitation. Beads were washed three times with lysis buffer containing 0.25 M NaCl, and eluted by resuspending in 20 µl of 1× LDS sample buffer containing 1 mM DTT.

4.16. Protein purification, crystallization and structure determination

Parkin S65N (Parkin\(^{S65N}\)) (Δ84–143) was cloned into pET156P vector (DU56345) and expressed as His-SUMO fusion in E. coli BL21 cells, using conditions similar to those described in Chaugule et al. [74]. His-tagged Parkin\(^{S65N}\) was purified using Ni-NTA resin. Protein eluted from Ni resin was incubated overnight at 4°C with SENP1 protease to remove the His-SUMO tag, and dialysed in 20 mM Tris pH 7.5, 75 mM NaCl and 250 µM TCEP buffer. Dialysed protein was further incubated with Ni-NTA resin and tag-free Parkin\(^{S65N}\) was collected in the flow through, purified on Mono-Q and Superdex-75 columns (as described in [64]) and concentrated to 8 mg ml\(^{-1}\) for crystallization. Parkin\(^{S65N}\) was crystallized at 4°C in 100 mM BIS-TRIS pH 5.5, 200 mM LiSO\(_4\) and 20% PEG3350 by using a vapour diffusion method under sitting drop. Crystals were flash frozen in 20% glycerol, the native dataset was collected at ID30A-1 beamline, European Synchrotron Radiation Facility (ESRF, Grenoble). Data were processed using Mosflm and Aimless in CCP4 (CCP4, 1994). Parkin\(^{S65N}\) structure was determined by molecular replacement using Phaser in CCP4, WT-Parkin (pdb id: 5C1Z) was used as the search model. The initial model obtained from Phaser was further constructed and refined using Coot [75] and REFMAC5 in CCP4 [76], respectively. The final model of Parkin\(^{S65N}\) shows excellent geometry (electronic supplementary material, table S4).

4.17. Human genetic analysis

4.17.1. Case 1 (S65N-M70)

Patient DNA samples were screened for variants using HaloPlex targeted sequencing of 82 selected PD-associated loci (Agilent Technologies, Santa Clara, CA, USA). DNA was extracted from peripheral blood by standard procedures. Sequencing was performed with a MiSeq sequencer (Illumina, San Diego, CA, USA), variant calling with Genome Analysis Toolkit [77] and the annotation with ANNOVAR [78]. The variants were confirmed by independent DNA sequencing method, Sanger sequencing. For the c.194G>T variant in PARK2 we used the following PCR and sequencing primers for PCR and sequencing: 5’-CTCGCA TTCATGTTTGACATTTCC; 5’-ATGCTCATGCAGACTG
CACTAAAG; sequencing 5’-CCTGCTGTCAGTGTGCAG AATG. The frequency of variants was screened from ExAC (http://exac.broadinstitute.org/) and gnomAD browsers (http://gnomad.broadinstitute.org) [79], the potential pathogenic effects were evaluated using CADD C-score [42] and conservation using UniProt [80].

4.17.2. Case 2 (S65N-F60)

We downloaded the clinical data of case 2 (ID 3185) from the Parkinson’s Progression Markers Initiative (PPMI) database (www.ppmi-info.org/data) on 13 August 2018. PPMI is a multi-centre, on-going longitudinal and observational study, which contains clinical, imaging and biological data from 454 PD patients and 215 control patients currently stored at the Laboratory of Neuro Imaging (LONI) database at University of California, Los Angeles (UCLA). The cohort consists of 620 females and 828 males. The open-access repository is available online after registration at http://www.ppmi-info.org/. Informed consent was signed by the patients enrolled in the PPMI study. The patient’s DNA whole-genome sequence data were downloaded from PPMI repository on 8–11 September 2018 and we filtered all coding variants in 82 PD-associated loci (used in-targeted sequencing panel of patient S65N-M70 (ID3185) excluding mitochondrial DNA) with a CADD C-score of over 20 and a carrier frequency less than 1%. Polyphen-2 [81] HVAR-based predictions are provided for each variant.

Ethics. All animal studies and breeding in Dundee were approved by the University of Dundee ethical review committee, and further subjected to approved study plans by the Named Veterinary Surgeon and Compliance Officer (Dr. Nairen Dennison) and permitted under a UK Home Office project licence in accordance with the Animal Scientific Procedures Act (ASPAA, 1986). Associated collaborative institutes which contributed to the present study (mouse behaviour and histology—Cardiff University, UK; mitochondrial respiration analyses—CNRS, Paris, FR) also received institutional ethical approval. Informed consent was obtained from Case 1. Ethical approval for the study (Dnr 432/19/9/07) was given by the Ethics Review Board of Helsinki University Central Hospital. We used UPDRS and Modified Hoehn and Yahr scales to evaluate current progression of the disease. Informed consent was signed by the patients enrolled in the PPMI study. The authors have agreed to PPMI Data Use Agreement. The manuscript was reviewed by PPMI Data & Publications Committee (DPC) prior to submission.

Data accessibility. Coordinates and structure factors have been deposited into the PDB database (PDB ID 6HUE).

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