The Parkinson’s disease-associated protein DJ-1 plays a positive nonmitochondrial role in endocytosis in Dictyostelium cells

Suwei Chen1,2, Sarah J. Annesley1, Rasha A. F. Jasim1,3, Vanessa J. Musco1, Oana Sanislav1 and Paul R. Fisher1,*

ABSTRACT

The loss of function of DJ-1 caused by mutations in DJ1 causes a form of familial Parkinson’s disease (PD). However, the role of DJ-1 in healthy and in PD cells is poorly understood. Even its subcellular localization in mammalian cells is uncertain, with both cytosolic and mitochondrial locations having been reported. We show here that DJ-1 is normally located in the cytoplasm in healthy Dictyostelium discoideum cells. With its unique life cycle, straightforward genotype-phenotype relationships, experimental accessibility and genetic tractability, D. discoideum offers an attractive model to investigate the roles of PD-associated genes. Furthermore, the study of mitochondrial biology, mitochondrial genome transcription and AMP-activated protein kinase-mediated cytopathologies in mitochondrial dysfunction have been well developed in this organism. Unlike mammalian systems, Dictyostelium mitochondrial dysfunction causes a reproducible and readily assayed array of aberrant phenotypes: defective phototaxis, impaired growth, normal rates of endocytosis and characteristic defects in multicellular morphogenesis. This makes it possible to study whether the underlying cytopathological mechanisms of familial PD involve mitochondrial dysfunction. DJ-1 has a single homologue in the Dictyostelium genome. By regulating the expression level of DJ-1 in D. discoideum, we show here that in unstressed cells, DJ-1 is required for normal rates of endocytic nutrient uptake (phagocytosis and, to a lesser extent, pinocytosis) and thus growth. Reduced expression of DJ-1 had no effect on phototaxis in the multicellular migratory slug stage of Dictyostelium, but resulted in thickened stalks in the final fruiting bodies. This pattern of phenotypes is distinct from that observed in Dictyostelium to result from mitochondrial dysfunction. Direct measurement of mitochondrial respiratory function in intact cells revealed that DJ-1 knockdown stimulates whereas DJ-1 overexpression inhibits mitochondrial activity. Together, our results suggest positive roles for DJ-1 in endocytic pathways and loss-of-function cytopathologies that are not associated with impaired mitochondrial function.

KEY WORDS: Dictyostelium, DJ-1, Endocytosis, Macropinocytosis, Mitochondrial dysfunction, Parkinson’s disease, Phagocytosis, Respiration

INTRODUCTION

Attention was first drawn to the role of DJ-1 in Parkinson’s disease (PD) with the report by Bonifati et al. (2003) of the first two DJ-1-related PD cases, involving a 14 kb deletion from a Dutch kindred and an L166P mutation from an Italian background. Human DJ-1 is a protein of 189 amino acids encoded by the ~24 kb DJ1 gene (also known as PARK7) at chromosome 1p36. Although the early-onset PD caused by deletions or mutations of DJ-1 appears to be rare, Choi et al. (2006) suggested that DJ-1 might also play a crucial role in sporadic late-onset PD, the majority of PD cases, because greater oxidative damage to DJ-1 and elevated DJ-1 protein levels were found in the postmortem brains of sporadic PD patients. Therefore, it is very important to understand how DJ-1 exerts its function both in healthy cells and in familial and idiopathic PD.

Various putative functions of DJ-1 in PD have been proposed, including roles as a redox-sensitive chaperone, antioxidant, transcriptional regulator, protease and protein deglycase (Shendelman et al., 2004; Taira et al., 2004; Xu et al., 2005; Chen et al., 2010; Richarne et al., 2015). DJ1 was also shown to interact with other PD-linked genes, such as PINK1 and α-synuclein, which have been reported to cause PD through mitochondrial dysfunction (Belina et al., 2005; Dev et al., 2003). These interactions imply that DJ-1 might function as an indirect regulator in PD. Nevertheless, the possible role of DJ-1, which is implied in the pathology of PD, remains poorly understood. In addition, the subcellular localization of DJ-1 has been very controversial, because the cytoplasm, nucleus and mitochondria have all been proposed as its site of residence in the cell (Bonifati et al., 2003; Canet-Avilés et al., 2004; Zhang et al., 2005; Junn et al., 2009).

The Dictyostelium mitochondrial disease model is well established and features characteristic and reproducible phenotypic outcomes that in most cases depend on chronic hyperactivity of the energy-sensing protein kinase AMPK (Francione et al., 2011). These aberrant phenotypes include impaired growth and phototaxis and abnormal morphogenesis. If loss of DJ-1 function causes pathology by a mechanism involving impaired mitochondrial function, it should phenocopy the effects of mitochondrial disease. We show here that this is not the case in the Dictyostelium model. Instead, Dictyostelium DJ-1 is localized in the cytoplasm, where its loss causes cytopathological defects in two endocytic pathways, phagocytosis and macropinocytosis, that are unaffected by mitochondrial dysfunction. In support of this, we use Seahorse respirometry on intact cells to show that knockdown of DJ-1 causes a small but significant activation of mitochondrial respiratory function, whereas overexpression inhibits mitochondrial activity.

RESULTS

A single homologue of human DJ-1 was identified in the D. discoideum proteome

The protein sequence of human DJ-1 was used at DictyBase with a Basic Local Alignment Search Tool (BLAST) search, and a single
homologous protein encoded in the *D. discoideum* genome was identified. The local sequence alignment is shown in Fig. 1.

**Dictyostelium DJ-1 is localized in the cytoplasm, not in the mitochondria**

The subcellular localization of DJ-1 in mammals is controversial, with conflicting reports of mitochondrial localization (Zhang et al., 2005; Canet-Aviles et al., 2004). To examine the subcellular localization of *Dictyostelium* DJ-1, we first made in silico predictions using Web-based software, including MitoProt II, Helical Wheel and Predotar. The results showed that DJ-1 does not have a characteristic mitochondrial targeting signal in the form of a positively charged amphipathic helix at its N-terminus and is unlikely to be localized to the mitochondria, while Predotar predicted that an endoplasmic reticulum (ER) location might be possible (Fig. S1 and Table S1).

To determine whether the prediction of a nonmitochondrial location for *Dictyostelium* DJ-1 was correct, we created *D. discoideum* cell lines expressing a DJ-1:GFP fusion protein and examined the cells by deconvolution fluorescence microscopy. Fig. 2 shows that DJ-1 was predominantly cytoplasmic, with no evidence of localization in the mitochondria. This was true both in fixed cells (Fig. 2) and in live cells (Fig. S3) and was confirmed by immunofluorescence microscopy of fixed cells using an anti-GFP antibody to detect the GFP (Fig. S4). A western blot separately confirmed that the DJ-1:GFP fusion protein is expressed and has the expected molecular mass in transformants containing the fusion protein construct (Fig. S5).

To determine whether the cytoplasmic localization of the fusion protein was affected by oxidative stress, we grew cells for 24 h in the presence of inhibitory concentrations of H$_2$O$_2$ (Fig. 2; Fig. S6). The effective inhibitory concentrations were determined by measuring growth rates in these conditions at H$_2$O$_2$ concentrations ranging up to ~1.2 mM (Fig. 2E). The concentration giving 50% of maximal inhibition (IC$_{50}$) was found to be 150 µM, and growth was almost completely prevented at 300 µM. The cytoplasmic localization of DJ-1:GFP was unchanged by exposure of the cells to either of these concentrations (Fig. 2C,D).

**Generation of Dictyostelium transformants with altered DJ-1 expression**

To study the roles of DJ-1 in otherwise healthy cells, we created *Dictyostelium* transformants with altered levels of DJ-1 expression. Antisense-inhibition (pPROF688) and overexpression constructs (pPROF9690) were created and transformed into the parental *D. discoideum* strain AX2 (see Fig. S2 for maps of the plasmid constructs). The plasmid constructs in transformants undergo rolling circle replication to generate multiple copies of the construct, which are integrated randomly into the *D. discoideum* genome by recombination (Barth et al., 1998). This generates stable transformants containing various numbers of copies of the construct, so that each transformant expresses the gene at a different level. The number of copies of the inserted constructs was determined by qPCR, and relative expression levels were measured using qRT-PCR. The relationships between the DJ-1 expression levels and the copy numbers of the antisense and overexpression constructs (Fig. 3) were determined. The antisense inhibition construct reduced DJ-1 mRNA expression by up to about threefold (change of 1.65 qPCR threshold cycles), whereas overexpression resulted in as much as a 23-fold increase in expression (change of 4.5 qPCR threshold cycles) compared with AX2. Thus, the total range in expression levels was nominally about 70-fold from the greatest level of knockdown to the highest level of overexpression.

This approach of combining knockdown and overexpression with analysis of the copy number dependence of the outcomes offers several advantages. It is simple, reliable, lends itself to the study of essential genes and excludes the possibility of phenotypes being caused by unknown genetic events elsewhere in the genome, because such events are random, affect any given phenotype with low probability and are different in every transformant and uncorrelated with construct copy number. Furthermore, regression analysis of the phenotypic outcomes in multiple transformants over a range of copy numbers provides a more sensitive means of reliably detecting abnormalities than can be obtained in the study of one (or two) knockout mutants (which might also contain additional, unknown genetic alterations). In this case, we did not attempt isolation of a knockout strain because of the expectation that it could be lethal.

**Cytoplasmic DJ-1 is needed for normal rates of phagocytosis and micropinocytosis, and reduced levels do not phenocopy mitochondrial dysfunction**

To determine the effects of changing the levels of DJ-1 expression, the *D. discoideum* transformants expressing various levels of DJ-1 were analysed phenotypically. If PD cytopathology accompanying DJ-1 deficiency is caused by mitochondrial dysfunction, it should phenocopy the outcomes of mitochondrial disease in *D. discoideum*; these include slow growth, impaired slug phototaxis and defective fruiting body morphology, but no changes in phagocytosis or pinocytosis (except in some isolated respiratory complex deficiencies; Francione et al., 2011; Annesley et al., 2014).

Phototaxis was unaffected by altered levels of DJ-1. *D. discoideum* slugs are able to sense light sensitively and move towards it with great accuracy (Fisher, 2001). This enables the slug...
to migrate to the surface of the soil, which is an optimal location for culmination into a fruiting body and spore dispersal. The photosensory pathway was shown by Wilczynska et al. (1997), Kotsifas et al. (2002), Torija et al. (2006) and others to be sensitive to impaired mitochondrial function. The resulting defect in phototaxis is mediated by chronically hyperactive AMP-activated protein kinase (AMPK), an energy-sensing protein kinase involved in homeostatic regulation of mitochondrial ATP production (Bokko et al., 2007).

Irrespective of the copy number, phototaxis by slugs of the DJ-1 antisense-inhibited and overexpression transformants displayed highly accurate phototaxis resembling that of the wild type, as shown in Fig. 4. This is different from the features displayed by D. discoideum strains with mitochondrial dysfunction, which show disoriented phototaxis, and suggests that DJ-1 does not play a role in photosensory signal transduction and that its reduction does not cause mitochondrial dysfunction in normal conditions.

DJ-1 positively regulates growth on bacterial lawns and phagocytosis in D. discoideum

Mitochondrially diseased Dictyostelium strains showed decreased growth on bacterial lawns. To investigate whether DJ-1 is involved in regulating growth and whether it might be involved in mitochondrial dysfunction, the DJ-1 transfectants were analysed for their ability to grow on normal agar plates containing a lawn of Escherichia coli B2. The rate of plaque expansion was calculated and compared with wild-type AX2. Fig. 5A shows that DJ-1 knockdown decreases plaque expansion rates, whereas overexpression increases plaque expansion rates. This elevated rate of plaque expansion was also exhibited by cells expressing the DJ-1:GFP fusion protein (strain HPF1246), which grew 30% faster than wild type on E. coli B2 lawns ($P=1.8 \times 10^{-6}$, multiple linear regression of plaque diameters versus time).

The rate of D. discoideum plaque expansion on bacterial lawns is controlled by phagocytosis rate, growth rate and motility of the
amoebae. To determine whether the increased rate of plaque expansion on bacterial lawns could be explained by increased rates of phagocytosis, we measured the rate of uptake of fluorescently labelled bacterial prey. Fig. 5B shows that knockdown of DJ-1 expression reduced phagocytosis rates, whereas increased expression resulted in greater phagocytosis rates. The magnitude of the effect across the whole range of DJ-1 expression levels was two- to threefold, similar to the effect on plaque expansion rates. Not surprisingly, the phagocytosis and plaque expansion rates were also correlated with one another (not shown). These results suggest that the changes in plaque expansion rates were attributable to effects of DJ-1 levels on the phagocytosis rates. This is unlike most forms of mitochondrial disease in Dictyostelium, in which, except for some isolated Complex I-specific defects, growth on bacterial lawns is impaired but phagocytosis is unaffected (Francione et al., 2011).

DJ-1 modestly upregulates axenic growth and pinocytosis

Laboratory strains of D. discoideum are also able to grow axenically, without a bacterial food source, in nutrient broth (HL-5). To determine whether changing the expression of DJ-1 has effects on axenic growth, the generation time of wild-type AX2 and the DJ-1 antisense-inhibited and overexpression transfectants was measured. Fig. 6A shows that the growth rate increases (generation time decreases) modestly with increasing DJ-1 expression. Although statistically significant and consistent with the effects on growth on bacterial lawns, this effect is only small, with a 2 h (~20%) decrease in generation time over the ~70-fold range in DJ-1 mRNA expression levels between the highest copy numbers of the antisense and overexpression constructs. It is dissimilar in magnitude from the large impairment of growth in axenic medium observed in all mitochondrially diseased Dictyostelium strains (Francione et al., 2011).

To determine whether the foregoing changes in growth rates in liquid medium were attributable to changes in the ability of the transfectants to ingest nutrients from the liquid medium, the rates of pinocytosis were measured. The pinocytosis rates did correlate weakly with the expression of DJ-1 (Fig. 6B), changing by ~20% across the full range of DJ1 gene expression. This suggests that the slight effects on the generation time in liquid medium were a result of similar modest effects on the rate of pinocytosis. Except for some Complex I-specific defects, mitochondrial disease in Dictyostelium does not cause impairment of pinocytosis (Francione et al., 2011).

DJ-1 is required for normal fruiting body morphology

When their bacterial food source is depleted, D. discoideum amoebae aggregate and undergo multicellular differentiation, ultimately resulting in the formation of a fruiting body that consists of a sorus containing spores supported by a stalk and basal disc consisting of vacuolated cells (Strmecki et al., 2005). Mitochondrial dysfunction and activation of AMPK in D. discoideum results in altered fruiting body morphology, with fewer fruiting bodies that have shorter and thicker stalks (Kotsifas et al., 2002; Bokko et al., 2007). To investigate whether DJ-1 was involved in regulating normal fruiting body morphogenesis, the
mitochondrial respiratory activity directly in the parental AX2 strain. This is so, we used Seahorse respirometry (Lay et al., 2016) to assay damage to mitochondrial respiratory functions. To verify whether the cytosolic location of DJ-1 and the failure of DJ-1 knockdown to phenocopy mitochondrial dysfunction suggest that loss of function of this protein can cause cytopathology without causing an increase in the expression of DJ-1 did not result in any alterations in the expression levels were increased. The linear regression was statistically significant (F test). Error bars are the s.e.m. from three independent experiments.

fruiting bodies of the wild-type AX2 and DJ-1 transformants were observed. A reduction in the expression of DJ-1 resulted in aberrant fruiting bodies with larger sori and shorter, thicker stalks, whereas an increase in the expression of DJ-1 did not result in any alterations when compared with AX2 (Fig. 7). Although this phenotype is present in mitochondrially diseased Dictyostelium strains, it is also caused by lysosomal defects in Dictyostelium models for Batten disease (Chavan, 2015). The various forms of Batten disease are neurodegenerative disorders caused by mutations in lysosomal or ER proteins, and they produce lysosomal, vesicle trafficking and autophagy abnormalities (Narayan et al., 2006; Siintola et al., 2005; Wavre-Shapton et al., 2015). The short, thick stalks in DJ-1 knockdown strains thus constitute a phenotype which, in isolation, does not allow a distinction to be made between mitochondrial and lysosomal disorders.

**DJ-1 inhibits and its loss activates respiration by functionally normal oxidative phosphorylation complexes**

The cytosolic location of DJ-1 and the failure of DJ-1 knockdown faithfully to phenocopy mitochondrial dysfunction suggest that loss of function of this protein can cause cytopathology without causing damage to mitochondrial respiratory functions. To verify whether this is so, we used Seahorse respirometry (Lay et al., 2016) to assay mitochondrial respiratory activity directly in the parental AX2 strain and in DJ-1 antisense-inhibited and overexpressing strains. We found that reduced levels of DJ-1 expression slightly enhanced, whereas overexpression inhibited key parameters of mitochondrial respiratory function, namely the basal O2 consumption rate (OCR; Fig. 8A), the O2 consumption attributable to respiratory ATP synthesis (Fig. 8B), and the uncoupled respiration rate (Fig. 8C) and Complex I (Fig. 8D) activities. Regression analysis of O2 consumption by ATP synthesis versus basal OCR (Fig. 8E), and Complex I activity versus the uncoupled OCR (Fig. 8F) showed that the antisense, control and overexpression strains all fell on the same straight line. This shows that ATP synthase and Complex I are functionally normal, making the same relative contribution to respiration in the antisense and overexpression strains. Similar results were observed (Fig. S7) with all other assayed components of respiration. Thus, changes in the level of expression of DJ-1 affect only the total level of respiratory activity, not the functionality of individual complexes. We conclude that loss of DJ-1 does not impair but activates mitochondrial respiratory function, whereas overexpression causes clear reductions in all mitochondrial respiratory activity. These effects are not consistent with a protective role for DJ-1 in the mitochondria and must be indirect because the protein is not localized to the mitochondria.

**DISCUSSION**

Mutations of DJ-1 (14 kb deletion and L166P) have been found to be associated with autosomal recessive early-onset PD, which is considered to result from loss of function of the DJ-1 protein (Bonifati et al., 2003). Accordingly, DJ-1 is believed to play a normally protective role in the cell by functioning as a molecular chaperone, antioxidant, transcriptional regulator, protease and/or protein deglycase (Bonifati et al., 2003; Taira et al., 2004; Shendelman et al., 2004; Paterna et al., 2007; Clements et al., 2006; Olzmann et al., 2004). Mitochondrial dysfunction has been implicated in the pathogenesis of PD, and DJ-1 has been suggested to have a protective role in mitochondrial function (Larsen et al., 2011). However, Giaime et al. (2012) found that DJ-1 knockout...
does not impair mitochondrial respiratory function in primary mouse embryonic fibroblasts.

To exert a putative protective role in the mitochondria, DJ-1 needs to be localized to the mitochondria. Conflicting data in this regard have been presented in the literature. Zhang et al. (2005) found that DJ-1 localized to the mitochondrial matrix and inter-membrane space in mouse brain tissues and human neuroblastoma cells. However, Canet-Avlés et al. (2004) found that DJ-1 has very little specific localization to mitochondria in M17 human neuroblastoma cells, although treatment with paraquat (pQ2+) created an oxidative stress and led to the translocation of DJ-1 to the mitochondria. In the present study, three in silico bioinformatics tools (MitoProt II, Predotar and Helical Wheel) were used to predict the subcellular localization of DJ-1. The helical wheel plot of DJ-1 did not exhibit the characteristic positively charged amphiphilic α-helix at the N-terminus that constitutes the mitochondrial targeting
signal for most mitochondrial proteins (Fig. S1B). In addition, mitochondrial proteins usually contain an arginine residue, which can be recognized by mitochondrial processing peptidases and mitochondrial intermediate peptidases (Endo and Kohda, 2002; Mills et al., 2008). These enzymes remove the leader peptide upon import of the protein into the mitochondrial matrix, to produce the mature mitochondrial protein. DJ-1 does contain an arginine (R29) near the N-terminus, but the surrounding sequence does not conform to the consensus target site for mitochondrial processing peptidases (Lee et al., 2003).

Fluorescence microscopy using a GFP-tagged DJ-1 (Fig. 2; Figs S3, S4, S6) supported this, by showing that DJ-1 is cytoplasmic both in unstressed and in oxidatively stressed cells. Like the wild-type protein, expression of the DJ-1-GFP fusion protein caused accelerated growth on a bacterial lawn. This suggests that the GFP-tagged protein is functionally normal and that its subcellular location thus reflects that of the wild-type protein.

Although DJ-1 is localized in the cytoplasm, its loss could impair mitochondrial function indirectly. If so, mitochondrial respiration should be impaired by DJ-1 loss (knockdown) and enhanced by its overexpression. When we measured mitochondrial respiratory activity directly in intact, living Dictyostelium cells, we found that the reverse was true; DJ-1 knockdown resulted in a small, but statistically significant increase in mitochondrial respiration, whereas overexpression caused a reduction in the key parameters of mitochondrial respiratory activity. It is of interest that similar respirometric measurements in intact human cells recently revealed enhanced mitochondrial respiration both in lymphoblasts from idiopathic PD patients (Annesley et al., 2016) and in fibroblasts from Parkin-null genetic PD patients (Haylett et al., 2016).

*Dictyostelium* is an established mitochondrial disease model, with highly predictable and reproducible disease phenotypes. If the loss of DJ-1 causes mitochondrial respiratory dysfunction, the *Dictyostelium* model of PD created by DJ-1 knockdown would phenocopy the well-established outcomes of mitochondrial disease. The results reported here show that this does not happen. Firstly, the phototaxis defect that is observed in all mitochondrially diseased *Dictyostelium* strains (Wilczynska et al., 1997; Kotsifas et al., 2002; Bokko et al., 2007; Francione et al., 2009) was not present in DJ-1 knockdown strains. Secondly, the DJ-1 knockdown strains exhibited growth defects associated with commensurately impaired rates of endocytosis, a feature not present in mitochondrially diseased strains, with the exception of some isolated Complex I-specific defects (Kotsifas et al., 2002; Torija et al., 2006; Bokko et al., 2007). Thirdly, the growth defects observed in mitochondrially diseased strains are equally severe whether the cells are grown on bacterial lawns or in liquid medium. This was not the case with the DJ-1 knockdown strains, in which the impairment of phagocytosis and growth on bacterial lawns was much more severe than the slight effects on macrophagocytosis and growth in liquid medium. These results showing differential dependence of different types of endocytosis on DJ-1 are reminiscent of those of Kim et al. (2013), who reported that astocytes of DJ-1 knockout mice exhibit impaired lipid raft-dependent but not clathrin-dependent endocytosis. DJ-1 was associated with lipid rafts, where it was required for CD14-dependent endocytosis of the pattern recognition receptors TLR3 (recognizing double-stranded RNA) and TLR4 (recognizing bacterial lipopolysaccharide). These observations and the role of DJ-1 in phagocytosis in *Dictyostelium* are consistent with the reported role of lipid rafts in phagocytosis (Nagao et al., 2011).

Under nutrient deprivation *Dictyostelium* amoebae differentiate, chemotactically aggregate and undergo a transition to a multicellular differentiation programme that ultimately results in formation of a fruiting body that consists of a sorus containing spores and a long slender stalk and basid disc that contain dead, vacuolated cells, the end product of a form of autophagic cell death. This process, which is affected by defects both in mitochondrial respiration and in lysosomal function, results in more cells entering the stalk differentiation rather than the spore differentiation pathway (Bokko et al., 2007; Francione et al., 2011; Chavan, 2015). The result is fruiting bodies with short, thick stalks, as we observed in this work in our DJ-1 antisense-inhibited transformants (Fig. 7A). This suggests that DJ-1 plays a role in preventing cells from differentiating into stalk cells, possibly through preventing autophagic cell death.

The results presented here show that rather than impairing mitochondrial respiration, the loss or reduction of function of DJ-1 in Parkinson’s disease cells produces defects in particular endocytic pathways, downstream vesicle trafficking and related processes. At least 17 other Parkinson’s disease-related proteins also play normal and cytopathological roles in endolysosomal trafficking, and another six are associated with autophagic trafficking to the lysosome of defective organelles and protein aggregates (Abeliovich and Gitter, 2016). The outcome of reduced DJ-1 expression in *Dictyostelium* is chronic nutritional stress and slow growth, accompanied by elevated autophagic cell death in the form of short, thick stalks.

It has been suggested from work on cell lines and animal models that DJ-1 plays a protective role in cells, shielding them from the adverse downstream consequences of oxidative and other stresses (Bonifati et al., 2003; Taira et al., 2004; Inden et al., 2006; Paterna et al., 2007; Hwang et al., 2013). Although we did not explicitly stress the cells in most experiments reported in this paper, even healthy cells experience background levels of a variety of stresses including oxidative stress, unfolded proteins, DNA damage and the like. However, to determine whether DJ-1 translocates to the mitochondria under oxidative stress, we exposed growing cells to inhibitory concentrations of H$_2$O$_2$ for 24 h. The cytoplasmic localization of the DJ-1-GFP fusion protein was unaffected by this treatment. Given that DJ-1 has protective molecular chaperone, protease and protein deglycase activities, it could exert these functions normally in nonmitochondrial locations to protect endocytic and associated vesicle trafficking pathways from the cytopathological consequences of oxidative and other stresses. Our results do not allow us to distinguish between positive regulatory or protective roles for DJ-1 in endocytosis, but they do reveal that the loss of DJ-1 function can cause cytopathological consequences in particular endocytic pathways that are not associated with impaired mitochondrial function. It will be of interest in future work to determine whether these roles of DJ-1 role depend on its proteolytic, deglycation or chaperone functions.

The abnormal phagocytosis, growth and morphogenesis in DJ-1 knockdown strains are similar to those caused by high levels of ectopic expression in *Dictyostelium* of wild-type and mutant forms of another PD-associated protein, human $\alpha$-synuclein (Fernando, 2012). As in the work described in this paper, the $\alpha$-synuclein was not localized in the mitochondria but in the cytosol (albeit concentrated in the cortical regions), and the pattern of phenotypes was unlike that observed in mitochondrially diseased strains. In mammalian cells, mutant $\alpha$-synuclein (A30P) expression impairs proteasomal activity, possibly via interaction with a subunit of proteasome regulatory complexes (Ghee et al., 2000;
Tanaka et al., 2001). It will be of interest in future experiments to study potential interactions between DJ-1 and α-synuclein in the Dictyostelium cytosol.

The existence of nonmitochondrial endocytic defects resulting from reduced DJ-1 expression suggests that the cytopathological mechanisms underlying Parkinson’s disease include processes not involving mitochondrial dysfunction. However, this does not exclude the possibility of additional pathological mechanisms, particularly in oxidatively stressed cells. It will be valuable to examine this possibility in future work.

MATERIALS AND METHODS

Bioinformatic analysis of Dictyostelium DJ-1

A BLAST at DictyBase (the international dictyostelid genomics resource at http://dictybase.org; Basu et al., 2013) was used to identify the homologue of human DJ-1 in the D. discoideum proteome using the protein sequence of human DJ-1. The programs MitoProt II, Predotar and Helical Wheel were used to predict the possibility of subcellular localization of DJ-1.

Plasmid constructs

DJ-1 antisense construct pPROF688 and DJ-1 sense construct pPROF690 were created by subcloning a fragment of the DJ1 gene (75-479 bp) and the whole DJ1 gene into the vector pDNeo2 (Witke et al., 1987) and the vector pPROF267 (generated by S.J.A., unpublished data) by replacing the GFP gene cassette with the Tet cassette from pPROF74 and additional restriction enzymes sites included for cloning purposes. The construct pPROF693 was generated by insertion of the DJ1 gene in frame into pA15GFP for expression of DJ-1::GFP fusion protein.

D. discoideum strains and culture conditions

All experiments were conducted with D. discoideum parental strain AX2 and transformants (derived from it) (Wilczynska et al., 1997). Strains HPF1164-

Restriction sites at the 5'-end and 3'-end of the 405 bp gene fragment from the endogenous DJ1 gene (75-479 bp) were included for cloning purposes. The construct pPROF693 was generated by insertion of the DJ1 gene in frame into pA15GFP for expression of DJ-1::GFP fusion protein.

DNA and RNA molecular manipulation

General gene cloning and sequence analysis were conducted as described previously (Wilczynska et al., 1997; Kotsiás et al., 2002). Fragments of interest were amplified using gene-specific primers containing added restriction sites at the 5’ end for cloning and subcloning purposes. Constructs were verified by restriction endonuclease digestion and DNA sequencing [Australian Genome Research Facility (AGRF), Melbourne]. Sequence alignment and database searches were performed using software BioEdit and Web-based software at ExPASy (http://www.expasy.org).

Polymerase chain reaction

A 405 bp DJ1 gene encoding the DJ-1 antisense fragment was cloned, cloned into pUC18 and subcloned into pDNeo2 vector with primers DAF (5’-GGCAATTGGTTGGGCTAGAGG-3’) and DAR (5’-GGCAATTCGATCCGATACCTGTTGGCACC-3’). The length of DJ-1 was amplified, cloned into pUC18 and subcloned into pPROF267 with primers DOEF (5’-GGCAATTCGATGCCAATAACAAAAATA-TTTATTATATTTGAAAGG-3’) and DOER (5’-GGCAATTCGCCGA-GTTAAAAACCATTAAGTTTTACCTTTTTAGC-3’). The DJ1 gene without the stop codon was amplified and cloned into the pUC18 vector and subcloned into pA15GFP for expression of DJ-1::GFP with the same forward primer as DOEF and DGFPR (5’-GGCAATTCGATCGATAAAAA-CCTTAAAGGTCTTTTTACTTTTTTACC-3’).

Quantitative PCR (qPCR)

The construct copy numbers in D. discoideum transformants were measured by quantitative PCR using iQ SYBR Green Supermix as instructed by the manufacturer (Bio-Rad). The gDNA of D. discoideum AX2 was used to create a standard curve for estimation of the quantity of gDNA. The filamin gene (Annesley et al., 2007) was used as a reference housekeeping gene, and primers were designed using software Primerquest to amplify a 100 bp fragment from the endogenous filamin. The reaction was performed using an iCycler IQ Multicolor Real-Time PCR Detection System (Bio-Rad). The calculation of copy numbers for each gene was based on comparison of their average Ct values (threshold cycle) with those for filamin (control for gDNA concentration) in unknown and parental AX2 (control for gene’s quantity in chromosomal DNA). The linear relationship of the logarithm of the DNA amount (Starting Quantity) and its Ct value enables the calculation of gene copy numbers in transformants.

Quantitative one-time reverse transcriptase-PCR (qRT-PCR)

The RNA was quantitated by iScriptTM One-Step RT-PCR Kit. The RNA from all strains was extracted and treated with DNase I before it was mixed with SYBR Green RT-PCR reaction mix, primers and iScript reverse transcriptase. Two transformants was chosen randomly for use as negative controls, in which iScript reverse transcriptase was not added. The reaction was carried out in an iCycler IQ Multicolor Real-Time PCR Detection System (Bio-Rad), and the copy numbers of cDNA were calculated as described for qPCR.

Fluorescence microscopy

Axenically grown cells were allowed to settle onto glass coverslips for 30 min. For immunofluorescence, the HL-5 liquid media supplemented with 50 μg streptomycin ml⁻¹, 10 μg tetracycline ml⁻¹ and 100 μg ampicillin ml⁻¹. All antibiotics were removed when growing cells for and conducting all phenotypic assays. This ensures the stability of the transformants, as they are not maintained for long periods without selection, while also removing the possibility of an effect of the antibiotics themselves on the resulting phenotypes. Stock cultures for all strains were kept frozen in DMSO.

Isolation and molecular manipulation of DNA and RNA

DNA and RNA isolation

Plasmid DNA isolation was adapted from Birnboim and Doly (1979) and Birnboim (1983); and the PureLinkTM HiPure Plasmid Filter Purification Kit and the PureLinkTM HiPure Precipitation Module (Invitrogen) were used for the large-scale extraction of plasmid DNA. DNAzol (Molecular Research Center) and TRizol reagent (Gibco BRL) were used to isolate genomic DNA and RNA from D. discoideum transformants according to the instructions of the manufacturer. The CsCl isolation method was used for the large-scale isolation of D. discoideum genomic DNA as described in DictyBase (http://dictybase.org).
Otherwise, fixation was performed for 10 min in 300 μl 4% paraformaldehyde in PBS followed by 10 min in 4% paraformaldehyde plus 0.2% Triton X-100, then by two washes in PBS and 7 min incubation in 0.2 M glycine in PBS. The coverslip was then washed three times in PBS, once in dH2O and finally mounted onto a slide using 5 μl of mounting media with DAPI (Duolink).

The cells were observed with an Olympus BX 61TRF microscope. The digital images were captured with an Olympus DP80 camera. For deconvolution microscopy, the image was deconvolved after background subtraction, using Olympus cellSens Dimension 1.16 software. Deconvolution removes out-of-focus light to produce a result similar to laser confocal microscopy.

To examine the effect of oxidative stress, the same procedures were followed, except that the cells were exposed to inhibitory concentrations of H2O2, (150 and 300 μM) for 24 h in axenic medium before and during the Mitotracker Red staining.

**Transformation of D. discoideum and phenotypic analysis**

**Transformation of Dictyostelium**

All transformants were obtained using the Ca(PO4)2/DNA coprecipitation method developed by Nellen et al. (1984) with minor alterations and isolated by growing on Micrococcus luteus lawns on SM agar supplemented with 20 μg ml⁻¹ G418 described by Wilczynska and Fisher (1994).

**Phenotypic analysis of Dictyostelium strains**

**Plaque expansion**

Dictyostelium strains were inoculated in the centre of a Normal agar plate containing a lawn of E. coli B2, with four replicates for each strain. The plates were incubated at 21°C, and the diameter of the plaque was measured twice each day at ~8 h intervals for 100 h. The statistics software package ‘R’ was used to calculate and analyse the plaque expansion rate (in mm/h) using linear regression analysis.

**Phototaxis analysis**

The phototaxis assay was performed using the methods developed by Wilczynska and Fisher (1994) and Fisher and Annesley (2006). D. discoideum colonies growing on K. aerogenes lawns were collected and spotted onto charcoal agar plates. The plates were placed into black polyvinylchloride (PVC) boxes with a 4 mm hole drilled in one side and incubated at 21°C for 24-36 h with the hole facing a lateral light resource. The amoebae aggregated and formed slugs, which migrated over the agar surface leaving a trail of collapsed slime sheath, which was analysed and transferred to PVC discs and stained with 0.3% (v/v) Coomassie Blue R. The stained slug trails were digitized as described by Darcy et al. (1994) using a Summagraphics MM1201 digitizing tablet connected to a Linux workstation.

Growth in HL-5 broth

The axenic growth of D. discoideum strains was conducted and its growth rate measured as previously described (Bokko et al., 2007). The Dictyostelium cells were inoculated into HL-5 liquid medium and incubated at 21°C, shaking at 150 rpm. Cells were counted using a haemocytometer (Scientific Instruments) twice a day at an interval of 7-8 h for >100 h. The programmable software package ‘R’ was used for statistical analysis and calculation of generation time after log-linear regression analysis. In some experiments, to determine the inhibitory effects of oxidative stress on growth, the medium was supplemented with H2O2 at concentrations in the micromolar range and up to ~1.2 mM.

**Phagocytosis**

The phagocytosis rate of Dictyostelium strains was determined using the prey of E. coli cells, which express a fluorescent protein named DSRed (Maselli et al., 2002; Bokko et al., 2007). The E. coli DSRed cells were inoculated into Luria broth containing ampicillin (75 μg ml⁻¹) and 1 mM IPTG and incubated at 37°C until the density reached 2×10⁸ bacteria ml⁻¹ before being harvested and resuspended in 10-15 ml of 20 mM phosphate buffer. D. discoideum wild-type AX2 and transformants were grown, harvested, resuspended in 1 ml of 20 mM phosphate buffer and transferred into a scintillation vial and incubated with shaking (150 rpm) at 21°C for 30 min to starve the cells. One millilitre of the harvested E. coli DSRed cells was added to the scintillation vial. At the time points T0 (0 min) and T30 (30 min), a 400 μl aliquot was removed and added to duplicate 10 ml Falcon tubes containing 3 ml of 5 mM Na2SO4. The cells in Falcon tubes were harvested, washed, and lysed in 2 ml of 0.25% (v/v) Triton X-100 before the OD490 of the E. coli DSRed cells was measured using a spectrophotometer to allow calculation of the number of bacterial cells and the fluorescence per million bacteria (Maselli et al., 2002). The fluorescence for all transformants was measured in a Modulus fluorometer (Turner Biosystems, Sunnyvale, CA, USA) using a custom-manufactured module. Measurements were performed in duplicate at each time point, and the hourly consumption rate of bacteria by a single amoeba was calculated from the increase in fluorescence over 30 min, the fluorescence signal per million bacteria and the amoebal density.

**Statistical analysis**

Regression and correlation analysis was performed as previously described (Annesley et al., 2016).

This article is part of a special subject collection ‘Neurodegeneration: from Models to Mechanisms to Therapies’, which was launched in a dedicated issue guest edited by Aaron Gitler and James Shorter. See related articles in this collection at http://dmm.biologists.org/collection/neurodegenerative-disorders.

**Acknowledgements**

We thank Sophie Wilczynska and Sui Lay for technical advice, Brian Usher for reading and correction of the manuscript, and Jon Irom, who conducted preliminary Seahorse respirometry experiments.

**Competing interests**

The authors declare no competing or financial interests.

**Author contributions**


**Funding**

This work was supported by the Australian Research Council (DP140104276 to P.R.F. and S.J.A.). S.C. was the recipient of La Trobe University Postgraduate Research Award and Full Fee Remission Scholarship. R.A.F.J. was the recipient of a


