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GENETIC AND CELL BIOLOGICAL DISSECTION OF ALPHA-SYNUCLEIN TRAFFICKING DEFECTS
IN YEAST AND MAMMALIAN CELLS

by

CHING FERN SUE-ANN LEE

DISSERTATION

Submitted in partial satisfaction of the requirements for the degree of

DOCTOR OF PHILOSOPHY

in

BIOMEDICAL SCIENCES

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GRADUATE DIVISION

of the

UNIVERSITY OF CALIFORNIA, SAN FRANCISCO

Dedication

*To my parents Lee Lip Nyeon and Tan Geok Bee:
Thank you for everything.*

ACKNOWLEDGMENTS

I would like to give thanks to everybody who helped me along the long winding road of graduate school and made the journey so much better than the ordeal it could have been.

I really appreciate the freedom and independence in carrying out my research given to me by my supervisor, Dr. Paul Muchowski, and whose guidance and advice was never more than an open office door away. His enthusiasm for science and breadth of knowledge will always be inspirational to me. If not for his encouragement and insistence on learning to multitask, doubtless the last leg of this journey would have been infinitely more stressful.

A very special thank you goes to Dr. Vicente Sancenon, whom I had the good fortune to have worked closely with the first few years of graduate school. I will forever be grateful for his patience, mentorship and unstinting support all these years, and for the fond memories of our many impromptu language lessons.

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I am indebted to my friends Dr. Thomas Lie and Dr. Hankiat Ho for their generosity and kindness when I was trying to find my footing at the start of graduate school, and for their readiness to lend a listening ear or helping hand.

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In conclusion, I would like to thank the Agency for Science, Technology and Research board in Singapore for giving me this immense opportunity to pursue my undergraduate and graduate studies in the United States.

Genetic and cell biological dissection of alpha-synuclein trafficking defects in yeast and mammalian cells

Ching Fern S. Lee

α -Synuclein, a major player in Parkinson's disease pathogenesis, is thought to impair vesicle trafficking as a toxic gain of function through aggregation. Genetic screens for modifiers of α -synuclein toxicity have overwhelmingly identified a significant subset of genes involved in vesicle trafficking. While recent studies in yeast have shown that at toxic levels α -synuclein disrupts Rab homeostasis, causing an initial ER-to-Golgi block that precedes a generalized trafficking collapse, further studies in mammalian systems prove that several rabs downstream of ER-Golgi trafficking to rescue α -synuclein toxicity. Here, we show that constitutive expression of α Syn in yeast causes the accumulation of endocytic vesicles and impairs late-exocytic, early-endocytic and/or recycling trafficking and further, that this vesicle trafficking impairment can be attenuated by yeast casein kinase 1 and the small rab protein Ypt1p. Our work in mammalian cell culture models of Parkinson's disease demonstrate the ability of the human homologues of vacuolar protein sorting genes involved in endosomal transport to modulate the toxicity of α -synuclein. Furthermore, our findings suggest that α -synuclein-induced cytotoxicity is due to impairment in the endosomal trafficking pathway of the SH-SY5Y cells. Taken together, our results provide evidence of the potential contribution of endosome anomalies to the pathogenesis of Parkinson's disease.

CONTRIBUTIONS

Chapter 2 was submitted for publication to the journal *Human Molecular Genetics* entitled “Genetic Context-Dependent Modulation of α -synuclein Toxicity and Trafficking Defects by Phosphorylation of Serine 129” by Vicente Sancenon, Sue-Ann Lee, Christina Patrick, Janice Griffith, Amy Paulino, Angela Sia, Tiago F. Outeiro, Fulvio Reggiori, Eliezer Masliah, and Paul J. Muchowski. Figures 1 and 3H were contributed by Ching Fern S. Lee

The work and accompany figures in chapter 3 was submitted for publication to the *Journal of Neuroscience* entitled “Endosomal trafficking genes modulate α -synuclein toxicity in mammalian cells” by Sue-Ann Lee, Gaia Skibinski, Leonidas Stefanis, Guillermo Yudowski and Paul J. Muchowski. Figures 1-5, 7-8 and 9b-d were contributed by Ching Fern S. Lee

Aside from these items, the work presented in this thesis was conducted by its author, Ching Fern S. Lee, under the supervision of Dr. Paul J. Muchowski.

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CHAPTER 1 – GENERAL INTRODUCTION

GENERAL INTRODUCTION

Parkinson's disease (PD)

PD was first described by the English apocathery James Parkinson in his 1817 work “An essay on the shaking palsy”. A progressive neurodegenerative disorder, PD is second only to Alzheimer’s disease in causing neurodegeneration, and is estimated to affect 1% of the population over 65 years of age (de Rijk et al., 2000). Patients with PD are clinically diagnosed by symptoms such as muscle rigidity, and resting tremors. In advanced stages of the disease, PD is also associated with cognitive impairment. The clinical symptoms are pathologically correlated to the loss of neurons in the substantia nigra pars compacta, a brain region involved in the production of movement, as well as progressive loss of the neurotransmitter dopamine (Hornykiewicz, 1998). This observation led to the use of the dopamine precursor L-dihydroxyphenylalanine (L-DOPA) as a therapy to alleviate symptoms associated with PD. However, L-DOPA does not stop progressive neurodegeneration in patients with PD (Tintner et al., 2002) and despite the various drug therapies involving dopamine agonists, surgical treatments and physical therapies, no cure yet exists for this disease (Olanow, 2004).

Although the etiology of PD remains unclear, age and exposure to neurotoxins are established risk factors (Vanitallie, 2008) while nicotine and caffeine are purportedly protective against the disease (Ross et al., 2001). Until recently, PD was considered a non-genetic disease as the vast majority of cases are idiopathic. It has since been shown that multiple gene loci and genes are associated with both autosomal dominant and recessive familial forms of the disease. In particular, missense mutations in one of these associated genes, SNCA, results in A53T, A30P or E46K substitutions in the α -synuclein

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protein, each contributing to early-onset inherited PD (Polymeropoulos et al., 1997; Kruger et al., 1998; Zarranz et al., 2004). Multiplications of the wild-type SNCA gene as well as polymorphisms and variations in the length of the SNCA promoter region (Maraganore et al., 2006; Myhre et al., 2008; Sotiriou et al., 2009) also cause autosomal dominant PD, implying that increased concentrations of α -synuclein are sufficient to cause PD (Singleton et al., 2003). The SNCA gene product α -synuclein also plays a central role in the pathophysiology of idiopathic PD. Postmortem, diagnosis of PD is confirmed by the presence of Lewy bodies and Lewy neurites in the remaining surviving neurons. Lewy Bodies are intracellular inclusions of lipids and proteins, predominantly comprised of α -synuclein (Spillantini et al., 1997; Kuusisto et al., 2003).

The SNCA gene product α -synuclein (α SYN)

α SYN is a relatively small, 140 amino acid protein that is ubiquitously expressed in the brain and enriched in presynaptic nerve terminals (Jakes et al., 1994). In solution, it is a ‘natively unfolded’ protein with little secondary structure that takes on an amphipathic α -helical structure in the presence of phospholipids (Chandra et al., 2003). Over-expression of wild-type and mutant forms of α SYN in mice leads to aggregation of α SYN in brainstem and spinal cord neurons and motor phenotypes (Masliah et al., 2000; van der Putten et al., 2000; Giasson et al., 2002). On the other hand, α SYN knock-out mice do not exhibit impaired survival or brain function, nor is α SYN required for the basic neurotransmitter release machinery (Chandra et al., 2004).

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Although the exact physiological function of α SYN remains undetermined, it has been implicated in the maintenance of synaptic homeostasis and plasticity. In addition, it can also reduce hydrolysis of lipid droplets (Cole et al., 2002), as well as regulate the size of pre-synaptic vesicular pools in cell culture (Murphy et al., 2000). Analysis of a mouse model where the α SYN gene was deleted suggests that α SYN is necessary for the regulation of pre-synaptic dopamine neurotransmission (Cabin et al., 2002). In transgenic mice, α SYN appears to act as a molecular chaperone, assisting in the folding and refolding of Synaptic proteins (Chandra et al., 2005). α SYN has been linked to learning, development and plasticity (di Rosa et al., 2003; Sidhu et al., 2004), and most likely plays a role in synaptic vesicle recycling (Ben Gedalya et al., 2009; Nemani et al., 2010).

Several disease mechanisms that are not necessarily mutually exclusive have been suggested: first, aggregation of α SYN into a toxic oligomeric/protofibrillar/fibrillar species perturbs the structure and/or function of downstream targets; second, packaging and secretion of dopamine is disrupted; third, the ubiquitin-proteasome system is impaired; fourth, molecular chaperone function is impaired; fifth, mitochondrial function is impaired and/or oxidative stress is incurred, which may be related to impairment in the packaging of dopamine; and sixth, intracellular trafficking pathways and synaptic transmission are impaired (Goldberg et al., 2000; Goedert, 2001; Lotharius et al., 2002). Fragmentation of the Golgi apparatus has been observed in PD brains (Fujita et al., 2006) and in cells overexpressing α SYN (Gosavi et al., 2002), which is thought to be a specific consequence of toxic pre-fibrillar α SYN aggregation. α SYN is also suggested to impair

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ER-Golgi trafficking (Cooper et al., 2006). Additionally, redistribution of Synaptic SNARE proteins in α SYN transgenic mice and reduction in dopamine release has been shown to correlate with α SYN aggregation and locomotive defects (Garcia-Reitböck et al., 2010) while another study has demonstrated a loss of presynaptic proteins regulating endo- and exocytosis in α SYN transgenic mice and PD brains that is correlated with synaptic pathology (Scott et al., 2010).

In vitro studies suggest that α SYN protofibrils can bind and permeabilize acidic phospholipid vesicles (Volles et al., 2001; 2002). It has been proposed that this may lead to defective sequestration of dopamine into vesicles and subsequent generation of reactive oxygen species in the cytoplasm which contribute to neuronal dysfunction and cell death (Lotharius et al., 2002). Recently, α SYN has been found in human plasma and cerebral spinal fluid and has been shown to be secreted into the medium of cultured neuronal cells (El-Agnaf et al., 2003, 2006; Lee et al., 2005), suggesting that α SYN toxicity may be propagated through the extracellular matrix to neighboring cells.

Yeast and mammalian cell culture models of PD

If PD does indeed involve multiple disease mechanisms, it will be crucial to understand the genes and cellular pathways that are of primary significance for neuronal dysfunction and cell death from a temporal and spatial sense. The baker's yeast *Saccharomyces cerevisiae* is a powerful model organism to study the function and disease-causing attributes of α SYN in a PD context for two reasons. First, basic cellular mechanisms,

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such as replication, recombination, cell division, protein folding, intracellular transport and metabolism are well conserved between yeast and mammals. Secondly, genetically engineered yeast cells over-expressing heterologous human α SYN that were generated by Outeiro et al. (2003) to study the mechanisms of α SYN toxicity recapitulate many features observed in PD, including the formation of inclusion bodies, disruption of vesicle trafficking, impairment of proteasomal function, and dose-dependent toxicity. Third, genetic manipulations can be rapidly performed in the organism. Various yeast genetic screens have shown that α SYN toxicity is exacerbated or alleviated in different yeast gene deletion strains. Among the genes that enhance or suppress α SYN toxicity when deleted, a significant number was clustered in the functionally related categories of lipid metabolism and vesicle trafficking, and a high percentage of those genes have human orthologs (Willingham et al., 2003). By conducting studies in yeast, toxicity mechanisms that are relevant to PD and potential disease-modulating proteins might be uncovered that could contribute to the development of therapies for PD.

It must be acknowledged that yeast as a model system for studies relating to neurodegeneration has obvious limitations, for example, some genes important for modulating neurodegeneration may not be present in the yeast genome (such as those that encode caspases involved in apoptosis or growth factors). Thus, the validity of using yeast as a model organism for studying α SYN dependent pathogenic mechanisms of PD will only be established by performing complementary approaches in more physiologically relevant models of neurodegeneration. Human cell lines also allow for

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direct investigation of PD pathophysiology in a relatively short amount of time and labor. Although genetic manipulation is more limited than in yeast, the expression of specific genes can be readily suppressed or proteins of interest over-expressed in cell line culture systems, allowing for close study of their function. Furthermore, techniques for high-throughput screening can also be adapted for cell lines to develop novel therapeutic compounds.

As PD is characterized by the specific loss of dopaminergic neurons in the substantia nigra, it is unsurprising that the human neuroblastoma SH-SY5Y cell line, which has moderate levels of dopamine beta hydroxylase activity, is widely used as a neurotoxicity model for PD. When differentiated with retinoic acid, the SH-SY5Y cells acquire a neuronal phenotype and express high levels of the vesicular monoamine transporter 2 (Presgraves et al., 2004). Importantly, stable overexpression of wild-type α SYN in this cell line induces gradual degeneration of differentiated cells (Vekrellis et al., 2009) which recapitulates the progressive, age-related onset of sporadic PD. Thus, this cell line is a useful tool to dissect cell autonomous pathways that might regulate toxicity induced by elevations of WT α SYN. Results from studies in this cell line can be subsequently validated in *in vivo* and more physiological relevant models of PD.

The importance of vesicle trafficking pathways in α SYN-induced toxicity has been demonstrated by identification of vesicle trafficking as a major category of genes that modulate α SYN toxicity by multiple genetic screens. Furthermore, overexpression of small Rab GTPase proteins (Cooper et al., 2006; Gitler et al., 2008) and hVps41, which

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are involved in vesicle trafficking, have shown rescue α SYN toxicity. However, the site(s) of action impaired by α SYN toxicity and the mechanism by which these genetic modifiers alter α SYN toxicity remain poorly understood. We have sought to bridge this knowledge gap through a systematic analysis of genetic manipulation of several vesicle trafficking genetic modifiers on α SYN-induced toxicity and vesicle trafficking defects in the SH-SY5Y cell line.

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ABSTRACT

The aggregation of α -Synuclein (α Syn) is a neuropathological hallmark of Parkinson's disease and other Synucleinopathies. In the aggregates, α Syn is extensively phosphorylated, predominantly at serine 129 (S129). Recent studies in yeast have shown that, at toxic levels, α Syn disrupts Rab homeostasis, causing an initial ER-to-Golgi block that precedes a generalized trafficking collapse. However, whether α SYN phosphorylation modulates trafficking defects has not been evaluated. Here, we show that constitutive expression of α Syn in yeast impairs late-exocytic, early-endocytic and/or recycling trafficking. Although members of the casein kinase I (CKI) family phosphorylate partially α Syn at S129, they attenuate α SYN toxicity and trafficking defects by a phosphorylation-independent mechanism. However, phosphorylation of S129 modulates α Syn toxicity and trafficking defects in a genetic background-dependent manner. Abnormal endosome morphology, increased levels of the endosome marker Rab5, and co-localization of mammalian CKI with α SYN aggregates are observed in brain sections from α SYN-overexpressing mice and human synucleinopathies. Our results provide evidence of the potential contribution of endosome anomalies and CKI dysfunction to the pathogenesis of synucleinopathies.

INTRODUCTION

Synucleinopathies comprise a subset of neurodegenerative disorders characterized by the accumulation of cytoplasmic inclusions, or Lewy bodies, that contain the protein α -

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synuclein (α Syn) in selected populations of neurons [Parkinson's disease (PD) and dementia with Lewy bodies (DLB)] or in glia [multiple system atrophy (MSA)].

Although the etiology of these disorders is unknown, the discovery of mutations in the α Syn gene (*SNCA*) that cause PD implicates α SYN in the pathogenesis of synucleinopathies (Spillantini et al., 2000).

The precise cellular function of α Syn is unclear. α Syn is a presynaptic protein that stimulates the formation of synaptic vesicles and neuronal transmission *in vitro* and *in vivo* (Cabin et al., 2002; Liu et al., 2004; Chandra et al., 2005; Ben Gedalya et al., 2010). Importantly, the discovery that multiplications of the α SYN locus cause PD suggests that neurotoxicity is a quantitative trait of α Syn (Singleton et al., 2003). Therefore, overexpression of α Syn has been used to study the molecular mechanisms of disease pathogenesis in a variety of model systems. In addition to other phenotypes, overexpression of α Syn interferes with vesicular transport in cell-based and *in vitro* models, and in patients with PD (Gosavi et al., 2002; Fujita et al., 2006; Larsen et al., 2006; Lee et al., 2006; Thayanidhi et al., 2010). Yeast has proven useful as model to reconstitute α Syn dose-dependent cellular toxicity and trafficking defects. α Syn was shown to block ER-to-Golgi transport (Cooper et al., 2006) and other intracellular trafficking pathways (Gitler et al., 2008; Zabrocki et al., 2008) at toxic concentrations. These trafficking failures correlate with an accumulation of intracellular vesicles (Gitler et al., 2008; Soper et al., 2008). Interestingly, α Syn toxicity can be modulated by

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manipulating the expression of genes involved in cellular trafficking (Willingham et al., 2003; Cooper et al., 2006; Flower et al., 2007; Kuwahara et al., 2008; Liang et al., 2008; van Ham et al., 2008).

Posttranslational modifications of α Syn *in vivo* may play an important role in the pathogenesis of PD and other synucleinopathies. The most abundant modification of α Syn in Lewy bodies is the phosphorylation of serine 129 (S129) (Fujiwara et al., 2002; Waxman et al., 2008). This residue is located within a casein kinase (CK) consensus recognition site and is phosphorylated by yeast and mammalian CKs and other kinases in cellular and animal models. However, the relevance of S129 phosphorylation for pathogenesis remains controversial. Studies in rats and flies argue for protective, innocuous and detrimental effects of phosphorylation on neurodegeneration (Chen et al., 2005; Gorbatyuk et al., 2008; Azeredo da Silveira et al., 2009; McFarland et al., 2009). Moreover, whether phosphorylation influences α Syn-induced intracellular trafficking defects has not been evaluated.

In this study, we show that late-exocytic, early-endocytic and/or recycling transport of PM proteins is altered by constitutive expression of α Syn in yeast. Yeast casein kinase 1 (Yck1) attenuates this defect by a phosphorylation-independent mechanism. However, blocking α Syn phosphorylation dramatically enhances α Syn toxicity and trafficking defects in a strain-specific manner, suggesting that the genetic context determines the

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sensitivity to changes in the phosphorylation state of α Syn. We also report early endosome alterations and co-localization of mammalian CK1 δ with α Syn-positive inclusions in mouse models and human synucleinopathy brains, providing evidence that endosome anomalies and CK1 δ sequestration may contribute to the pathogenesis of synucleinopathies.

RESULTS

Overexpression of α Syn Causes Vesicles to Accumulate in Yeast

Wild-type (WT) α Syn-GFP ectopically expressed in yeast from the galactose-inducible promoter of the *GALI* gene accumulates in intracellular inclusions (Outeiro et al., 2003). The earliest inclusions form at 3.5 h of induction in the cell periphery and subsequently spread towards the cell interior (Gitler et al., 2008). Immuno-electron microscopy (IEM) studies revealed that the inclusions observed by fluorescence microscopy are α SYN-positive clusters of vesicles (Gitler et al., 2008; Soper et al., 2008). To further investigate the composition of these clusters, we examined the ultrastructure and the subcellular localization of α Syn by IEM over time in yeast expressing α Syn-GFP by the *GALI* promoter. Within the first 4 h of induction, α Syn-GFP immunoreactivity was almost exclusively observed at the plasma membrane (PM) (data not shown). At 6 h, we observed small clusters of vesicles in the vicinity of the PM (Fig. S1A and B). The vesicles were homogeneous in size (~20–40 nm in diameter), morphology and electron density, suggesting a common origin. At 12 h, the clusters were enlarged, and their

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vesicular content became heterogeneous in morphology and size (up to ~100 nm in diameter), consistently with a widespread trafficking defect (Gitler et al., 2008) (Fig. S1C and D). Notably, α Syn-GFP immuno-reactivity was detected on the surface of the vesicles at 6 h and 12 h, in agreement with previous reports showing that the α SYN inclusions observed by fluorescence microscopy correspond to these clusters.

Constitutive α Syn Expression Disrupts Late-Exocytic, Early-Endocytic and/or Recycling Trafficking in Yeast

Although the Lindquist group initially showed that α Syn-inclusions co-localize with Ypt1, an endoplasmic reticulum (ER)-to-Golgi trafficking marker (Cooper et al., 2006), a follow on study by the same group showed co-localization with diverse trafficking markers, including Ypt31 (late Golgi), Sec4 (secretory vesicles-to-PM), Ypt6 (endosome-to-Golgi), Vps21 and Ypt52 [early endosome (EE)-to-late endosome (LE)], and Ypt7 (LE-to-vacuole), indicating that α Syn disrupts multiple trafficking route (Gitler et al., 2008). To further investigate the origin of the accumulated vesicles, we evaluated the effect of constitutively expressing untagged α Syn from the promoter of the glycerol-3-phosphate dehydrogenase (*GPDI*) in a 2 micron plasmid on the steady-state localization of a series of GFP-tagged protein markers of intracellular trafficking (Lewis et al., 2000; Reggiori et al., 2000; 2001) (Fig. 1A). GFP-Snc1, a transmembrane exocytic SNARE (soluble N-ethylmaleimide-sensitive factor attachment protein receptor), is targeted to the PM through the secretory pathway and subsequently recycled for re-use via EE and the

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Golgi. Ste2-GFP, the transmembrane α -factor pheromone receptor, and GFP-Snc1-Sso1, an engineered variant of GFP-Snc1 containing a transmembrane domain of the SNARE Sso1, are targeted to the PM through the secretory pathway and, subsequently, after endocytosis, to the vacuolar lumen via EE and LE. The SNARE GFP-Pep12 is targeted to the membrane of the prevacuolar complex via the carboxypeptidase Y (CPY) biosynthetic pathway. The transmembrane proteins GFP-Phm5 and Sna3-GFP are targeted to the vacuolar lumen via the CPY pathway by ubiquitin-dependent and independent mechanisms, respectively. GFP-Nyv1-Snc1, an engineered variant of the SNARE Nyv1 containing the transmembrane domain of Snc1, is targeted to the vacuole membrane via the alkaline phosphatase (ALP) pathway.

To quantitatively assess the effect of α Syn on trafficking, we counted the percentage of cells exhibiting a mislocalization phenotype, considered as any anomaly in the localization pattern of a trafficking marker that differs from the pattern displayed by the majority (>70%) of cells not expressing α Syn. Constitutive expression of untagged α Syn from the *GPD1* promoter selectively altered the targeting of GFP-Snc1 to the PM and of GFP-Snc1-Sso1 and Ste2-GFP to the vacuole lumen in more than 50% of the cells, but not of GFP-Pep12 and GFP-Nyv1-Snc1 to the vacuole membrane or GFP-Phm5 and Sna3-GFP to the vacuole lumen (Fig. 1B and C). The trafficking routes that are unique to the protein markers perturbed by α Syn include Golgi-to-PM, PM-to-endosome and endosome-to-Golgi. These observations suggest that, at the steady state expression levels

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achieved by the *GPD1* promoter, α Syn impairs the delivery of proteins to the PM from the Golgi and/or their subsequent endocytic and recycling trafficking. In contrast, other markers that use the ER-to-Golgi pathway but bypass the PM (GFP-Pep12, GFP-Phm5, Sna3-GFP and GFP-Nyv1-Snc1) do not exhibit localization defects in α Syn expressing cells, suggesting that ER-to-Golgi trafficking is not impaired.

To confirm this hypothesis, we analyzed the subcellular distribution of α Syn and the exocytic SNARE Snc1 by co-IEM (Fig. 2). Consistent with the fluorescence microscopy studies, Snc1 immunoreactivity was detected in the α Syn-positive vesicular clusters, confirming anomalies in PM delivery, endocytic and/or recycling trafficking of Snc1. As α SYN has been reported to block the delivery of the dye FM 4-64 to the vacuole, but not its uptake (Outeiro et al., 2003), we propose that α Syn impairs post-endocytic and/or recycling trafficking that follows vesicle budding from the plasma membrane (Fig. 1A).

To gain further insights in the trafficking steps blocked by α Syn, we investigated the subcellular distribution of the trafficking marker Snc1-Sso1 and the dye FM 4-64 in two subsets of yeast trafficking mutants (Fig. S2A). First, in loss-of-function deletion mutants defective in intra-Golgi (*ypt31 Δ*), endocytic (*end3 Δ* , *ypt51 Δ*), recycling (*ypt31 Δ*), endosome-to-Golgi (*vps35 Δ*), and endosome-to-vacuole (*vps23 Δ* , *did3 Δ*) transport, endosome and vacuole homotypic fusion (*ypt7 Δ*) and actin remodeling (*sac6 Δ*). Second, in temperature sensitive secretory mutants defective in ER-to-Golgi (*sec7-4*, *sec18-1*),

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intra-Golgi (*sec7-4*), and Golgi-to-plasma membrane (*sec1-1*) transport at permissive (RT) and non-permissive (37°C) temperature. Among all the mutants studied *did3 Δ* and *vps23 Δ* appear to mimic more closely the mislocalization pattern of Snc1-Sso1 caused by α Syn, suggesting a late endocytic defect (Fig. S2B and C). However, the mislocalization phenotype in α Syn expressing cells seems to rather be unique, suggesting that multiple trafficking steps are affected, in agreement with a previous study (Gitler et al., 2008).

Yck1 Attenuates α Syn-Induced Toxicity and Trafficking Defects through a Phosphorylation-Independent Mechanism

There is increasing evidence that α Syn disrupts endocytic trafficking. For example, α Syn overexpression perturbs the subcellular distribution of the endocytic tracker FM 4-64 (Outeiro et al., 2003) and diverse endocytic protein markers (Gitler et al., 2008). The endocytic pathway is more vulnerable to insults in α Syn-transgenic (tg) worms (Kuwahara et al., 2008). Therefore, we reasoned that genes regulating endocytosis might contribute to modulate α Syn-induced growth defects and vesicle accumulations. To test this hypothesis, we assessed whether Yck1 and Yck2, two functionally redundant PM-associated members of the CKI protein family that promote the endocytosis of PM proteins (Marcha et al., 2000; 2002), modulate α Syn toxicity. For these studies, we generated a yeast strain carrying two stably integrated copies of the human α Syn gene fused to GFP under the control of the *GAL1* inducible promoter (which allows to control for gene-specific effects in non-inducing conditions) in the BY4741 strain (Table I). As positive and negative controls, we deleted the genes *TLG2*, a known α Syn toxicity

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modifier encoding a SNARE required for the targeting of Yck2 to the PM (Panek et al., 2000; Willingham et al., 2003), and *SPO14*, a non modifier gene encoding a yeast phospholipase D (Rose et al., 1995), respectively. In contrast to a previous study (Zabrocki et al., 2008), we found that deletion of *YCK1* and *YCK2* genes significantly increased the growth defect caused by α Syn (Fig. 3A and S3).

To confirm these genetic interactions, we reasoned that pharmacologic inhibition of CKI activity in yeast expressing α Syn should phenocopy the *yck1 Δ* or *yck2 Δ* alleles, and this effect should be more dramatic in yeast lacking either one of the two functionally redundant enzymes. Therefore, we tested the effect of the CKI-specific inhibitor D4476 on the viability of cells expressing α Syn. To make cells more sensitive to the compound, we knocked out the multidrug resistance gene *PDR1* in all the strains tested. Although *YCK1* or *YCK2* are not individually essential for cell growth, deletion of both genes results in growth arrest. As expected, the CKI-specific inhibitor D4476 decreased yeast growth in a concentration-dependent manner. Notably, this effect was more pronounced in cells expressing α Syn and was significantly increased in cells lacking one of the two redundant enzymes (Fig. S4), suggesting that CKI activity counteracts the detrimental effects of α Syn overload.

To determine whether the increase in growth inhibition caused by loss of CKI function correlates with increased trafficking defects, we studied the localization of mCherry

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tagged Snc1-Sso1 in WT and *yck1* Δ cells carrying two or zero integrated copies of the galactose inducible α Syn-GFP gene. In cells not expressing α Syn, mCherry-Snc1-Sso1 is correctly delivered to the vacuolar lumen (Fig. 3E). In contrast, expression of α Syn-GFP prevented the proper targeting of Snc1-Sso1 in ~30% of WT cells (Fig. 3E and F). Note that the defect in these cells is less marked than in cells constitutively expressing untagged α Syn from a 2 micron plasmid, where ~75% of cells are affected (Fig. 1C). However, deletion of *YCK1* did not aggravate this phenotype (Fig. 3E and F), indicating that the enhancement of growth defects by the *yck1* Δ mutation is not due to an enhancement of trafficking defects.

Next, we investigated the ability of *YCK1* to reverse α Syn-induced toxicity and trafficking defects (Fig. 3G and H). We observed that *YCK1* overexpression attenuates the growth defect caused by 2 copies of the α Syn-GFP gene in WT and *yck1* Δ cells. In addition, in contrast to the absence of trafficking defect enhancement upon deletion of *YCK1*, overexpression of *YCK1* significantly reduced the percentage of cells showing abnormal localization of GFP-Snc1-Sso1 in cells constitutively expressing α Syn (Fig. 3H). Interestingly, Ypt1, a Rab GTPase that also suppresses α Syn toxicity (Cooper et al., 2006), decreased mislocalization of GFP-Snc1-Sso1 to the same extent. These results suggest that Yck1 may alleviate α Syn toxicity by, at least in part, directly promoting PM endocytosis.

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α Syn contains a consensus CKI phosphorylation site on S129 that is phosphorylated by yeast and mammalian CKI *in vitro* and *in vivo* (Okochi et al., 2000; Zabrocki et al., 2008). To assess whether α Syn is phosphorylated at S129 in yeast, we monitored the levels of total and phosphorylated α Syn (pS129) over time in WT cells carrying 2 copies of the α Syn-GFP gene. Both α Syn and its phosphorylated form were detected after 1 h of inducing α Syn expression, indicating that α Syn is rapidly phosphorylated in yeast (Fig. 3B). To test whether CKI modulates directly or indirectly the phosphorylation of α Syn at S129 in our model, we compared the relative levels of pS129 in the WT, *yck1* Δ and *yck2* Δ strains after 1 h of induction. The *spo14* Δ strain was included as negative control. As previously shown, we observed a modest (~30%) decrease in the relative levels of pS129 in the *yck1* Δ and *yck2* Δ mutants compared to the WT strain (Fig. 3C and D), confirming that CKI contributes partially to the phosphorylation of S129.

To determine whether the attenuation of growth and trafficking defects by Yck1 are mediated by phosphorylation of α Syn, we measured the levels of pS129 in WT and *yck1* Δ cells transformed with a plasmid for the overexpression of *YCK1* or the corresponding empty vector at 5.5 and 11 h of induction (Fig. 3I). As control, we treated cells with a combination of the phosphatase inhibitors (PI) okadaic acid and activated Na_3VO_4 . *YCK1* overexpression did not increase α Syn phosphorylation in either WT or *yck1* Δ cells, suggesting that the attenuation of toxicity and trafficking defects by *YCK1* is not mediated by phosphorylation.

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Phosphorylation Regulates the Toxicity and Trafficking Defects Caused by α Syn in a Context-Dependent Manner

The role of S129 phosphorylation on disease pathogenesis is unclear, as contradictory results have been published in different models (Chen et al., 2005; Gorbatyuk et al., 2008; Azeredo da Silveira et al., 2009; Chau et al., 2009; Kragh et al., 2009; McFarland et al., 2009). To investigate the effect of S129 phosphorylation on α Syn-induced toxicity and trafficking defects in yeast, we generated strains that stably express WT α Syn or the phosphorylation mutants S129A or S129E from one or two genomic loci in the BY4741 strain background (Table I). As expected, α Syn reduced cell growth in a dose-dependent manner (Fig. 4A). However, replacement of S129 by A or E did not alter α Syn toxicity or expression levels (Fig. 4A and B). These results suggest that phosphorylation does not modulate α Syn toxicity. However, the S129 phosphorylation status appears to govern α Syn neurotoxicity in at least a fly and rat model (Chen et al., 1992; Gorbatyuk et al., 2008), but not in two other models (Azeredo da Silveira et al., 2009; Mc Farland et al., 2009) Therefore, we reasoned that variations in the genetic background of the models may account for the differential sensitivity of cells to the α Syn phosphorylation status.

To test this hypothesis, we generated strains that stably express WT α Syn or the phosphorylation mutants S129A or S129E from one or two genomic loci in the W303-1A genetic background (Table I). This strain carries a mutation in the *YBPI* gene that

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increases its sensitivity to oxidative stress (Veal et al., 2003), a known mechanism of α Syn toxicity (Witt et al., 2006). Whereas one copy of any of the three α Syn alleles had no impact on yeast growth, two copies were detrimental in an allele-specific manner (Fig. 4C). While the S129A mutation, that prevents phosphorylation, significantly increased the growth defect caused by WT α Syn, the S129E mutation, that mimics phosphorylation, had no effect, suggesting that preventing phosphorylation enhances α Syn toxicity in the W303-1A strain background. Interestingly, the S129A mutation caused a significant ~6-fold increase in the percentage of cells with α Syn inclusions in comparison to WT α Syn without altering expression levels (Fig. 4D-F), suggesting that blocking phosphorylation of S129 enhances trafficking defects caused by α Syn.

To confirm this hypothesis, we studied the trafficking of the dye FM 4-64 in the strains with 2 copies of the WT α Syn gene, or the S129A and S129E mutations in the W303-1A background. As previously reported (Outeiro et al., 2003), WT α Syn impaired the delivery of the dye to the vacuolar membrane (Fig. 4G and H). The S129A mutation enhanced this defect, indicating that the enhancement of toxicity correlates with increased trafficking defects. Importantly, these defects were typically observed in cells with α Syn inclusions (Fig. 4I), regardless of the α Syn variant expressed, confirming that the formation of inclusions is an indication of underlying trafficking defects and suggesting a molecular link between phosphorylation and trafficking.

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To verify whether the modulation of α Syn toxicity by Yck1 observed in the BY4741 derived strains is mediated by S129 phosphorylation or an independent mechanism, we deleted or overexpressed *YCK1* in strains expressing 2 copies of the WT α Syn gene, or the S129A and S129E mutations in the W303-1A background. Unexpectedly, either deletion or overexpression of *YCK1* did not alter the growth defect of these strains, whether expressing WT α Syn or the S129 mutations (Fig. 4J). These observations demonstrate that the genetic modification of a toxic phenotype is profoundly influenced by the genotype and may explain paradoxical observations reported in different models.

Evidence of Endosome Anomalies and CK1 δ Mislocalization in α Syn Tg Mice and in Synucleinopathy Brains

To determine if defects in early-endocytic trafficking are a conserved pathological feature of Synucleinopathies, we studied the subcellular localization of the EE protein marker Rab5 in brain tissues from a tg mouse model of Synucleinopathy (Masliah et al., 2000) and human DLB/PD. In tg mice, overexpression of human α Syn results in the formation of α Syn-positive inclusion-like structures in the neocortex, hippocampus, and substantia nigra by two months of age (Masliah et al., 2000). In non tg mice, Rab5 labeled discrete punctuate endosomes in the cytosol of cortical neurons at six months of age whereas α Syn stained discrete puncta in the cell periphery. However, in tg animals, Rab5 labeled abnormally swollen endosomes in neurons that that contained α Syn-positive intracellular inclusions (Fig. 5). Interestingly, these outsized endosomes co-localized with small

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granular aggregates of α Syn, but were excluded from large Lewy-body-like inclusions. Similarly, in cortical sections of human control subjects, Rab5 and α Syn exhibited a punctuate pattern that in some cases co-localized. However, in human DLB/PD cases, Rab5 stained abnormal endosomal compartments that co-localized with α Syn granular aggregates but not with Lewy bodies. While the nature of the enlarged Rab5-positive endosomes is unknown and they may not be equivalent to the accumulation of vesicles observed in yeast overexpressing α Syn, the presence of this abnormal endosomes suggest a dysfunction of the endocytic pathway in α Syn tg mice.

To examine the early-endocytic trafficking machinery in pathological states *in vivo*, we analyzed by western blot the levels of Rab5, and two other EE markers, Rab4 and EEA1, in the α Syn tg mice and in a tg mouse model of Alzheimer's disease (AD), a non-strict form of Synucleinopathy in which a processed fragment of α Syn deposits in extracellular amyloid plaques. In this model, expression of mutant human amyloid precursor protein (APP) leads to the formation of plaques in the frontal cortex by 4 months of age (Rockenstein et al., 2001). Interestingly, at 6 months of age, both models exhibited elevated levels of monomeric and high molecular weight (HMW) species of α Syn in detergent-insoluble brain fractions (Fig. 6A and B). This change correlated with an accumulation of low mobility forms of Rab5, but no alterations in the mobility or levels of Rab4 or EEA1.

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To validate these observations, we analyzed Rab5, Rab4 and EEA1 levels in two subgroups of human amyloidopathies, including DLB/PD and AD. Consistent with the mouse studies, detergent-insoluble HMW species of α Syn accumulated in strict Synucleinopathies and AD cases compared to age-matched control subjects (Fig. 6C and D). In addition, levels of Rab5, but not Rab4 or EEA1, were markedly elevated in DLB/PD and AD relative to controls, suggesting upregulation or reduced turn-over of Rab5 in the two subgroups. As in the mice models, Rab5 exhibited a mobility shift in all the amyloidopathy cases studied, whereas the mobility of Rab4 or EEA1 was unchanged. Although the functional significance of the Rab5 mobility shift is unknown, the co-localization of α Syn granular aggregates with enlarged endosomes, and the correlation between accumulation of α Syn HMW species and Rab5 suggest a causative role for α Syn in early endosome dysfunction.

To investigate a possible involvement of mammalian CKI proteins in the pathogenesis of Synucleinopathies *in vivo*, we studied the subcellular localization of CKI δ , involved in vesicle transport (Milne et al., 2001; Yu et al., 2002), in brain sections from α Syn tg mice and human DLB/PD (Fig. 7). As expected, CKI δ localized predominantly to the cell periphery in cortical neurons from non-tg animals. In contrast, CKI δ co-localized with α Syn inclusions in tg animals. Importantly, this association was conserved in neuronal inclusions in human DLB/PD, consistent with the notion that CKI δ may be sequestered by α Syn inclusions in Synucleinopathies.

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Elevated levels of CK1 δ mRNA have been detected in AD brains (Yasojima et al., 2000), suggesting upregulation of CK1 δ as a compensatory response in AD. To investigate whether CK1 δ is upregulated in Synucleinopathies, we analyzed the levels of CK1 δ by western blot in brains from α Syn and APP tg mice and human DLB/PD and AD cases (Fig. 6B and D). We did not detect any significant changes in the levels of CK1 δ in mice models or human synucleinopathies, indicating that CK1 δ is not upregulated in response to α Syn accumulation. Unexpectedly, CK1 δ levels were also unchanged in AD cases, suggesting that the observed mRNA upregulation in AD does not lead to increased CK1 δ Synthesis, or that the upregulation is tissue-specific and undetectable in whole brain homogenates.

DISCUSSION

A number of recent studies have shown that α Syn overexpression causes vesicle trafficking defects in a wide variety of model systems (Gosavi et al., 2002; Cooper et al., 2006; Fujita et al., 2006; Larsen et al., 2006; Lee et al., 2006; Gitler et al., 2008; Kuwahara et al., 2008; Soper et al., 2008) by perturbing SNARE function (Darios et al., 2010; Garcia-Reitböck et al., 2010; Thayanidhi et al., 2010). In yeast, an early effect of expressing α Syn by a strong galactose-inducible system is an ER-to-Golgi block that precedes a global trafficking failure (Cooper et al., 2006; Gitler et al., 2008). This trafficking collapse is accompanied by the formation of α Syn-positive vesicular clusters

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that co-localize with protein markers of several trafficking routes, including ER-to-Golgi, intra-Golgi, Golgi-to-PM, EE-to-LE, and LE-to-vacuole (Gitler et al., 2008; Soper et al., 2008). The presence of endosome-to-Golgi markers in the clusters is controversial since Gitler and colleagues detected Ypt6, but Soper and colleagues failed to detect Vps17 or Vps29. Importantly, the Rab GTPase Ypt1 and the SNARE Ykt6, involved in ER-to-Golgi vesicle-mediated transport, suppresses α Syn-induced trafficking defects (Cooper et al., 2006; Gitler et al., 2008; Thayanidhi et al., 2010)

In this study, we present evidence of the steady-state impairment of late-exocytic, early-endocytic and/or recycling trafficking by constitutive expression of α Syn in yeast from the *GPM1* promoter. In agreement with previous studies, we observed that trafficking defects coincide with an accumulation of α Syn-positive vesicles that originate in the vicinity of the cell surface and progressively expand towards the cell interior. The vesicles co-label with Snc1, an exocytic SNARE that is targeted to the PM and subsequently internalized and recycled for re-use via EE and the Golgi, implying that at least some of the vesicles originate in the Golgi or the PM. We propose that, in our system, α Syn blocks a trafficking step that follows vesicle budding from the Golgi or the PM and precedes fusion to target membranes. However, we cannot exclude the possibility that the observed vesicles constitute a cellular response to cope with the α Syn overload by compartmentalizing the toxic protein.

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In our studies, α Syn did not impair the targeting of a number of protein trafficking markers traversing the ER and the Golgi towards the vacuole, indicating that ER-to-Golgi transport is unaffected in our model. The discrepancy between our findings and previous studies may be reconciled by differences in the expression levels, toxicity and duration of the insult attained by distinct expression systems (Mumberg et al., 1994; 1995). Whereas prior studies used a galactose-inducible promoter, our studies used a constitutive promoter to assess the effects of α Syn expression on protein trafficking. Interestingly, in the current study, we show that Ypt1 rescues the mislocalization of GFP-Snc1-Sso1 caused by constitutive α Syn expression. Although it is well established that Ypt1 functions in ER-to-Golgi trafficking, this protein also facilitates the recycling of internalized membrane material (Lafourcade et al., 2004). Therefore, we propose that Ypt1 rescues α Syn toxicity by promoting, at least in part, the recycling of PM proteins. Consistent with this interpretation, Ypt6, which is involved in endosome-to-Golgi and intra-Golgi retrograde transport (Luo et al., 2003), was also shown to partially suppress α Syn toxicity (Cooper et al., 2006; Gitler et al., 2008). Thus, although it is conceivable that the trafficking defects that we observed might be secondary to the sustained imposition of the primary ER-to-Golgi block, in our system, α Syn appears to directly impair late-exocytic, early-endocytic and/or recycling trafficking without affecting other pathways.

Our observations contribute to accumulating evidence that trafficking defects are a conserved mechanism of pathogenesis in human Synucleinopathies. In yeast, Rab

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GTPases governing multiple trafficking steps are sequestered by α Syn-induced vesicle clusters (Gitler et al., 2008). Similarly, in humans, members of the Rab family implicated in exocytosis (Rab3a), endocytosis (Rab5) and polarized traffic (Rab8a) interact aberrantly with α Syn in DLB and co-localize with α Syn glial inclusions in MSA (Dalfo et al., 2004; 2005). Conversely, Rab1 (involved in ER-to-Golgi transport), Rab3a and Rab8a are neuroprotective in cellular and animal models in which α Syn is overexpressed (Cooper et al., 2006; Gitler et al., 2008). In catecholaminergic cells α Syn impairs exocytosis, leading to an accumulation of docked vesicles (Larsen et al., 2006). Finally, clusters of dense core vesicles have been observed in the perimeter of Lewy bodies (Forno et al., 1976; Watanabe et al., 1977; Soper et al., 2008).

Our study provides evidence of anomalies in endosome morphology and the endocytic Rab5 in pathological states *in vivo*. In mouse models and human synucleinopathies, early endosomes are abnormally enlarged in cortical neurons and Rab5 co-localizes with α Syn granular inclusions and accumulates abnormally in detergent-insoluble fractions from brain lysates. In contrast, the levels of two other EE markers, Rab4 and EEA1, were unchanged. Although both Rab4 and Rab5 are involved in early endocytic trafficking, they differ in their functional specialization. Whereas Rab5 regulates the fusion between endocytic vesicles and early endosomes, as well as the homotypic fusion between early endosomes (Stenmark et al., 2001), Rab4 controls the function or formation of endosomes involved in endocytic recycling (van der Sluijs et al., 1992). Likewise,

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although EEA1 is a Rab5 effector (Simonsen et al., 1998), accumulation of Rab5 may not necessarily affect EEA1 levels. Therefore, α Syn appears to selectively alter Rab5 expression and function without altering the levels of downstream effectors. In agreement with our observations, inhibition of Rab5 GTPase activity results in the formation of unusually large early endocytic structures (Stenmark et al., 1994), a phenotype mimicked by the overexpression of α Syn. These alterations suggest that endocytic trafficking defects might also occur and contribute to neuronal dysfunction in Synucleinopathies. In striking similarity to our yeast studies, an RNAi screen in the nematode *C. elegans* showed that endocytosis-defective mutants potently exacerbate α Syn neurotoxicity (Flower et al., 2007). Worms that over-expressed α Syn displayed decreased neurotransmitter release, similar to endocytosis-defective mutants. These authors also reported that the knock down of a CK1 gene enhances α Syn toxicity, and showed that α Syn phosphorylated at S129 accumulated in mutants defective in endocytosis (Kuwahara et al., 2008).

In agreement with this model, we found that deletion of *YCK1* or *YCK2*, two redundant kinases of the CKI family that promote the endocytosis and delivery of PM proteins to the vacuole, led to an increase in α Syn toxicity. Interestingly, *yck1* Δ cells accumulate cargo normally destined for the vacuole in an endocytic compartment, but do not affect trafficking through the CPY and ALP pathways to the vacuole (Marcha et al., 2002). These results are further supported by our previous studies in which the yeast SNARE

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Tlg2 was identified as a loss-of-function enhancer of α Syn toxicity (Willingham et al., 2003). Tlg2 participates in endosome-to-Golgi recycling and is required for targeting Yck2 to the PM (Panek et al., 2000), suggesting that exacerbation of α Syn toxicity in *tlg2* Δ cells might be due, at least in part, to decreased CKI activity at the PM. Although we did not detect any significant increase in trafficking defects upon deletion of *YCK1*, we observed a reduction in α Syn-induced growth and trafficking defects upon overexpression of *YCK1*. Although Yck1 contributes modestly to the phosphorylation of α Syn at S129, our results indicate that the attenuation of the toxicity and trafficking defects is not mediated by increased phosphorylation of α Syn. Thus, it is conceivable that CKI activity protects against α Syn toxicity by directly promoting PM endocytosis. This hypothesis is consistent with the observation that knocking down the *C. elegans YCK1* ortholog *csnk-1* by RNAi causes synaptic deficits selectively in α Syn transgenic worm (Kuwahara et al., 2008).

The function of S129 phosphorylation in physiological and pathological conditions is unclear. While only a small fraction of α Syn is phosphorylated in the healthy brain, α Syn is hyperphosphorylated at S129 in pathological lesions (Fujiwara et al., 2002; Hirai et al., 2004; Waxman et al., 2008). However, the relevance of S129 phosphorylation to disease pathogenesis is unknown since conflicting observations have been reported. Mimicking phosphorylation has been shown to be neuroprotective (Gorbatyuk et al., 2008) or innocuous (Azeredo da Silveira et al., 2009; MacFarland et al., 2009) in rats, but

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detrimental in *Drosophila* (Chen et al., 2005) and SH-SY5Y cells (Chau et al., 2009; Kragh et al., 2009). We showed that, in yeast, the effect of S129 phosphorylation on α Syn toxicity is strain-specific. Blocking S129 phosphorylation is innocuous in BY4741-derived strains, but markedly increased the toxicity and trafficking defects caused by α Syn in W303-1A-derived strains, supporting a protective role for phosphorylation in a background-specific manner. Interestingly, W303-1A carries a mutation in the *YBPI* gene that abolishes the oxidative stress response and increases the sensitivity to oxidative stress. This genetic variability could be responsible for the differential sensitivity between the two strain backgrounds to S129A α Syn. Consistent with this hypothesis, α Syn causes oxidative stress and ROS accumulation and increase the vulnerability of yeast to hydrogen peroxide. Conversely, antioxidants and genes involved in the stress response suppress α Syn toxicity in yeast (Griffioen et al., 2006; Liang et al., 2008).

Taken together, our studies indicate that α Syn toxicity is linked to trafficking defects and that this phenotype is modulated by phosphorylation-dependent and independent pathways. For example, the attenuation of toxicity and trafficking defects by *YCK1* appears to be uncoupled from S129 phosphorylation. However, the relative contribution of each pathway to α Syn toxicity appears to be dependent on the global genetic landscape of the cell.

A previous study by Zabrocki and colleagues showed that Yck1, Yck2, Yck3 and CKII

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phosphorylate α Syn at S129 (Zabrocki et al., 2008). However, while deletion of *YCK1* and *YCK2* modestly alleviated an α Syn-induced growth defect and stabilized α Syn at the PM, deletion of *YCK3* and the four subunits of CKII (*CKA1*, *CKA2*, *CKB1* and *CKB2*) exacerbated the growth defect and resulted in α Syn accumulation in intracellular compartments. The latter observation is consistent with the genetic context-dependent enhancement of α Syn toxicity and inclusion formation by the S129A allele we report in this study. Therefore, despite some discrepancies regarding the effects of casein kinases on α Syn toxicity, the general conclusion arising from both studies is that impairment of endocytic trafficking can at least partially account for increased α Syn toxicity.

There is substantial evidence that mammalian CKs phosphorylate α Syn at S129 in cultured cells and *in vivo* (Okochi et al., 2000; Ishii et al., 2007; Waxman et al., 2008). In neurons, a number of mammalian CKI isoforms associate with Synaptic vesicles, and the phosphorylation of CKI substrates is thought to regulate Synaptic vesicle trafficking and neurotransmission. Mammalian CK substrates include proteins implicated in Synaptic vesicle formation (AP-3 adaptor complex) (Faundez et al., 2000), docking and fusion (p65) (Bennett et al., 1993), and exocytosis (Synaptotagmin I) (Davletov et al., 1993), or in the storage of neurotransmitters (VMAT2) (Krantz et al., 1997). Interestingly, some CKI mRNA isoforms (α , δ and ϵ , but especially δ) are dramatically upregulated in the hippocampus and associated with tau-containing neurofibrillary tangles in AD and other dementias (Yasojima et al., 2000). Here, we describe for the first time the co-localization

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of CK1 δ with Lewy bodies in DLB/PD, suggesting sequestration and loss of CK1 δ activity in Synucleinopathies. However, we did not detect any increase in the levels of CK1 δ protein in mice models or human DLB/PD cases, revealing that upregulation of CK1 δ is not a compensatory mechanism in synucleinopathies.

Based on our observations and previous studies, we have generated a model to describe the cascade of pathogenic events that lead to neuronal dysfunction and death in synucleinopathies (Fig. 8). As α Syn is normally a synaptic-vesicle associated protein, we hypothesize that, under physiological conditions, CK1 δ regulates neurotransmission by phosphorylating synaptic proteins, including α Syn. Under pathological conditions, the progressive accumulation of α Syn may lead to sequestration of Rab GTPases and deficits in synaptic trafficking and neurotransmission. CK1 δ -dependent phosphorylation of synaptic substrates may play a protective role by attenuating vesicular trafficking defects and restoring synaptic transmission. However, when all binding sites in synaptic vesicles are saturated, excess α Syn may associate with other compartments, including endosomes, leading to sustained defects in synaptic vesicle homeostasis and neurotransmission. In addition, excess α Syn deposited in Lewy bodies may irreversibly sequester CK1 δ and other vesicle-associated proteins, resulting in loss of CK1 δ activity and reduced protection against these defects. In summary, our study points that endosome defects and CK1 δ dysfunction may be relevant for the pathogenesis of synucleinopathies.

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TABLES

Table I. Strains used in this study

Strain	MT ¹	Genotype	Source
BY4741	MATa	<i>his3Δ1 leu2Δ0 met15Δ0 ura3Δ0</i>	
FRY346	MATa	BY4741 <i>TP11pr-8xMYC-SNC1::URA3</i>	This study
Y5563	MAT α	<i>can1Δ::MF1pr-HIS3 hyp1Δ his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 LYS2+</i>	
VSY1	MATa	BY4741 <i>ade2Δ0::SNCA(WT)-GFP NatR</i>	This study
VSY2	MAT α	Y5563 <i>trp1Δ0::SNCA(WT)-GFP URA3+</i>	This study
VSY4	MAT α	VSY2 <i>ade2Δ0::SNCA(WT)-GFP NatR</i>	This study
VSY57	MATa	VSY4 <i>yck1Δ0::KanR</i>	This study
VSY58	MATa	VSY4 <i>yck2Δ0::KanR</i>	This study
VSY59	MATa	VSY4 <i>tlg2Δ0::KanR</i>	This study
VSY60	MATa	VSY4 <i>spo14Δ0::KanR</i>	This study
<i>yck1Δ</i>	MATa	BY4741 <i>yck1Δ0::KanR</i>	
<i>yck2Δ</i>	MATa	BY4741 <i>yck2Δ0::KanR</i>	
<i>spo14Δ</i>	MATa	BY4741 <i>spo14Δ0::KanR</i>	
<i>tlg2Δ</i>	MATa	BY4741 <i>tlg2Δ0::KanR</i>	
<i>pdr1Δ</i>	MATa	BY4741 <i>pdr1Δ0::KanR</i>	
<i>did3Δ</i>	MATa	BY4741 <i>did3Δ0::KanR</i>	
<i>end3Δ</i>	MATa	BY4741 <i>end3Δ0::KanR</i>	
<i>rcy1Δ</i>	MATa	BY4741 <i>rcy1Δ0::KanR</i>	
<i>sac6Δ</i>	MATa	BY4741 <i>sac6Δ0::KanR</i>	
<i>vps23Δ</i>	MATa	BY4741 <i>vps23Δ0::KanR</i>	
<i>vps35Δ</i>	MATa	BY4741 <i>vps35Δ0::KanR</i>	
<i>ypt7Δ</i>	MATa	BY4741 <i>ypt7Δ0::KanR</i>	
<i>ypt31Δ</i>	MATa	BY4741 <i>ypt31Δ0::KanR</i>	
<i>ypt51Δ</i>	MATa	BY4741 <i>ypt51Δ0::KanR</i>	
RSY255	MAT α	<i>ura3-52 leu2-3,-112</i>	
RY782	MAT α	<i>his4-619 ura3-52 sec1-1</i>	
RY112	MATa	<i>his4-619 ura3-52 leu2-3,-112 trp1-289 sec 7-4</i>	
RY271	MAT α	<i>his4-619 ura3-5 sec18-1</i>	
VSY64	MAT α	VSY4 <i>pdr1Δ0::KanR</i>	This study
VSY65	MATa	VSY57 <i>yck1Δ0::kanRΔ0::LEU2</i>	This study
VSY66	MATa	VSY65 <i>pdr1Δ0::KanR</i>	This study
W303-1A	MATa	<i>can1-100 his3-11 15 leu2-3 112 trp1-1 ura3-1 ade2-1</i>	
VSY67	MATa	W303-1A <i>ura3-1::pRS306 URA3+</i>	This study
VSY68	MATa	W303-1A <i>ura3-1::GAL1pr-SNCA(WT)-GFP URA3+</i>	This study
VSY69	MATa	W303-1A <i>ura3-1::GAL1pr-SNCA(S129A)-GFP URA3+</i>	This study
VSY70	MATa	W303-1A <i>ura3-1::GAL1pr-SNCA(S129E)-GFP URA3+</i>	This study
VSY71	MATa	VSY67 <i>trp1-1::pRS304 TRP1+</i>	This study
VSY72	MATa	VSY68 <i>trp1-1::GAL1pr-SNCA(WT)-GFP TRP1+</i>	This study
VSY73	MATa	VSY69 <i>trp1-1::GAL1pr-SNCA(S129A)-GFP TRP1+</i>	This study
VSY74	MATa	VSY70 <i>trp1-1::GAL1pr-SNCA(S129E)-GFP TRP1+</i>	This study
VSY75	MATa	VSY71 <i>yck1Δ0::KanR</i>	This study
VSY76	MATa	VSY72 <i>yck1Δ0::KanR</i>	This study
VSY77	MATa	VSY73 <i>yck1Δ0::KanR</i>	This study
VSY78	MATa	VSY74 <i>yck1Δ0::KanR</i>	This study
VSY79	MAT α	Y5563 <i>trp1Δ0::pRS405 LEU2+</i>	This study
VSY80	MAT α	Y5563 <i>trp1Δ0::SNCA(WT)-GFP LEU2+</i>	This study
VSY81	MAT α	Y5563 <i>trp1Δ0::SNCA(S129A)-GFP LEU2+</i>	This study
VSY82	MAT α	Y5563 <i>trp1Δ0::SNCA(S129E)-GFP LEU2+</i>	This study
VSY83	MAT α	VSY79 <i>pdr1Δ0::pRS465 URA3+</i>	This study
VSY84	MAT α	VSY80 <i>pdr1Δ0::SNCA(WT)-GFP URA3+</i>	This study
VSY85	MAT α	VSY81 <i>pdr1Δ0::SNCA(S129A)-GFP URA3+</i>	This study
VSY86	MAT α	VSY82 <i>pdr1Δ0::SNCA(S129E)-GFP URA3+</i>	This study

¹Mating type

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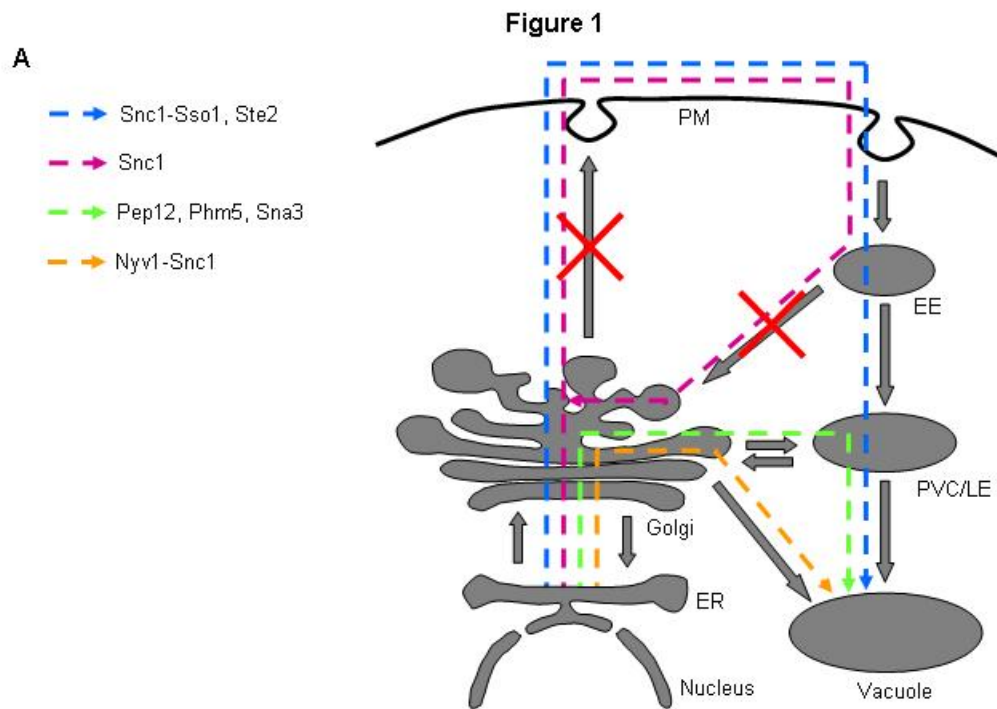
Table II. Characteristics of human cases analyzed in this study

Group	Age (years)	Gender M/F¹	Blessed score (range)	Braak stage (range)	Plaques per mm²	Tangles per 0.1 mm²	Lewy bodies	Brain weight (grams)
Non demented (n=4)	83+/-2	2/2	0-1	0-1	0.25	0	0	1150+/-40
AD (n=6)	81+/-2	3/3	13-33	5-6	25+/-3	5+/-1	0	1070+/-35
DLB/PD (n=8)	83+/-1	5/3	6-33	2-4	28+/-3	2+/-1	3+/-1	1110+/-60

¹Males/Females

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FIGURES



CHAPTER 2 – GENETIC CONTEXT-DEPENDENT MODULATION OF α -SYNUCLEIN TOXICITY AND TRAFFICKING DEFECTS BY PHOSPHORYLATION OF SERINE 129

Figure 1

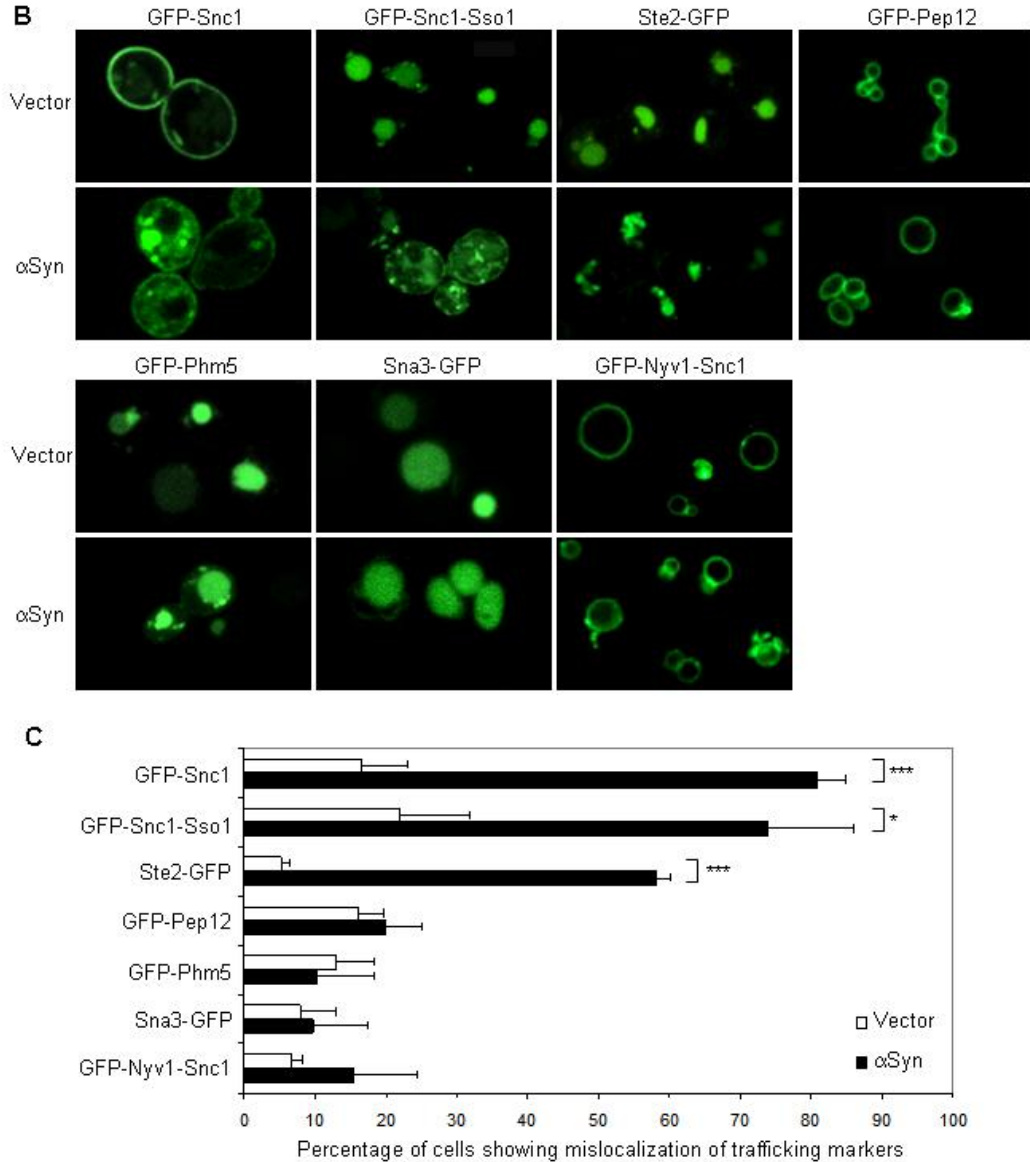


Figure 1. α Syn overexpression causes the mislocalization of late-exocytic and early-endocytic protein markers. (A) Schematic representation of the routes tracked by the indicated protein markers in yeast. Red crosses indicate putative trafficking steps blocked by constitutive α Syn expression. EE: early endosome; ER: endoplasmic reticulum; PM:

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plasma membrane; PVC/LE: prevacuolar complex/late endosome. (B) Effect of αSyn on the localization of the indicated protein trafficking markers. The BY4741 strain co-transformed with plasmids for the expression of the indicated protein markers and untagged WT αSyn under the control of a *GPD1* constitutive promoter or the corresponding empty vector was photographed in log phase. (C) Quantification of the percentage of cells from (B) exhibiting mislocalization of the indicated trafficking markers. Error bars represent standard deviations of three experiments. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; student's t test.

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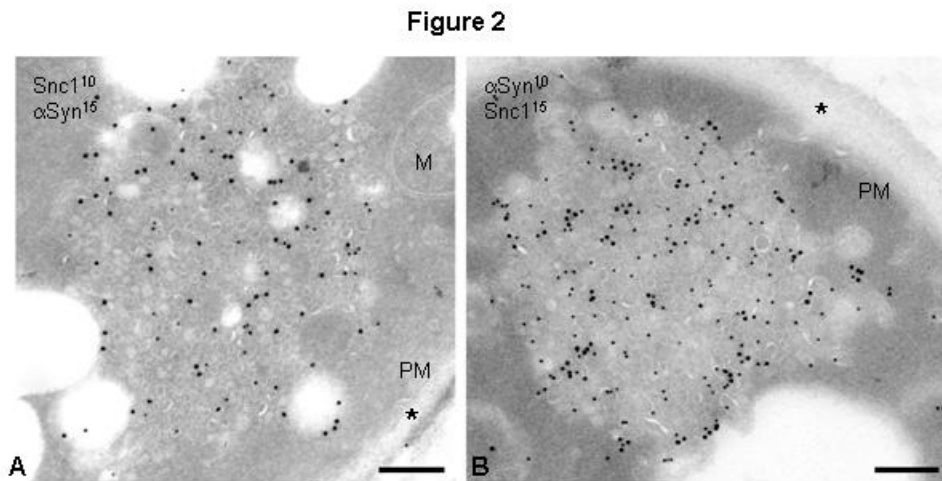
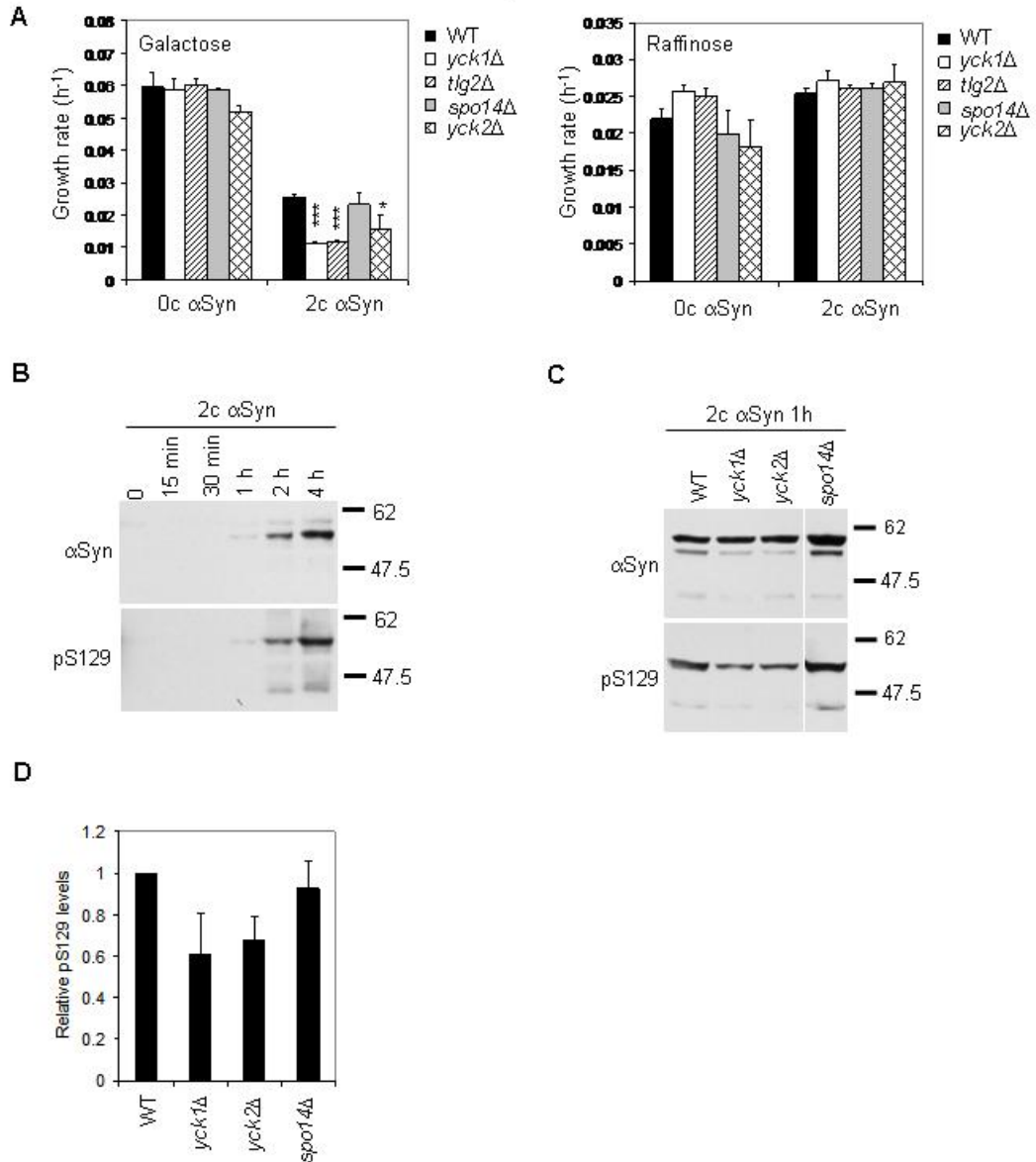


Figure 2. α Syn-induced vesicular clusters contain the exocytic SNARE Snc1. The strain FRY346 carrying an integrated $\delta xMYC$ -*SNC1* fusion and transformed with a plasmid for the expression of α Syn-GFP under the control of a constitutive *GPD1* promoter was grown to log phase, and cells were processed for IEM. In the left panel (A), cryosections were first incubated with anti-myc antibodies and then with anti GFP antibodies (α Syn¹⁵, 15-nm gold particles; Snc1¹⁰, 10-nm gold particles) whereas in the right panel (B) the sequence of the antibodies was inverted (α Syn¹⁰, 10-nm gold; Snc1¹⁵, 15-nm gold particles). PM, plasma membrane; M, mitochondria; *, cell wall. Bar, 200 nm.

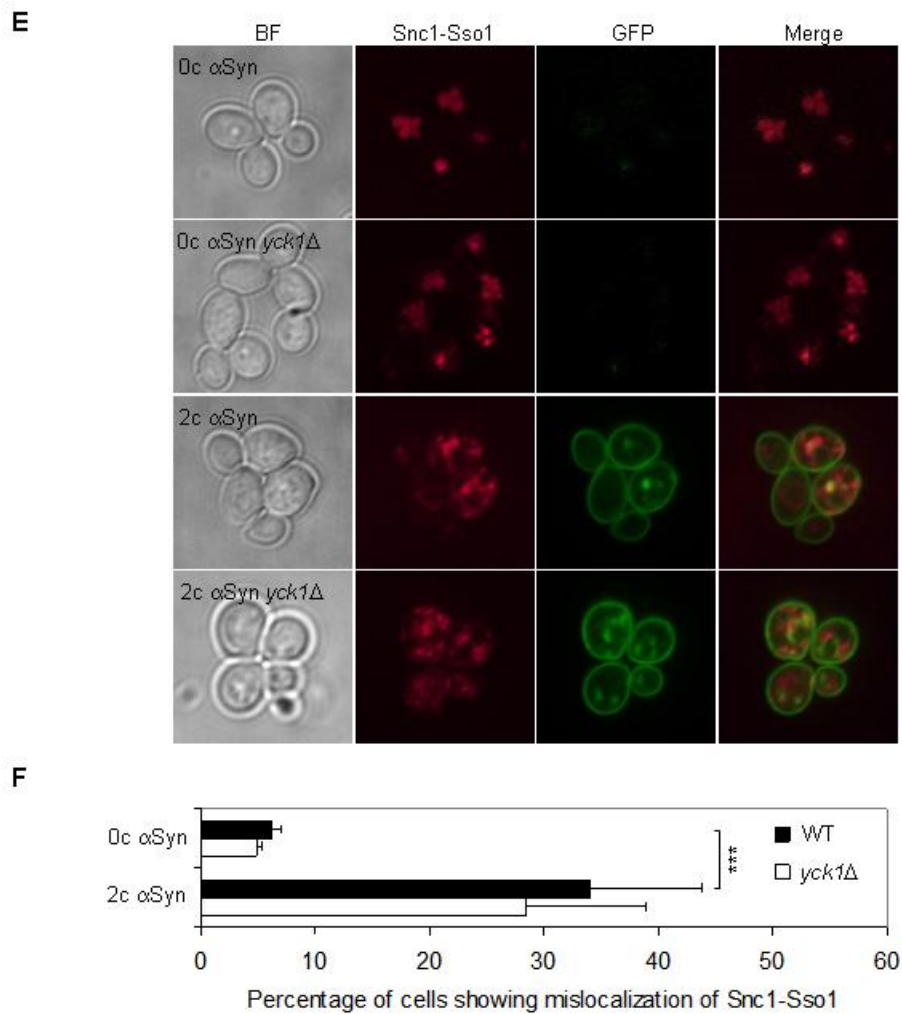
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Figure 3



CHAPTER 2 – GENETIC CONTEXT-DEPENDENT MODULATION OF α -SYNUCLEIN TOXICITY AND TRAFFICKING DEFECTS BY PHOSPHORYLATION OF SERINE 129

Figure 3



CHAPTER 2 – GENETIC CONTEXT-DEPENDENT MODULATION OF α -SYNUCLEIN TOXICITY AND TRAFFICKING DEFECTS BY PHOSPHORYLATION OF SERINE 129

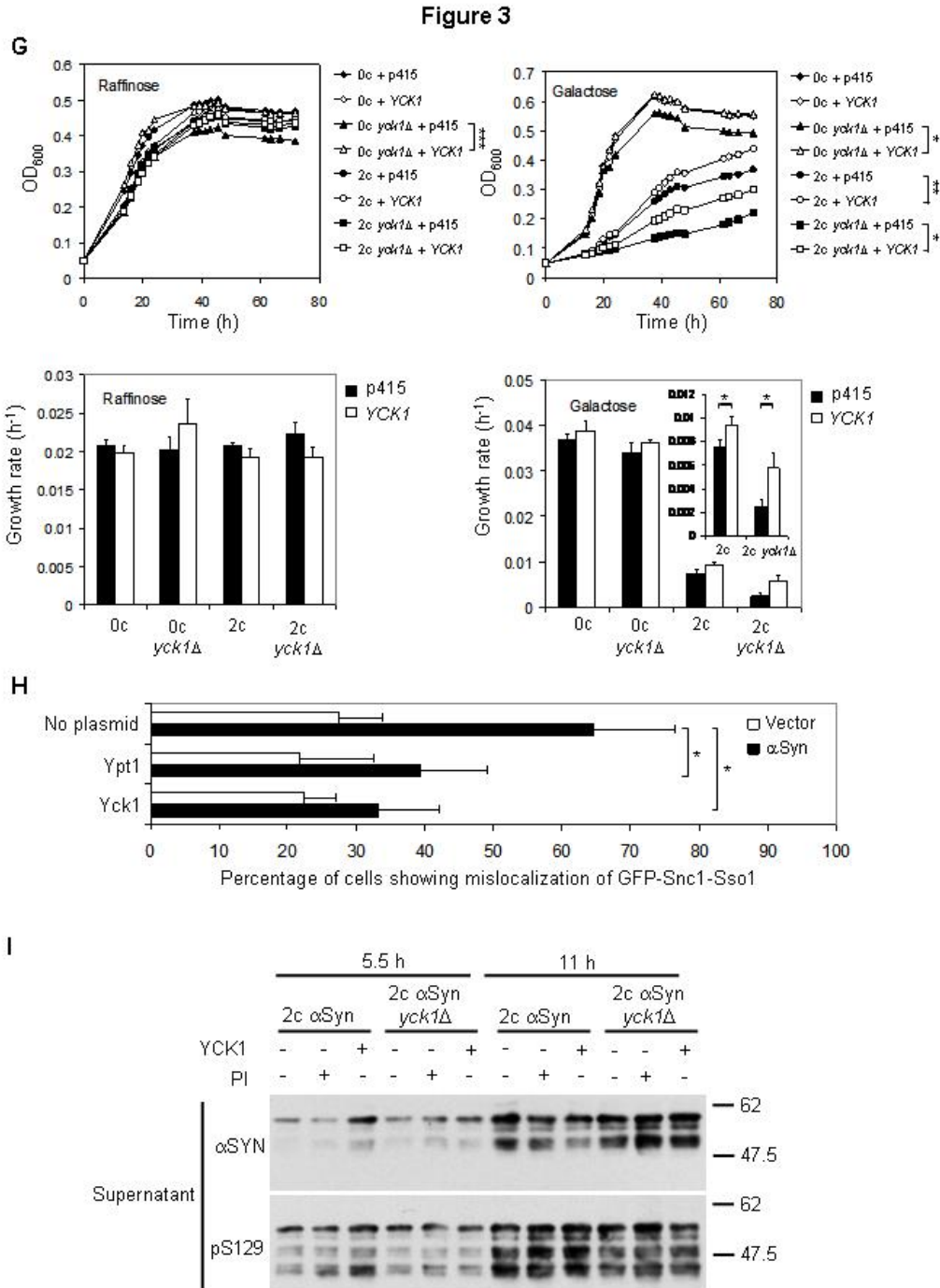


Figure 3. Yck1 attenuates α Syn-induced toxicity and trafficking defects through a

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S129 phosphorylation-independent mechanism. (A) Deletion of CKI genes (*yck1* Δ , *yck2* Δ) enhances the growth defect caused by α Syn overexpression in the BY4741 genetic background. Growth rates of WT cells or the indicated mutant strains containing either two copies (2c) or no copies (0c) of the α Syn gene in the BY4741 genetic background in conditions that do (galactose) or do not (raffinose) induce the expression of α Syn. The *tlg2* Δ and *spo14* Δ mutants are included as positive and negative controls, respectively. Growth rates were determined as the slope of the growth curves shown in Fig. S3 during logarithmic phase. (B) Kinetics of α Syn induction and phosphorylation in WT cells containing 2 copies of the α Syn gene in the BY4741 genetic background. Cells were grown to logarithmic phase ($OD_{600} \sim 0.8$) in raffinose-containing media and expression of α Syn was induced with galactose. Aliquots were collected at the indicated times and levels of phosphorylated (pS129) and total α Syn were analyzed by western blot. The soluble fraction is shown. The earliest α Syn was detected after 1 h of induction. (C) Deletion of CKI genes reduces moderately α Syn phosphorylation. The indicated strains were induced for 1 h and analyzed by western blot as described in (B). (D) Quantification of the S129 phosphorylation levels were estimated as the ratio of the band densities of phosphorylated relative to total α Syn from (C). (E) Deletion of *YCK1* does not enhance the defects in the trafficking of the marker Snc1-Sso1 caused by α Syn. WT or *yck1* Δ cells containing 2 copies (2c) or no copies (0c) of the α Syn-GFP gene in the BY4741 genetic background were transformed with a plasmid for the expression of trafficking marker mCherry-Snc1-Sso1, induced overnight in galactose-containing media

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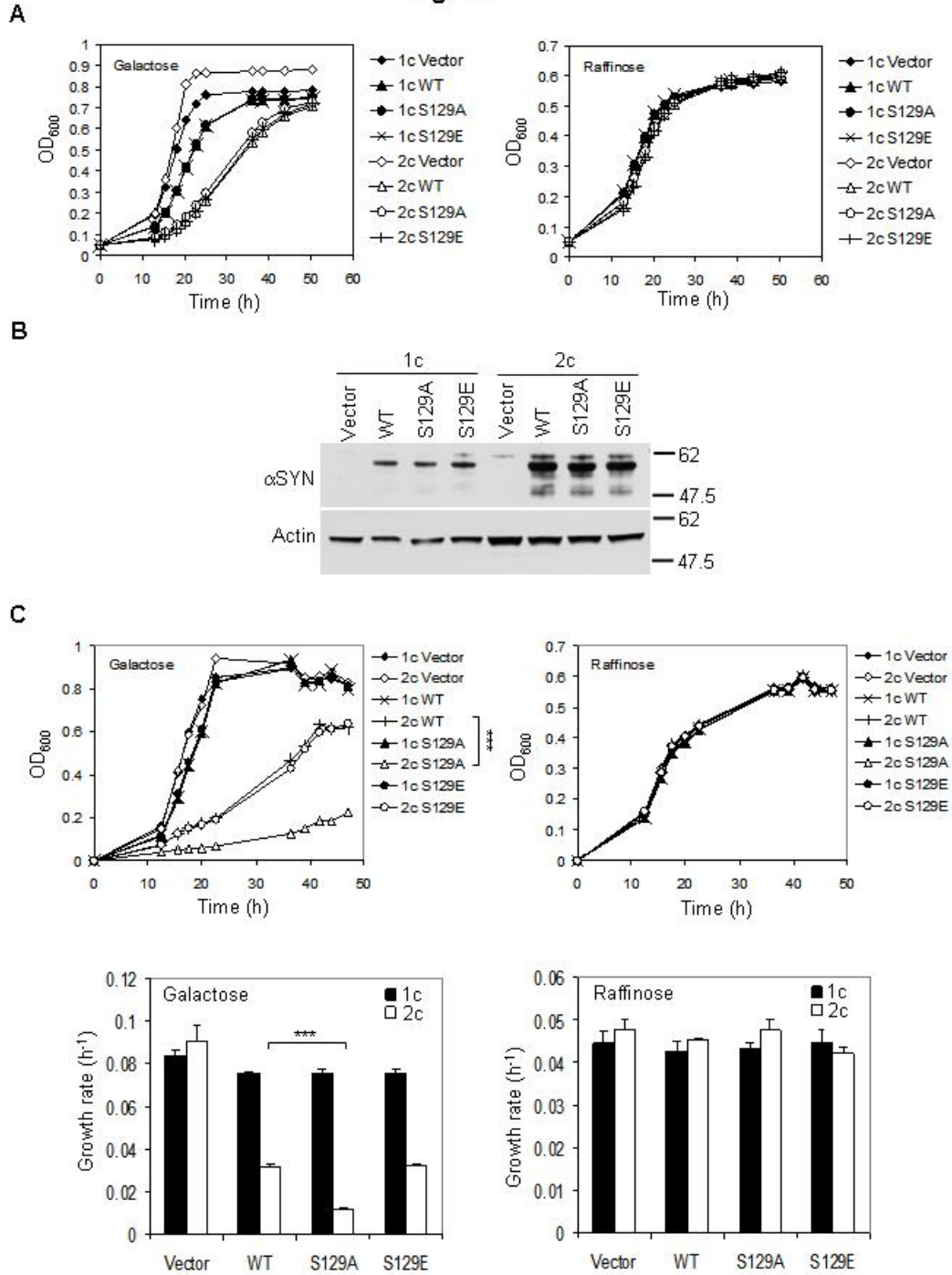
and imaged in logarithmic phase. (F) Quantification of the percentage of cells from (E) showing mislocalization of Snc1-Sso1. (G) Overexpression of *YCK1* attenuates α Syn-induced growth defects. Growth curves (upper panels) and growth rates (lower panels) of WT or *yck1* Δ cells containing 2 copies (2c) or no copies (0c) of the α Syn-GFP gene in the BY4741 genetic background and transformed with a plasmid for the over-expression of *YCK1* or the corresponding empty plasmid (p415). Growth rates were determined as the slope of the growth curves during logarithmic phase. (H) Yck1 and Ypt1 partially restore targeting of GFP-Snc1-Sso1 to the vacuolar lumen. BY4741 cells expressing GFP-Snc1-Sso1 were transformed with either untagged WT α Syn under the control of a constitutive *GPD1* promoter or the corresponding empty vector and the indicated plasmids for the over-expression of *YPT1* or *YCK1*. After transfer to a galactose-containing medium, cells were photographed in logarithmic phase. The percentage of cells exhibiting mislocalization of GFP-Snc1-Sso1 is shown. (I) Overexpression of *YCK1* does not increase α Syn phosphorylation at S129. WT or *yck1* Δ cells containing 2 copies (2c) or no copies (0c) of the α Syn-GFP gene in the BY4741 genetic background and transformed with a plasmid for the over-expression of *YCK1* or the corresponding empty plasmid were grown to logarithmic phase in raffinose-containing medium and induced with galactose. Aliquots were collected at the indicated times for western blot analysis. The indicated cultures were treated with the phosphatase inhibitors (PI) okadaic acid and activated Na_3VO_4 for 15 min before being collected. Error bars represent standard deviations from three experiments in panels (A), (F), (G) and (H) and two experiments in

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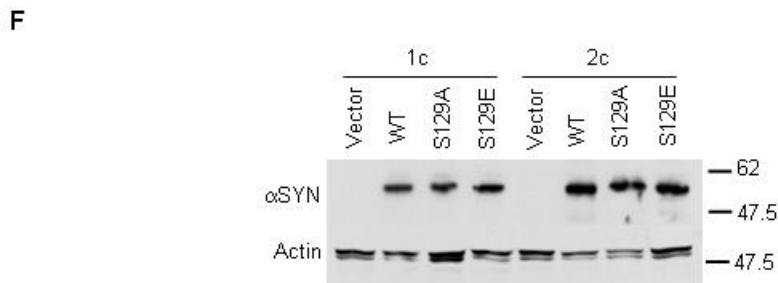
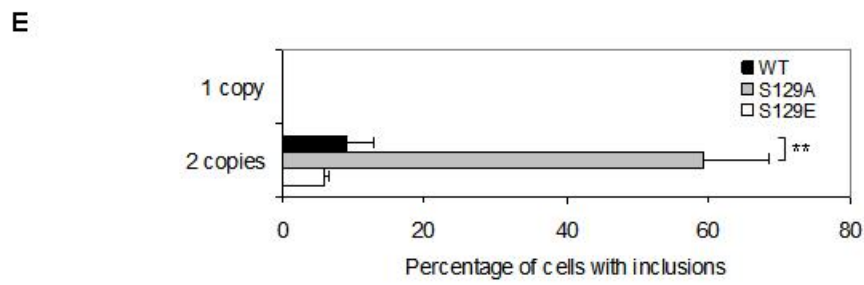
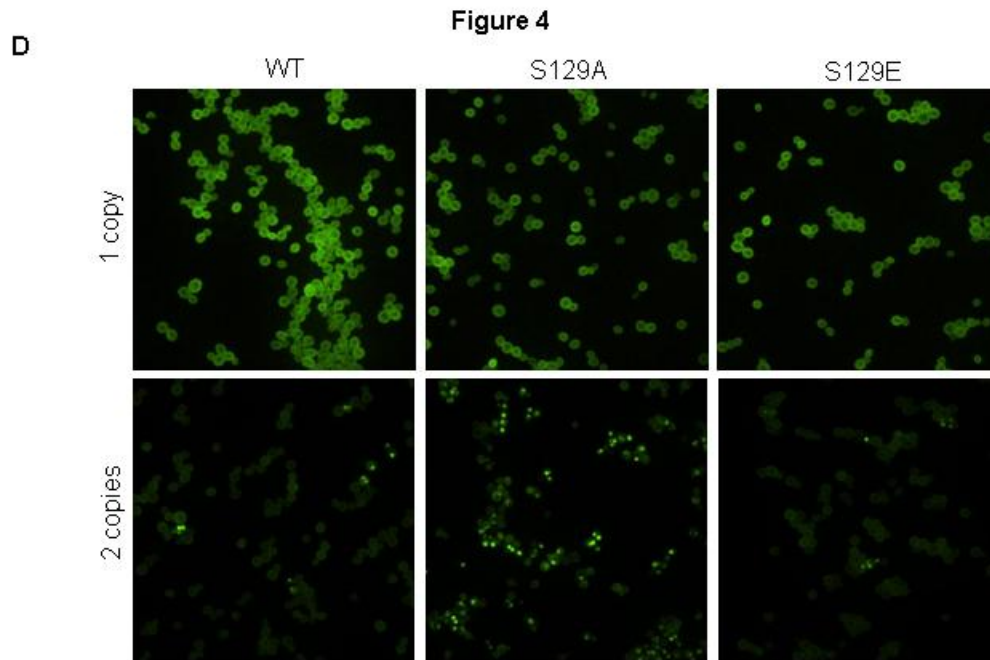
panel (D). * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; (A), (F), (G, lower panels), and (H), student's t test; (G, upper panels), ANOVA for repetitive measurements.

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Figure 4

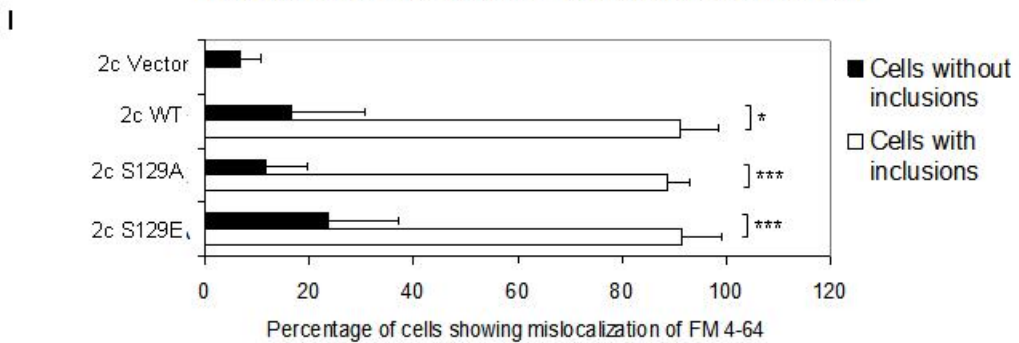
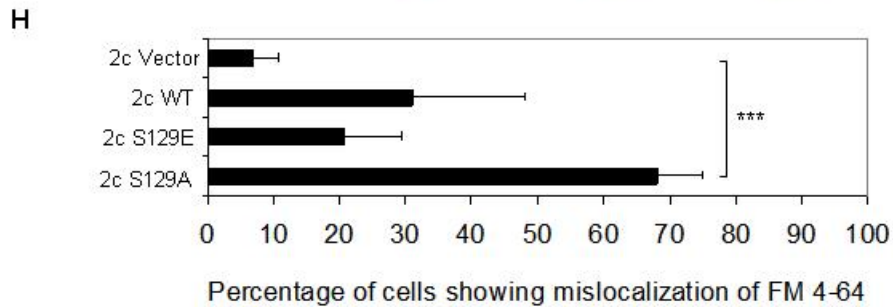
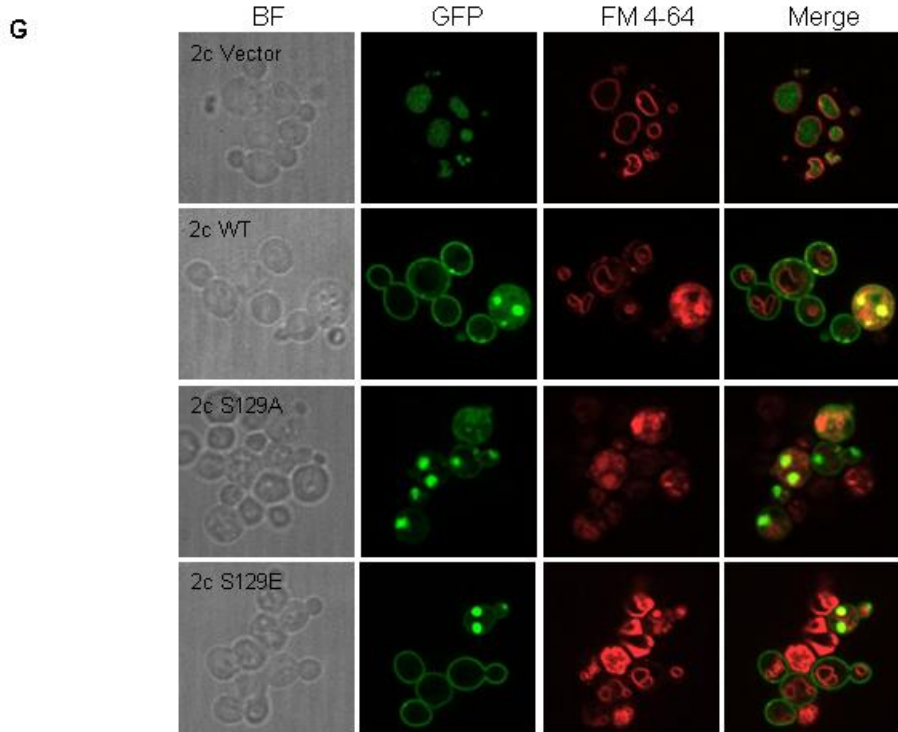


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Figure 4



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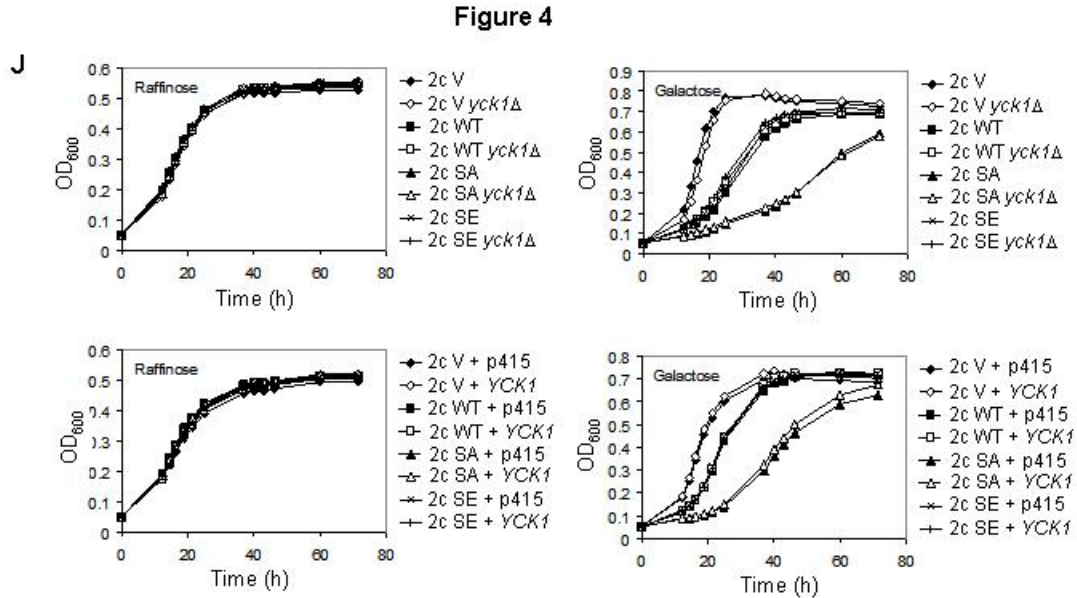


Figure 4. Preventing phosphorylation of S129 increases α Syn-induced toxicity and trafficking defects in a genetic context-dependent manner. (A) Growth curves of strains containing one (1c) or two (2c) copies of either the wild type (WT) α Syn gene or the phosphorylation mutants (S129A, S129E) or the corresponding empty vector in the BY4741 genetic background in conditions that do (galactose) or do not (raffinose) induce the expression of α Syn. (B) S129 mutations do not alter the levels of α Syn in the BY4741 background. Western blot of strains from (A) grown for 8 h in galactose-containing medium. (C) Growth curves (upper panels) or growth rates (lower panels) of strains containing one (1c) or two (2c) copies of either the wild type (WT) α Syn gene or the phosphorylation mutants (S129A, S129E) or the corresponding empty vector in the W303-1A genetic background in conditions that do (galactose) or do not (raffinose)

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induce the expression of α Syn. Growth rates were determined as the slope of the growth curves during logarithmic phase. (D) Localization of α Syn in the strains from (C) photographed in logarithmic phase. (E) Quantification of the percentage of cells from (D) exhibiting α Syn inclusions. (F) S129 mutations do not alter the levels of α Syn in the W303-1A background. Western blot of strains from (C) grown for 8 h in galactose-containing medium. (G) Preventing S129 phosphorylation enhances mislocalization of FM 4-64 caused by α Syn in the W303-1A background. Strains from (C) were co-stained with the dye FM 4-64 and imaged in logarithmic phase. (H) Quantification of the percentage of total cells from (G) showing mislocalization of the dye FM 4-64. (I) Quantification of the percentage of cells with and without inclusion from (G) showing mislocalization of FM 4-64. Typically, cells with inclusions display anomalies in the localization pattern of FM 4-64. (J) Deletion or overexpression of *YCK1* in the W303-1A background does not modify α Syn-induced growth defects. Growth curves of strains from (A) in which *YCK1* was either deleted (*yck1* Δ , upper panels) or overexpressed (*YCK1*, lower panels) in conditions that do (galactose) or do not (raffinose) induce the expression of α Syn. SA, S129A; SE, S129E. In panels (C), (E), (H), and (I), error bars represent standard deviations from three experiments. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; (C, lower panels), (E), (H), and (I), student's t test; (C, upper panels), ANOVA for repetitive measurements.

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Figure 5

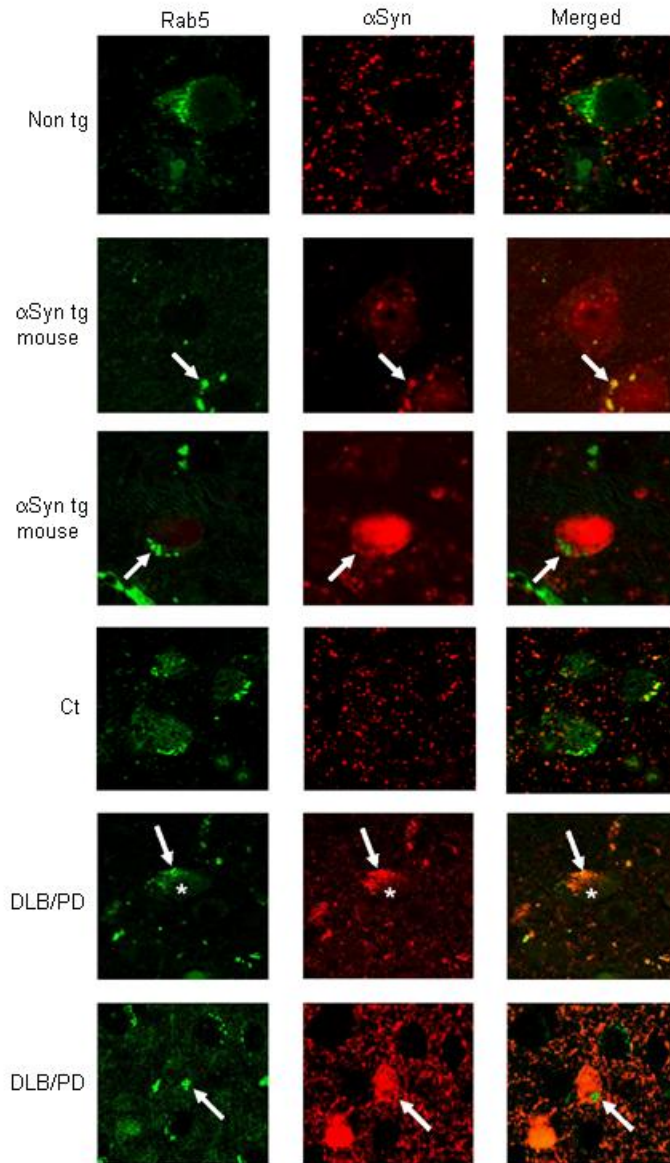


Figure 5. Abnormal endosome morphology in α Syn Tg Mice and in synucleinopathy brains. Abnormally enlarged Rab5-positive endosomes co-localize with granular inclusions of α Syn and accumulate in the vicinity of α Syn inclusions in α Syn tg mice

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and human DLB/PD. Cortical sections from α Syn tg mice or DLB/PD cases were double-labeled with antibodies against α Syn and Rab5 and detected with Tyramide Red or fluorescein isothiocyanate (FITC)-conjugated secondary antibodies, respectively. Images of non tg animals and control (Ct) subjects are included for reference. Arrows indicate the Rab5-positive compartments.

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Figure 6

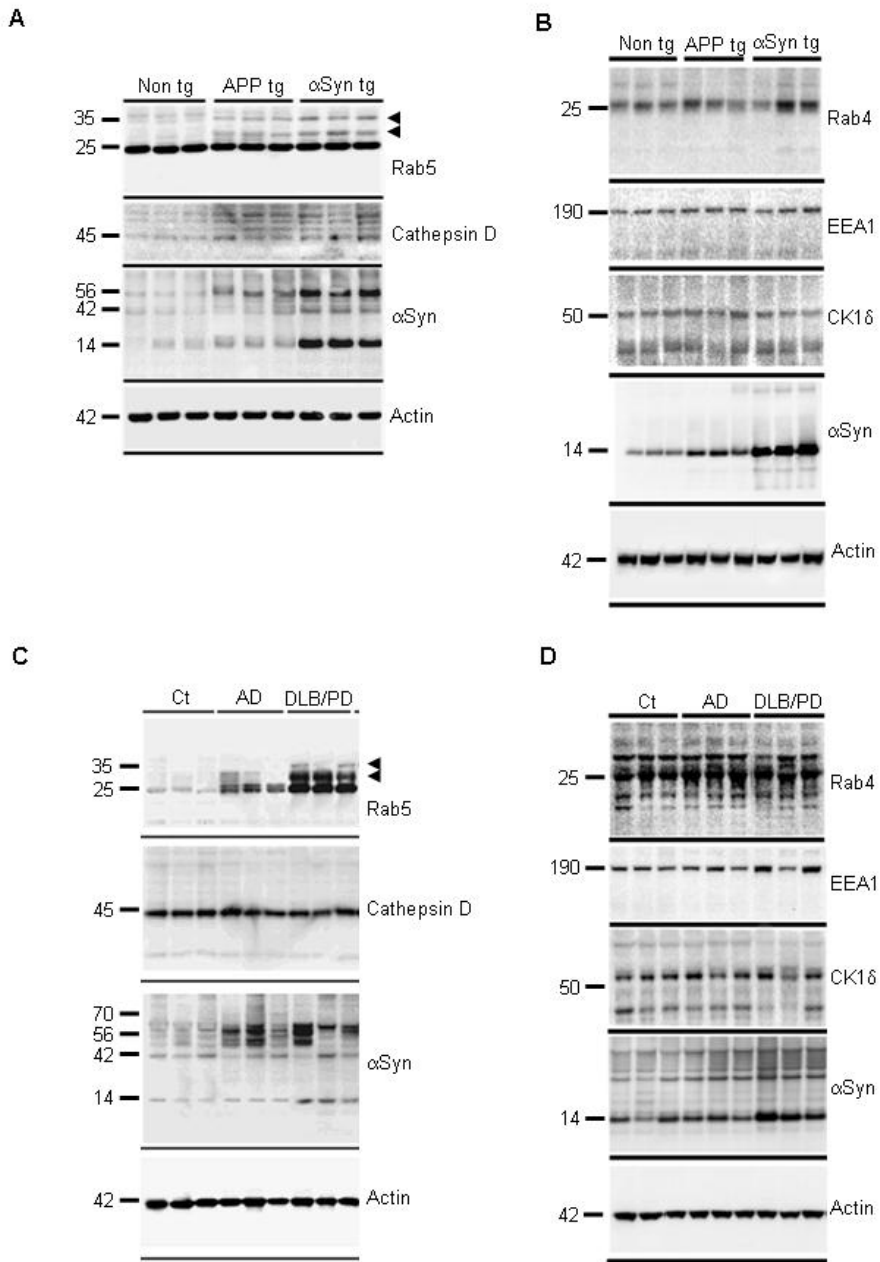


Figure 6. Anomalies in the mobility and levels of the early endosome marker Rab5, but not Rab4, EEA1 or CK1 δ , in mice models and human synucleinopathies. Brain

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particulate fractions from α Syn tg, APP tg, or non-tg mice (A and B) or from human DLB/PD or AD patients or control (Ct) subjects (C and D) were analyzed by western blot with the indicated antibodies. Arrowheads indicate Rab5 low mobility forms.

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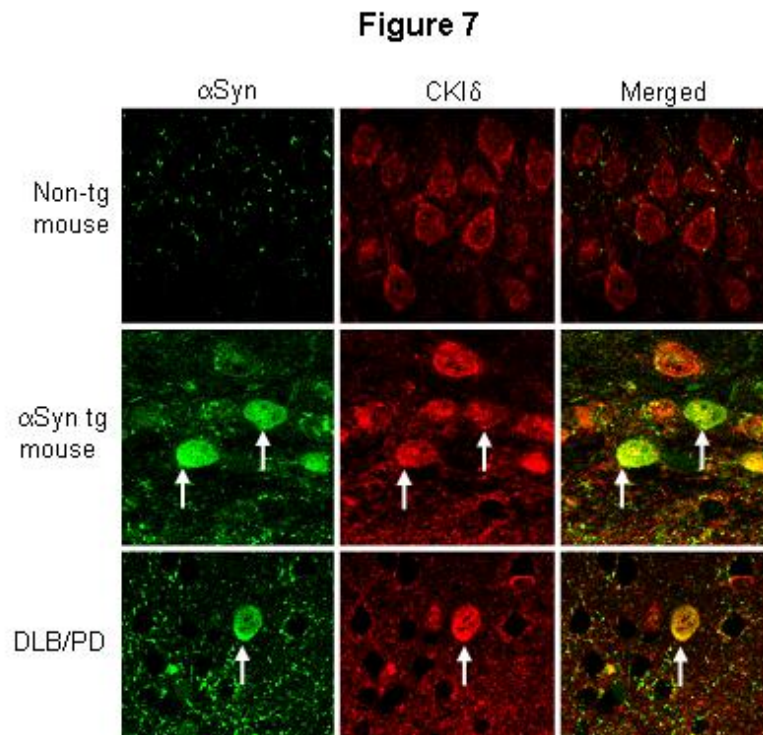


Figure 7. CKI δ co-localizes with α Syn inclusions in α Syn tg mice and human DLB/PD. Cortical sections from non-tg mice, α Syn tg mice, or human DLB/PD cases were double-labeled with antibodies against α Syn and CKI δ and detected with FITC and Tyramid Red-conjugated secondary antibodies, respectively. Arrows indicate the α Syn-positive inclusions.

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Figure 8

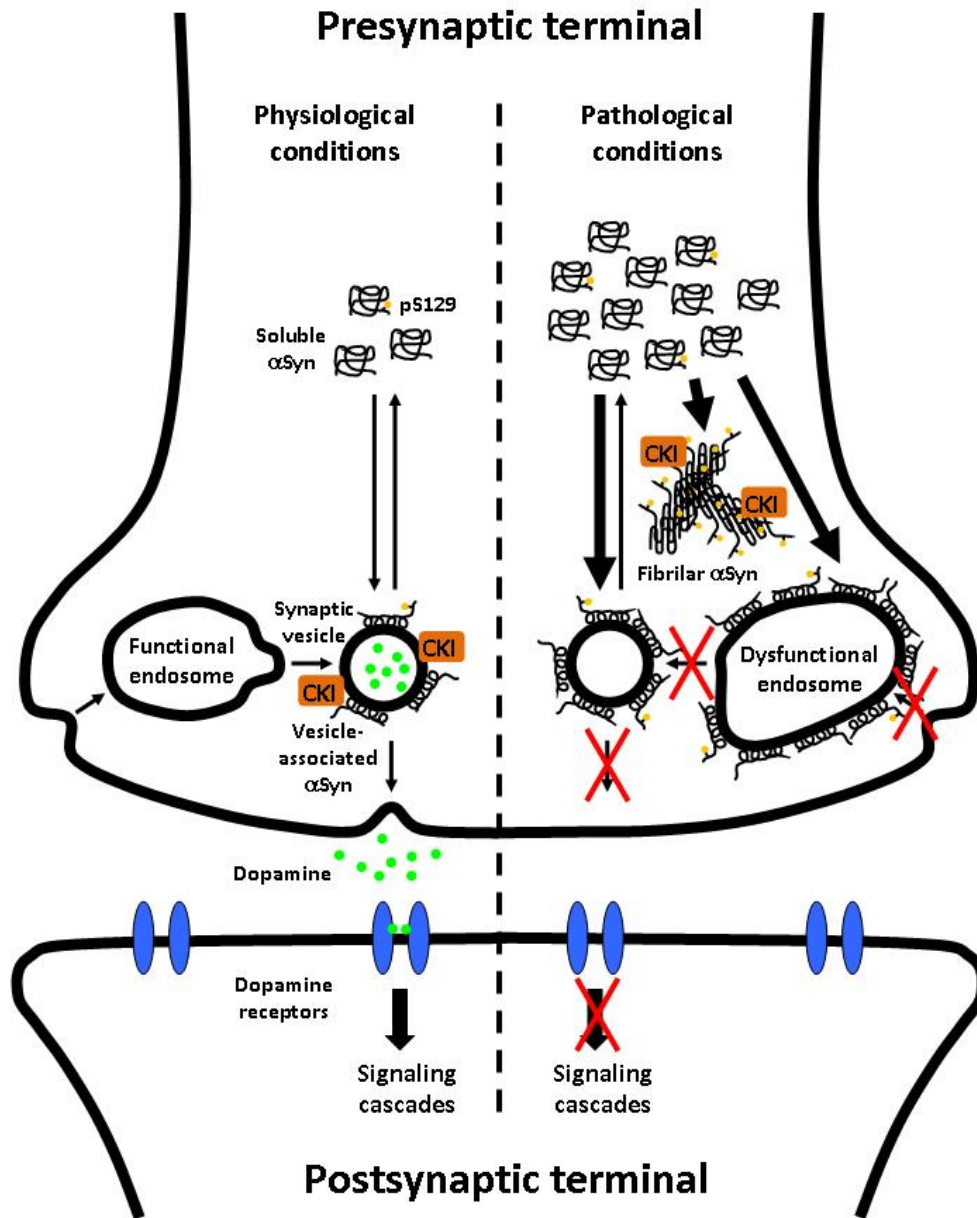


Figure 8. A model depicting how α Syn accumulation may cause neurotransmission defects in PD. We hypothesize that, under normal conditions, CKI regulates α Syn function and possibly association with Synaptic vesicles and neurotransmitter release by

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phosphorylating synaptic proteins, including α Syn at S129. Under pathological conditions in which α Syn accumulates and synaptic trafficking and neurotransmission are compromised, CKI may play a protective role in attenuating vesicular trafficking defects and restoring synaptic transmission. However, when all binding sites in synaptic vesicles are saturated, excess α Syn may associate with other compartments, such as endosomes, leading to abnormally enlarged endosomes and defects in synaptic vesicle homeostasis and neurotransmission. In addition, excess α Syn may form insoluble fibrillar deposits that sequester CKI, depleting CKI activity and enhancing synaptic defects. Red crosses indicate possible trafficking steps blocked by α Syn.

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Figure S1

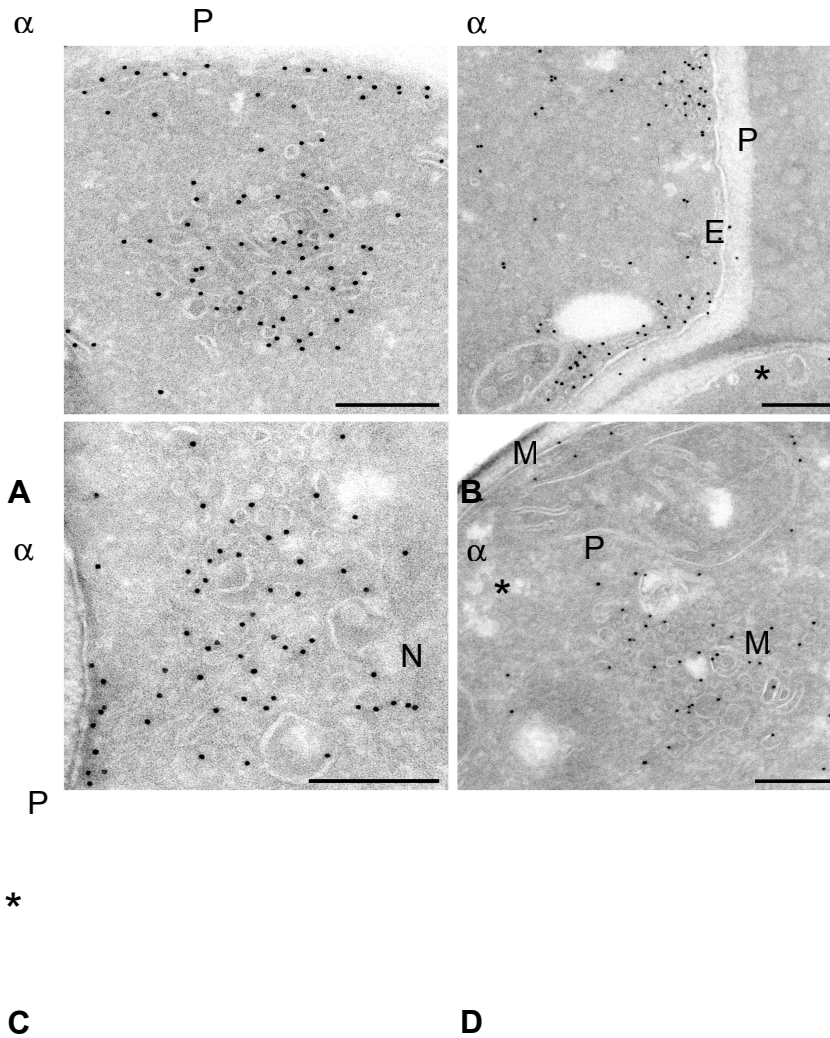


Figure S1. Expression of α Syn in yeast cells leads to the formation of clusters of vesicles. α Syn-GFP expression was induced in the yeast strain BY4741 for either 6h (A and B) or 12h (C and D) and cells were fixed and processed for IEM. At both time points, α Syn (α Syn¹⁰, 10-nm gold particles) is detected on the PM but also on the surface of vesicles that accumulate in cytoplasmic clusters. PM, plasma membrane; ER, endoplasmic reticulum; N, nucleus; M, mitochondria; *, cell wall. Bar, 200 nm.

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ABBREVIATIONS

AD, Alzheimer's disease; CK, casein kinase; CPY, carboxypeptidase Y; DLB, dementia with Lewy bodies; EE, early endosomes; ER, endoplasmic reticulum; GFP, green fluorescent protein; GPD, glyceraldehyde-3-phosphate dehydrogenase; IEM, immunoelectron microscopy; LE, late endosomes; PD, Parkinson's disease; PM, plasma membrane; S129, serine 129; α Syn, α -Synuclein; SNARE, soluble N-ethylmaleimide-sensitive factor attachment protein receptor; WT, wild type.

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ABSTRACT

α -Synuclein (α SYN), a major player in Parkinson's disease pathogenesis, is thought to impair vesicle trafficking as a toxic gain of function through aggregation. Genetic screens for modifiers of α SYN toxicity have overwhelmingly identified a significant subset of genes involved in vesicle trafficking. Through shRNA-mediated gene knock down and overexpression studies, we show that genetic manipulation of Stx7, Vps24, Vps28, Vps34, Vps45 and Vps52, genes involved in endosomal transport, is sufficient to modulate the toxicity of α SYN in a SH-SY5Y cell line and rat primary cortical neurons. Furthermore, we demonstrate that α SYN toxicity correlates with impairments in exocytosis, increase in constitutive receptor recycling of the transferrin receptor and enlargement of the Golgi apparatus. These abnormalities in the vesicle trafficking pathways can be altered by genetic modifiers of α SYN toxicity. Our findings are indicative of a key role for early endosomal trafficking in α SYN pathogenesis.

INTRODUCTION

Parkinson's disease (PD), a common movement disorder generally affecting individuals above the age of 60, is caused by degeneration of dopaminergic neurons in the *substantia nigra pars compacta* region of the brain (reviewed by Moore et al., 2005).

Intracytoplasmic inclusions termed Lewy bodies, a hallmark of PD, are found in the affected neurons (Lücking and Brice, 2000), and are primarily comprised of the protein α SYN (Baba et al., 1998). A highly conserved protein of 140 amino acid residues that is ubiquitously expressed in the brain and found abundantly in presynaptic terminals

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(George and Clayton, 1998), α SYN has been implicated in the pathogenesis of both sporadic and familial forms of PD (Polymeropoulos et al., 1997; Kruger et al., 1998; Chiba-Falek et al., 2006; Mizuta et al., 2006). While the physiological function of α SYN remains poorly understood, overexpression of the protein in cultured cells has been shown to inhibit phospholipase D (Jenco et al., 1998), induce the oxidative stress and the unfolded protein response (Cookson and van der Brug, 2008), cause proteasome dysfunction (Lindersson et al., 2004; Betarbet et al., 2005), impair vesicle trafficking (Cooper et al., 2006; Gitler et al., 2008) and inhibit neurotransmitter release (Abeliovich et al., 2000; Nemani et al., 2010).

Impairment of any of these key cellular processes could understandably cause neuronal toxicity. In order to develop effective therapeutic treatments for PD however, it is essential to distinguish between direct pathogenic effects of the α SYN protein and indirect consequences of abnormal α SYN interactions. Multiple genetic screens have been conducted in *Saccharomyces cerevisiae* (Willingham et al., 2003; Cooper et al., 2006; Flower et al., 2007) and *Caenorhabditis elegans* (Hamamichi et al., 2008; van Ham et al., 2008) to identify genes that protect cells from α SYN toxicity. In these screens, genes involved in vesicle trafficking and lipid metabolism were over-represented as modifiers of α SYN toxicity. However, the physiological relevance of these studies needs to be ascertained as these organisms do not natively express a synuclein homolog.

In this study, we used a WT α SYN –Tet-off inducible SH-SY5Y cell culture system that

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has been shown to exhibit α SYN toxicity when α SYN expression is induced in differentiated cells (Vekrellis et al., 2009) to determine whether vesicle trafficking genes can modulate α SYN toxicity. We show that down-regulation of human orthologs of yeast vacuolar protein sorting (Vps) genes increase α SYN toxicity. Furthermore, overexpression of these human orthologs is protective against α SYN toxicity in the SH-SY5Y cell culture model, as well as in primary neuronal cultures. Here we show that human orthologs of VPS genes are both necessary and sufficient to modulate α SYN toxicity in SH-SY5Y cells. Thus, manipulation of the expression of Vps genes might be a neuroprotective strategy to treat PD and other synucleinopathies.

RESULTS

Validation of yeast genetic modifiers of α SYN toxicity in SH-SY5Y cells

Our prior genetic screens in yeast identified genes involved in vesicle trafficking as both potent enhancers and suppressors of α SYN-induced toxicity (Willingham et al., 2003). As a first step, we sought to confirm that vesicle trafficking genes also modulated α SYN-induced toxicity in mammalian cells. For that purpose, we decided to study 11 yeast genetic modifiers involved in vesicle trafficking based on the functional homology of their human orthologs (table 1). We designed shRNA against the human orthologs of the yeast genetic modifiers to study the effect of regulating their expression levels in a SH-SY5Y cell line stably transfected with wild type- α SYN under the control of a Tet-off promoter (Vekrellis et al., 2009). In this cell line, we found that induction of α SYN induces toxicity, resulting in the retraction of neuronal processes and membrane blebbing

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(fig. 1), approximately 7 days after induction and differentiation as measured by the amount of LDH released into culture media by dead cells (Fig.2a). We confirmed our result using an alternate assay for cell death based on the fluorescence of the dye calcein-AM in the LIVE/DEAD assay (Fig. 2b).

We observed between 30 and 50 % knockdown of gene expression through transfection of the shRNA constructs (fig. 3a), with a transfection efficiency of approximately 40% (fig. 3a). 10 of the 11 genetic modifiers tested in this study are orthologs of yeast loss of function enhancers of α SYN toxicity. Syntaxin 7 (Stx7), a SNARE involved in homotypic late endosome fusion and late endosome to lysosome fusion, is the ortholog of the yeast vacuolar SNARE, Vam3, a loss of function suppressor of α SYN toxicity. Knockdown of Stx7 showed 30% suppression of α SYN-induced toxicity compared to the scrambled shRNA control (Fig. 3b), corroborating results of our yeast studies. . Despite knockdown of up to 40% at the mRNA level, the three loss of function enhancer human orthologs of Tlg2, a Golgi SNARE, Syntaxin1a, Syntaxin 12 and Syntaxin 16 did not alter α SYN-induced toxicity. 53% & 46% knockdown of Cog6 and Rabgef1 respectively induced toxicity independent of α SYN (data not shown). Strikingly, knocking down expression levels of the human orthologs of yeast vacuolar sorting (Vps) genes, Vps24, Vps28, Vps34, Vps45 and Vps52 all significantly increased α SYN-induced toxicity by 25-60% (Fig. 3c), validating our observations in yeast that Vps genes are potent loss of function enhancers of α SYN-induced toxicity.

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Expression of Vps24, Vps28 and Stx7 reduces α SYN toxicity in differentiated SH-SY5Y cells

We next overexpressed Stx7, Vps24, Vps28, Vps34 and Vps45 in the α SYN overexpressing SH-SY5Y cell line. To confirm proper expression and localization patterns for these proteins, we subcloned the full length cDNAs into a vector encoding a C-terminal mcherry tag. The majority of the mcherry-tagged proteins showed a punctate localization, consistent with their predicted localization pattern in cells (Fig. 4). We found that overexpression of Vps34-mcherry and Vps45-mcherry did not affect α SYN-induced toxicity in the SH-SY5Y cells. Overexpression of Vps24-mcherry and Vps28-mcherry, which function in endosomal cargo sorting as members of the endosomal sorting complex required for transport (ESCRT) complexes downstream of Vps34 did have a small but significant reduction of α SYN-induced toxicity. Surprisingly, overexpression of Stx7-mcherry also decreased α SYN-induced toxicity by approximately 20%, which was comparable to the approximate 20% decrease of α SYN-induced toxicity observed by the overexpression of Vps24-mcherry and Vps28-mcherry. (Fig. 5a, b).

Expression of Vps34 and Stx7 rescues α SYN toxicity in rat primary cortical neurons

We next tested the ability of Stx7 and Vps34 to rescue α SYN-induced toxicity in rat primary neurons transfected with WT human α SYN. Cumulative risk of death curves indicate that primary neurons expressing α SYN have a significantly greater risk of death than control cells (*p < 0.0001, log-rank test). Overexpression of Vps34 and Stx7 resulted in almost complete abolishment of α SYN-induced toxicity (Fig. 6). Together

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with our experiments in differentiated SH-SY5Y cells, these results suggest that overexpression of Vps24, Vps28, Vps34 and Stx7, genes involved primarily in early endosomal trafficking, modulate α SYN-induced toxicity.

α SYN-induced Golgi abnormalities do not correlate with modulation of toxicity by genetic modifiers in differentiated SH-SY5Y cells

Neuronal Golgi fragmentation has been reported in several neurodegenerative diseases (Fujita et al., 2002; Gonatas et al., 2006), including PD (Gosavi et al., 2002; Fujita et al., 2006) and it has been suggested that Golgi fragmentation is specifically due to α SYN aggregation. We stained differentiated SH-SY5Y cells with and without overexpression of α SYN with the GM130 antibody to assay the morphology of the Golgi over several days. We observed no differences in Golgi morphology between the α SYN expressing and non-expressing cells in the days leading to α SYN-induced toxicity. However, we found significantly enlarged, albeit unfragmented, Golgi in α SYN-overexpressing cells close to onset of α SYN-induced toxicity (Fig. 7a, b). We next determined if modulation of α SYN-induced toxicity by vesicle trafficking genes is correlated to the magnitude of Golgi enlargement in SH-SY5Y cells. Although knockdown of Vps24, Vps28 and Vps34 exacerbates α SYN toxicity, they decreased Golgi size in α SYN expressing cells relative to the scrambled control. Knockdown of Vps45 and Vps52 had no effect on Golgi enlargement, despite their exacerbation of α SYN toxicity. We also observed a lack of effect on Golgi enlargement due to the suppression of toxicity by Stx7 knockdown. (Fig.

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7c). These results suggest that that genetic modification of α SYN toxicity in SH-SY5Y cells does not correlate with enlargement of Golgi, suggesting that this phenotype is unlikely to play a primary role in toxicity.

α SYN-induced exocytosis impairment does not correlate with modulation of toxicity by genetic modifiers in differentiated SH-SY5Y cells

Our studies in yeast suggest that a post-endocytic and/or early exocytic step in yeast is impaired by the overexpression of α SYN (Sancenon et al.t, manuscript in review). In addition, studies in *C. elegans* also implicate the endocytic pathway in α SYN-induced toxicity (Kawahara et al., 2008). To examine if α SYN-expression interferes with exocytosis, we studied the retention of the lipophilic dye FM1-43 in SH-SY5Y cells with or without overexpression of α SYN. KCl depolarization evokes exocytosis, which is followed by compensatory endocytosis that traps FM1-43 in the retrieved vesicles. Subsequent repolarization by KCl results in fusion of FM1-43 labeled vesicles with the plasma membrane and the release of dye into the extracellular medium. This results in decreased fluorescence within the cell, which is a measure of exocytosis. We found that the fluorescence intensity of FM1-43 in α SYN-overexpressing cells was significantly stronger compared to non α SYN-overexpressing cells after the second KCl depolarization event, indicating increased retention of FM1-43 in the α SYN-overexpressing cells (Fig. 8a, b). This suggests impairment in exocytosis in α SYN overexpressing cells.

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Stimulated exocytosis of synaptic vesicles is temporally coupled to endocytosis of vesicular membrane and inhibition of Rab5 has been shown to reduce endo-exocytic rates at the synapse, possibly due to inhibition of membrane exchange between synaptic vesicles and the early endosome. (Wucherpfennig et al., 2003). Active recruitment of Vps34 to the early endosome by Rab5 results in a local enrichment of phosphoinositol-3-phosphate (PI3P, which is critical for endosomal trafficking. We wanted to determine whether exacerbation of α SYN-induced toxicity due to the knock down of Vps34 was correlated with changes in FM1-43 retention in differentiated SH-SY5Y cells. We co-transfected cells with scrambled shRNA or shRNA against Vps34 and examined retention of FM1-43 in successfully transfected cells. Despite significantly exacerbating α SYN toxicity, knock down of Vps34 gene expression had no effect on the increased retention of FM1-43 in α SYN-overexpressing cells (Fig. 8c)

α SYN-induced increase in constitutive receptor recycling is nullified by Vps34 knockdown in SH-SY5Y differentiated cells.

Vesicles labeled by FM1-43 constitute a 'fast recycling' pool of vesicles (Sara et al., 2002) that likely involves the early endosome (Maxfield et al., 2004). A separate pool of vesicles termed the 'slow storage pool' regulated by Rab11 (Filipeanu et al., 2006) is involved in the recycling of constitutive receptors, e.g. the transferrin receptor. To determine whether this slow recycling endocytosis pathway is impaired by α SYN overexpression, we performed total internal reflection fluorescence to image differentiated SH-SY5Y cells transfected with GFP-tagged transferrin receptor (TfR).

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Fusion of TfR containing vesicles with the plasma membrane is termed an 'insertion event' and the number of insertion events of TfR in the cell plasma membrane is representative of TfR recycling activity. Regardless of aSYN overexpression, insertion events in the differentiated SH-SY5Y cells were exclusively 'transient' events, characterized by rapid dispersion of TfR after insertion into the plasma membrane (Fig. 9a) (Yudowski et al., 2006). We found that cells overexpressing α SYN displayed significantly more insertion events and thus an increase in TfR recycling (Fig. 9b), further suggesting α SYN-induced perturbations in the exo-endocytic pathway. We also tested the effect of Vps34 and Stx7 knockdown on the increase in TfR recycling induced by α SYN-overexpression. The decrease in Vps34 gene expression in α SYN-overexpressing cells markedly reduced TfR recycling activity to normal levels found in cells without α SYN-overexpression. However, knock down of Stx7 or overexpression of Stx7 and Vps34 did not alter the increased TfR recycling activity in α SYN overexpressing cells (Fig. 9c).

DISCUSSION

The pioneering yeast genetic screen for modifiers of α SYN toxicity by Willingham et al. (2003) identified multiple genes involved in vesicle trafficking. Since then, other genetic screens in model organisms of PD (Cooper et al., 2006; Hamamichi et al., 2008; Liang et al., 2008) have also identified vesicle trafficking genes as a major gene category in modulating α SYN toxicity. Our findings described represent a systematic study on the effect of modulating vesicle trafficking genes on α SYN toxicity and pathogenesis in an inducible WT- α SYN SH-SY5Y cell line. We show that manipulating the gene expression

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level of endosomal trafficking genes by shRNA exacerbates α SYN-induced toxicity in differentiated SH-SY5Y cells, while knockdown of Stx7 ameliorates α SYN-induced toxicity. We also demonstrate that overexpression of Vps24, Vps28 and Stx7 reduces α SYN-induced toxicity in the SH-SY5Y cell line while expression of Stx7 and Vps34 is sufficient to rescue α SYN-induced toxicity in primary cortical neurons.

Recent studies have implicated impairments in mammalian orthologs of yeast Vps genes in neurodegeneration. A missense mutation in Vps54, a co-complex protein of Vps52, which results in depletion of the Golgi associated retrograde protein (GARP) complex is reportedly responsible for motor neuron degeneration in a murine model of amyotrophic lateral sclerosis (Schmitt-John et al., 2005). Deletion of Vps34 in sensory neurons has been reported to induce rapid neurodegeneration through endosomal defects (Zhou et al., 2010). Furthermore, overexpression of Vps41 has been shown to be neuroprotective in various invertebrate and cellular models of PD (Ruan et al., 2009). In agreement with these findings, we found that decreased expression of Vps genes involved in endosomal trafficking, Vps24, Vps28, Vps34, Vps45 and Vps52, enhance α SYN-induced toxicity in a neuronal cell line. Conversely, overexpression of Vps24, Vps28 and Stx7 were sufficient to reduce α SYN toxicity. While overexpression of Vps34 and Vps45 had no effect on α SYN toxicity in the SH-SY5Y cells, overexpression of Vps34 almost completely ameliorates α SYN-induced toxicity in primary cortical neurons. The lack of rescue by Vps34 overexpression in the SH-SY5Y cells might be due to several reasons. One possibility is that Vps34 regulates endosomal trafficking in a complex with p150 and

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Beclin 1 (reviewed by Lindmo et al., 2006), thus suppression of α SYN toxicity might require overexpression of multiple members of Vps34 complex. Another possibility is that the Vps34 overexpression does reduce α SYN toxicity in the SH-SY5Y cells but low transfection efficiency masked the decrease in toxicity in transfected cells when overall toxicity was measured. This would account for the lack of observed rescue of α SYN toxicity in the SH-SY5Y cells compared to the rescue seen in neurons where individual transfected neurons were tracked for survival. Alternatively, lower expression levels of the Vps34 cDNA construct in the SH-SY5Y cells compared to neurons might account for the lack of α SYN toxicity rescue in the cell line.

Results from mechanistic experiments in yeast suggested α SYN induced impairment in a post-endocytic and/or early exocytic pathway (Sancenon et al., manuscript in review). We observed a similar defect in differentiated SH-SY5Y cells where α SYN overexpression induced an abnormal retention of FM1-43, reflecting a defect in KCl stimulated exocytosis. A similar retention of FM1-43 induced by α SYN has recently been reported in neurons from α SYN transgenic mice by Scott et al. (2010) and in a PC12 cell line expressing α SYN by Garcia-Reitböck et al. (2010). We also observed an increase in constitutive receptor recycling of the transferrin receptor in α SYN overexpressing cells. Given the role of several of the genetic modifiers in endosomal trafficking, we hypothesize that the exacerbation of α SYN toxicity upon knockdown of the genetic modifiers might be due to a worsening of the α SYN-induced endo-exocytosis defects. We

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cannot rule out the possibility that exacerbation of α SYN-induced toxicity by decreased levels of Vps genes is due to disruptions in the lysosomal system, given the role of the ESCRT complex and associated proteins, Vps24, Vps28 and Vps34, in lysosomal degradation of proteins (reviewed by Hurley and Emr, 2006). However, we did not observe a change in α SYN protein levels in cells treated with shRNA against the Vps genes (data not shown), suggesting that an impairment in α SYN degradation is not responsible for the exacerbation of α SYN-induced toxicity.

Strikingly, we found that knock down of Vps34 gene expression mimicked the effects of α SYN on vesicle trafficking in wild-type cells, inducing enlargement of the Golgi, abnormal retention of FM1-43, an increase in transferrin receptor recycling (Fig. 7d, 8d, 9d), and impairment in neurotransmitter release in neurons (R. Edwards, personal communication). Furthermore, the conditional knock out of Vps34 in mice is thought to induce rapid neurodegeneration through defects in endosomal trafficking rather than autophagy (Zhou et al., 2010). It is conceivable that toxicity cause by α SYN accumulation may be due to an impairment of trafficking at the early endosome, which is regulated in part by Vps34. Depletion of Vps34 in α SYN overexpressing cells would presumably exacerbate the early endosome trafficking impairment, leading to the observed increase in α SYN toxicity.

Vps34, the only class III PI3K in mammalian cells, converts PI to phosphatidyinositol-3-phosphate, a phospholipid that establishes the identity of the early endosome and

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therefore is critical for trafficking at the early endosome (Gillooly et al., 2003). Vps34 is recruited to early endosomes by the small GTPase Rab5 (Yan and Becker, 2007). It has been shown that Rab5 accumulates in enlarged endosomes that colocalizes with α SYN in both α SYN transgenic mice and PD patient brains (Sancenon et al., manuscript in review). Furthermore, direct interaction between Rab5 and α SYN has been reported (Dalfó et al., 2004), suggesting that pathogenesis of α SYN involves early endosome trafficking. Given that the bulk of exocytosed vesicles are derived from endosomes, impairment of Rab5 function and therefore early endosome trafficking affects rates of endocytosis and exocytosis (Stenmark et al., 1994), which could explain the abnormal retention FM1-43 in the α SYN-overexpressing SH-SY5Y cells.

We speculate that cells compensate for the exocytosis block due to early endosome impairment by upregulating alternate pathways for exocytosis to maintain proper balance of membranes and proteins at the plasma membrane. One pathway is the route that the transferrin receptor takes through recycling endosomes, which is regulated by a different set of Rabs, namely Rab4 and 11 (Deneka and van de Sluijs, 2002) and not affected by specific Vps34 inhibition (Johnson et al., 2006). This would account for the observed increase in transferrin receptor recycling in both the α SYN-overexpressing SH-SY5Y cells and non α SYN-overexpressing cells with Vps34 gene knockdown. As recycling endosomes are closely associated with the trans-Golgi network (Ang et al., 2004), the enlarged Golgi seen in cells under those conditions might be related to the increase in recycling endosomal activity and further indicative of increased secretion.

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In addition to maintaining normal operational status quo of the secretory pathway and plasma membrane, upregulation of transferrin receptor recycling may be a cellular coping mechanism to eliminate unwanted molecules and even toxic α SYN species. Indeed, Emmanouilidou et al. (2010) recently reported exosome-dependent α SYN secretion into the extracellular medium of SH-SY5Y cells. Exosomes, small intraluminal vesicles formed within multivesicular bodies that fuse with the plasma membrane, purportedly clear unwanted proteins from the cell and establish cell-independent signaling (van Niel et al., 2006). Notably, the role of exosomes and secretion of the amyloid precursor protein and prion proteins has already been implicated in the pathogenesis of other neurodegenerative diseases such as Alzheimer's disease and Creutzfeldt-Jakob disease respectively (reviewed by Vella et al., 2008). Exosome formation is regulated by the recycling endosome Rab 11 (Savina et al., 2002), and an increase in a Rab11-associated protein Rab4 has been observed in α SYN transgenic mouse brains (unpublished data), further linking α SYN pathogenesis to an upregulation of the constitutive receptor recycling pathway. We observed that knock down of Vps34 in α SYN-overexpressing SH-SY5Y cells exacerbates α SYN toxicity that is correlated with persistent retention of FM1-43, and strikingly, ablation of the enlarged Golgi phenotype and a sharp decrease in transferrin receptor recycling. This suggests that the double insult of α SYN accumulation and Vps34 knock down overwhelms the cells' endosomal trafficking capabilities such that upregulation of alternate secretory pathways is impeded. If upregulation of constitutive receptor recycling is a pathogenic compensatory mechanism for α SYN-induced

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endosomal defects, overexpression of a protein that promotes trafficking to the recycling endosome could rescue α SYN toxicity. Indeed, Gitler et al. (2008) have demonstrated that α SYN toxicity in neurons is ameliorated by overexpression of Rab8, a regulator of transferrin receptor trafficking and putative mediator of membrane recycling that partially colocalizes with the recycling endosome marker Rab11 on small vesicles (Hattula et al., 2006).

Similar to other highly polarized cells, the health and proper function of neurons undoubtedly depends on proper delivery of proteins to the axonal or somadendritic membrane surface to ensure received signals are spatially separated from transmitted signals. Polarity of neurons is regulated at the level of endosomes (reviewed by Schmidt and Haucke, 2007). An impairment in endosome trafficking would therefore conceivably lead to mislocalization of important presynaptic terminal proteins, affecting neurotransmitter release among other consequences. Not only has the redistribution of SNAREs been reported in the striatum of PD patients, as well as a mouse model of PD with a corresponding reduction in exocytosis and dopamine release (Garcia-Reitböck et al. 2010; Scott et al., 2010), impairment in neurotransmitter release is clearly linked to neurodegeneration (Dong et al., 2003; Zhang et al., 2009; Nemani et al., 2010; Shen, 2010).

In conclusion, our findings demonstrate that genetic manipulation of vesicle trafficking genes can modulate α SYN-induced toxicity in mammalian cells, and that trafficking at

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the early endosome may be critical to α SYN pathogenesis. The mechanism of action is likely to involve regulation of the exo-endocytic pathways, thereby exacerbating or counteracting the toxic effects of α SYN on the trafficking machinery of the cell, or perhaps even modulating the propagation of neurodegeneration from cell to cell due to extracellular secretion of α SYN. Further studies on the interaction of vesicle trafficking genes with α SYN will be important to elucidate the mechanism of vesicle-trafficking related α SYN pathogenesis and may give rise to novel therapeutic targets for PD.

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TABLE

Yeast gene	Loss of function effect in yeast	Mammalian homologue	Mammalian gene function
Vam3	suppressor	Stx7	Late endosome fusion
Cog6	enhancer	Cog6	Retrograde Golgi trafficking
Vps9	enhancer	Rabgef1	Homotypic endosomal fusion
Tlg2	enhancer	Stx1a	PreSynaptic vesicle trafficking
Tlg2	enhancer	Stx12	Early and recycling endosomal trafficking
Tlg2	enhancer	Stx16	Trans-Golgi network trafficking
Vps24	enhancer	Vps24	Trans-Golgi network and endosomal trafficking
Vps28	enhancer	Vps28	Trans-Golgi network and endosomal trafficking
Vps34	enhancer	Vps34	Endosomal trafficking
Vps45	enhancer	Vps45	Trans-Golgi network trafficking
Vps52	enhancer	Vps52	Retrograde Golgi trafficking

Table 1. Loss of function yeast genetic modifiers of α SYN toxicity and corresponding mammalian orthologs.

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FIGURES

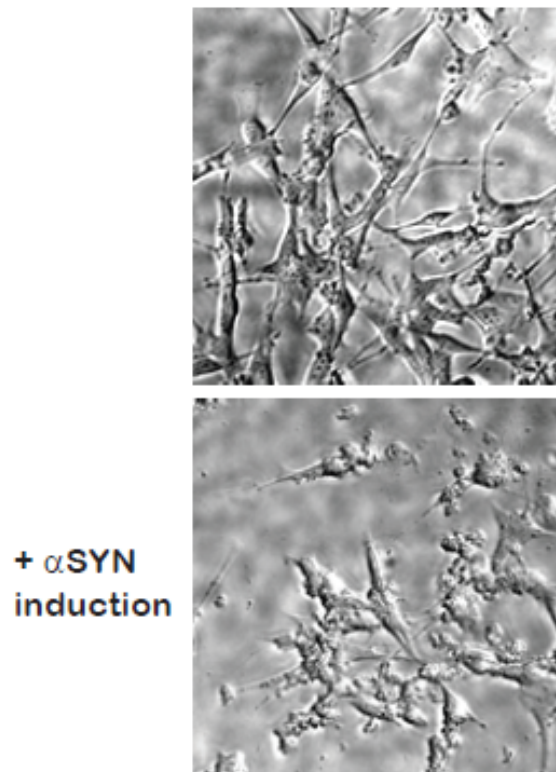


Figure 1. WT aSYN expression causes retraction of neuritic processes, membrane blebbing, and eventually death. Representative bright field photomicrographs of SH-SY5Y cells with or without α SYN induction at day 7 of differentiation are shown.

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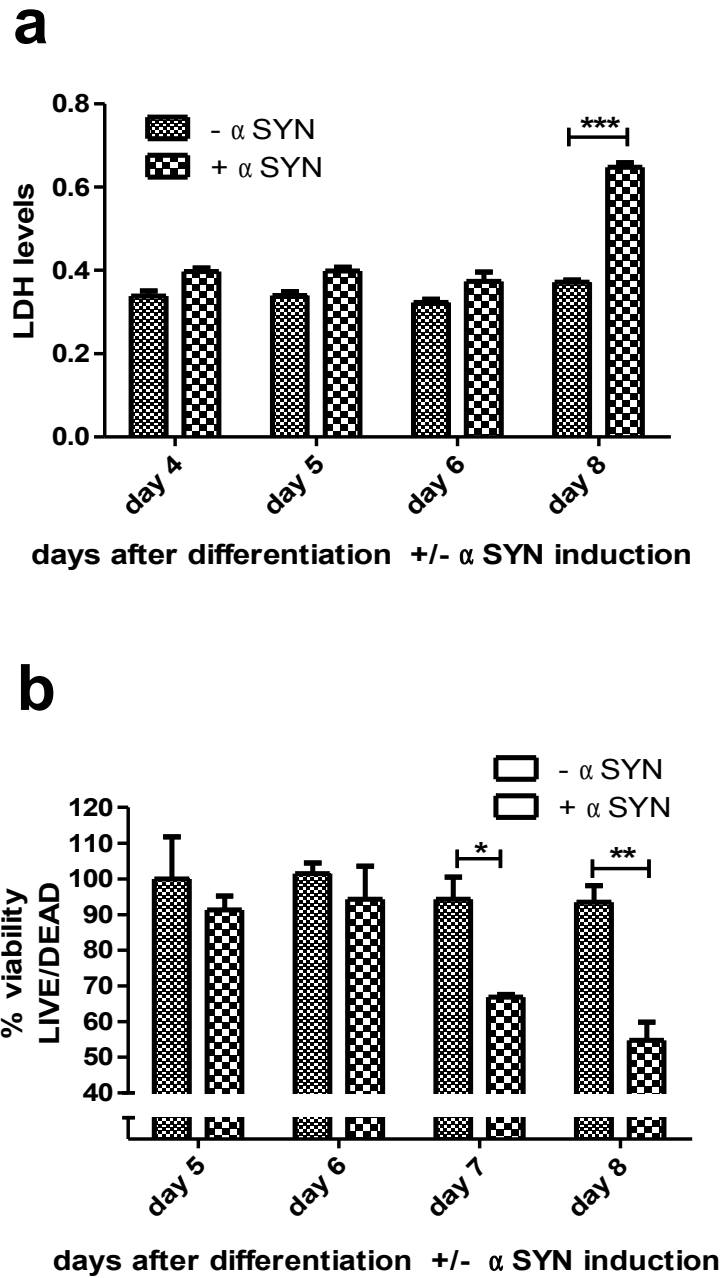
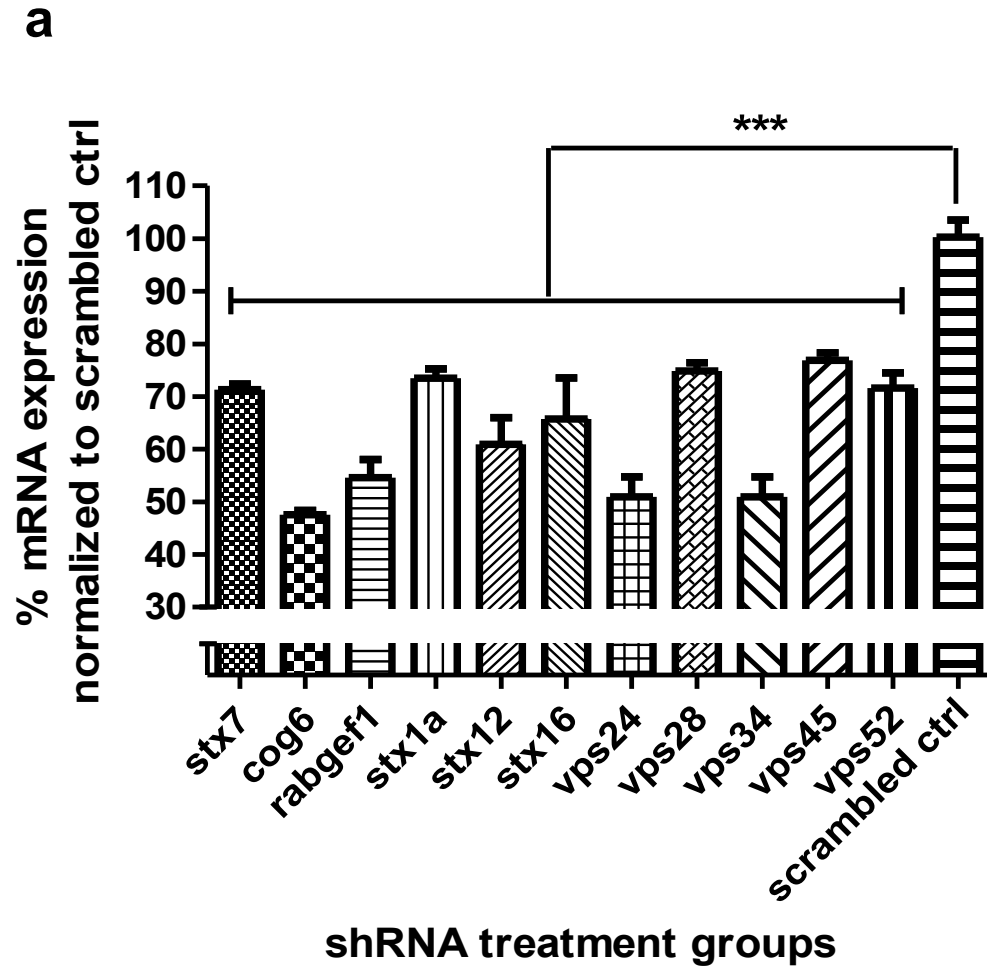


Figure 2. Overexpression of α SYN induces toxicity in differentiated SH-SY5Y cells after 6 days. (a) Culture medium was collected from differentiated SH-SY5Y cells with or without overexpression of α SYN over a time course of 8 days and the levels of LDH in the medium was assayed as a function of cell death (b) Differentiated SH-SY5Y cells

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with or without overexpression of α SYN were stained with LIVE/DEAD reagents as a measure of cell viability over a time course of 8 days. *P<0.05, **P<0.01, ***P<0.001; 2 way anova with Bonferroni posthoc analysis. Mean \pm SEM, n = 3 experiments.

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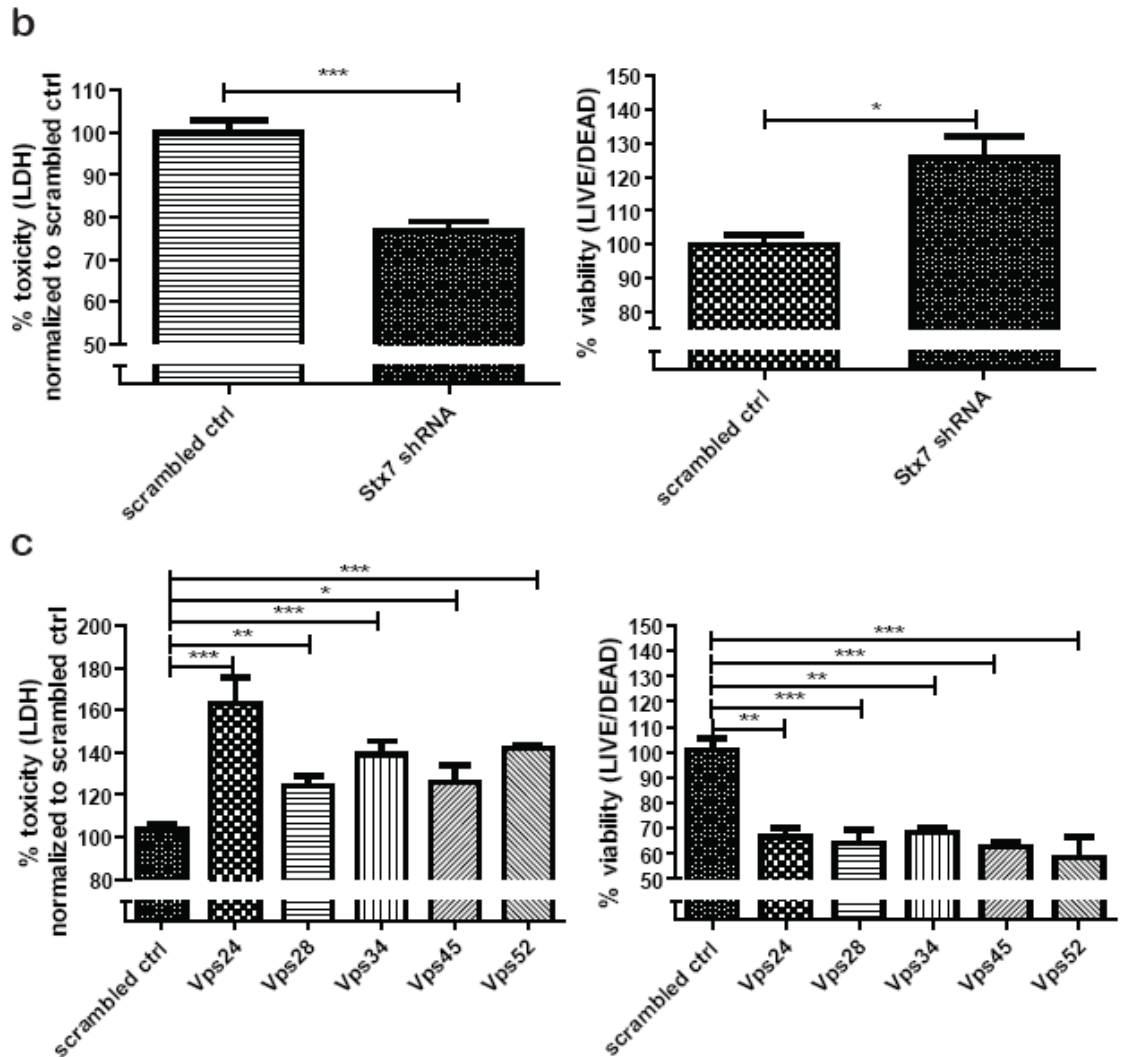


Figure 3. Knock down of gene expression of human orthologs of yeast genetic modifiers modulates α SYN-induced toxicity in differentiated SH-SY5Y cells. Culture medium was collected from cells 7 days after differentiation and toxicity was assayed by the levels of LDH present. (a) Transfection of shRNA against vesicle trafficking genes results in 30-50% decrease in gene expression compared to scrambled shRNA control, which was set to 100%. *** P<0.001, one way ANOVA. (b) Knock down of Stx7 gene

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expression decreased α SYN-induced toxicity in differentiated cells compared to cells transfected with scrambled shRNA control in the LDH and LIVE/DEAD assays. (c)

Knock down of gene expression of human Vps genes showed significant increases in α SYN-induced toxicity compared to cells transfected with scrambled shRNA control in the LDH and LIVE/DEAD assays. **P<0.01, ***P <0.001, Student's t-test. Mean \pm SEM, n = 3 experiments.

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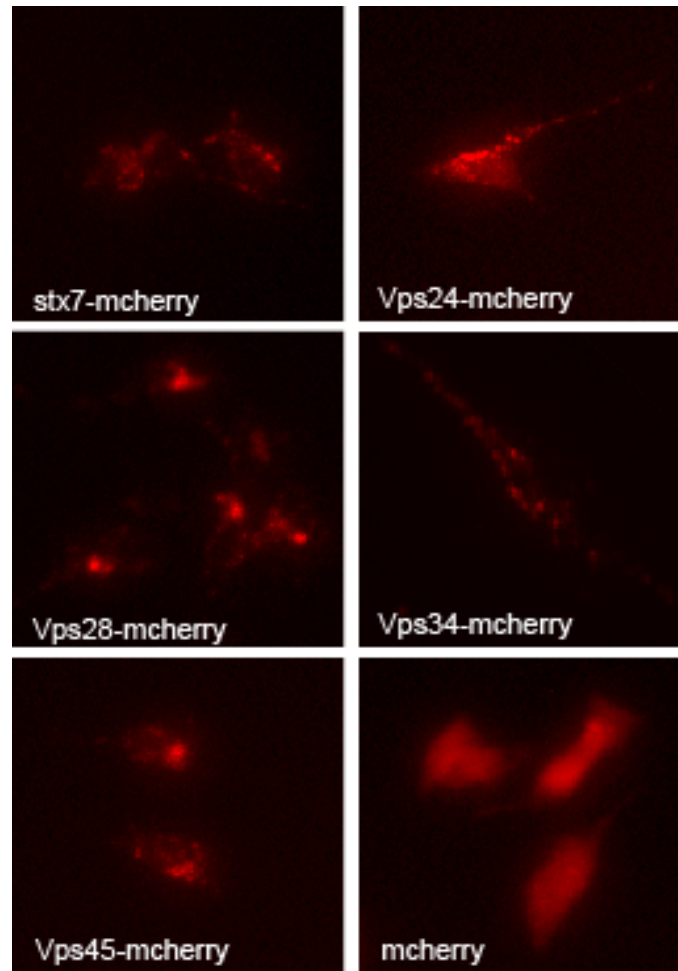


Figure 4. Expression of genetic modifier fusions to mcherry in SH-SY5Y cells.

Punctate localization of mcherry tagged Stx7, Vps24, Vps28, Vps34, Vps45 and mcherry in SH-SY5Y cells consistent with their predicated localization pattern.

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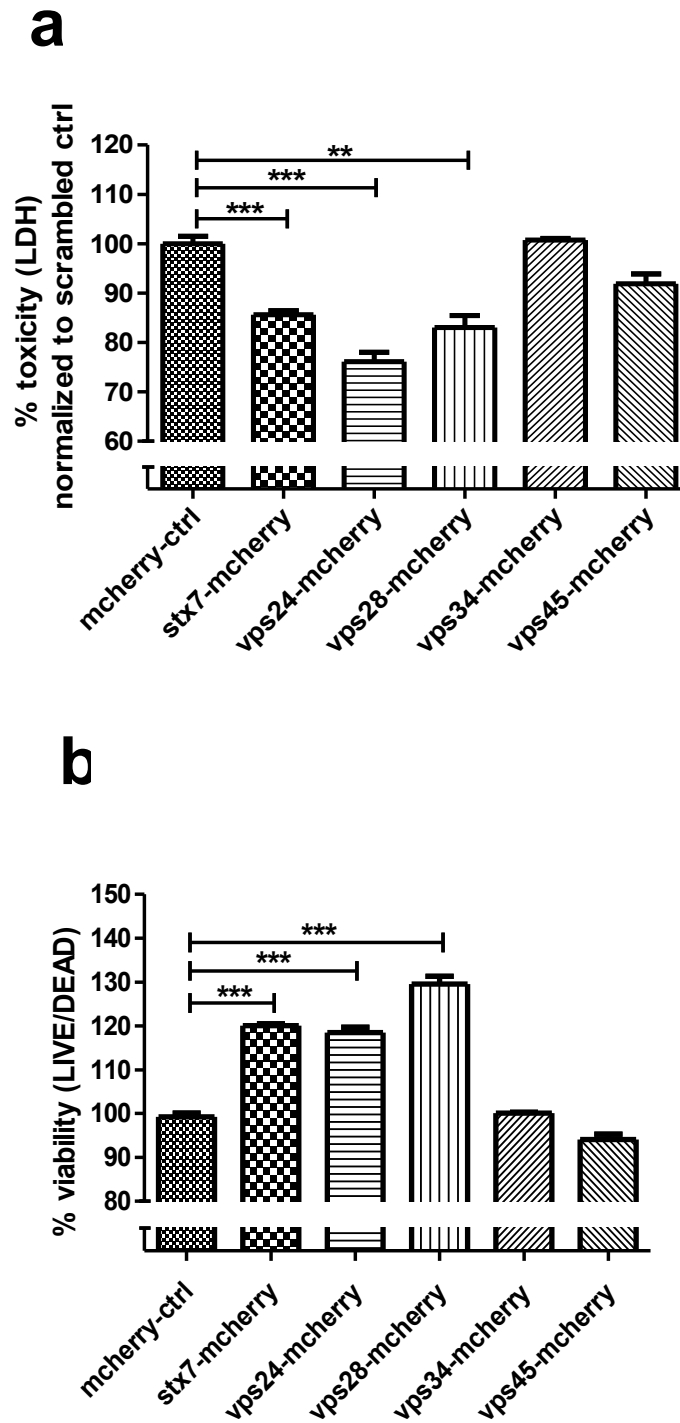


Figure 5. Expression of Vps genes is sufficient to rescue α SYN toxicity in SH-SY5Y cells. SH-SY5Y cells transfected with mcherry-tagged Stx7, Vps24, Vps28, Vps34,

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Vps45 and the mcherry vector and differentiated for 7 days were assayed for αSYN-induced toxicity by the (a) LDH assay and (b) LIVE/DEAD assay. **P<0.01, ***P<0.001, Student's t-test. Mean n ± SEM, n = 3 experiments.

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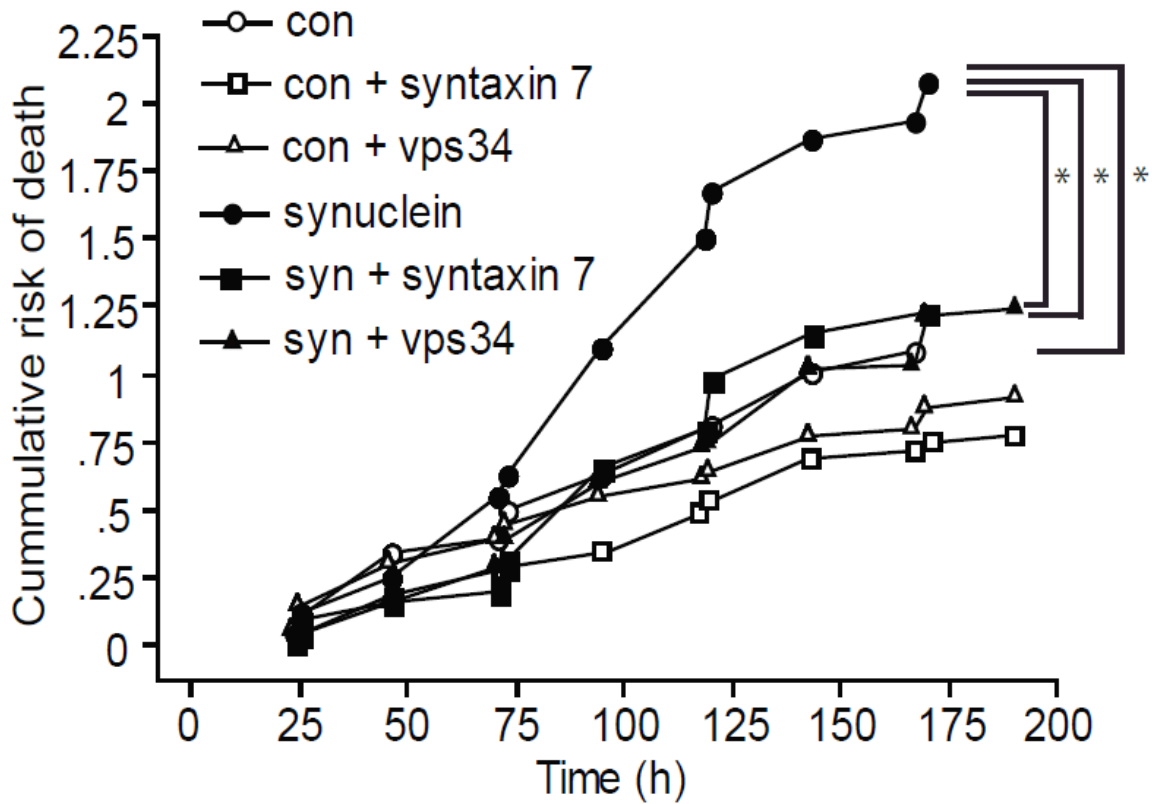


Figure 6. Overexpression of Stx7 and Vps34 rescues α SYN toxicity in rat cortical neurons. Rat cortical neurons were transfected five days after plating with Venus (a variant of yellow fluorescent protein), α SYN (SYN) or vector control (con), and either with or without modifiers Vps34 or Stx7. Cumulative risk of death curves indicate that primary neurons expressing α SYN have a significantly greater risk of death than control cells (* $p < 0.0001$, log-rank test). Overexpression of Vps34 and Stx7 significantly reduced α SYN-induced toxicity (* $p < 0.0001$). Neurons were combined from 3

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independent experiments and p values were calculated with the log rank test, n = 115-200 neurons per group.

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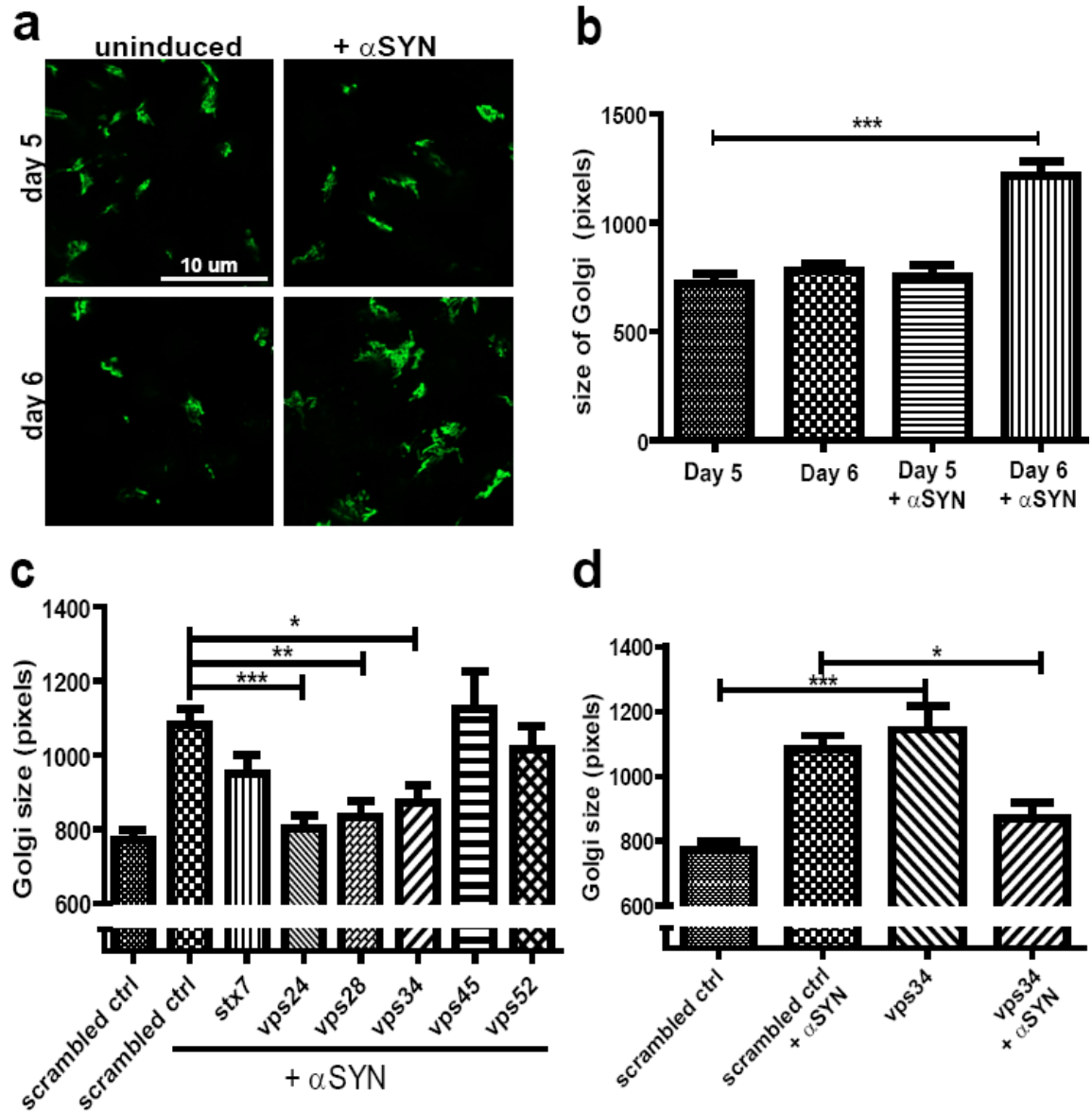


Figure 7. α SYN-induced Golgi abnormalities do not correlate with modulation of toxicity by genetic modifiers. (a) Confocal microscopy of SH-SY5Y cells 5 or 6 days post differentiation with or without overexpression of α SYN stained with α GM130. (b) Quantification of Golgi surface area. *** P <0.001, one way ANOVA. Mean \pm SEM, n = 3 experiments, > 50 cells per experiment. (c) Quantification of the effect of knocking down expression of vesicle trafficking genes on α SYN-induced Golgi phenotype in SH-SY5Y

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cells 6 days post differentiation. (d) Quantification of Golgi size in day 6 post-differentiation SH-SY5Y cells without without α SYN-overexpression transfected with scrambled shRNA or Vps34 shRNA. *P <0.05, **P<0.01, ***P<0.001, Student's t-test. Mean \pm SEM, n = 3 experiments. 1 pixel represents 61 nm.

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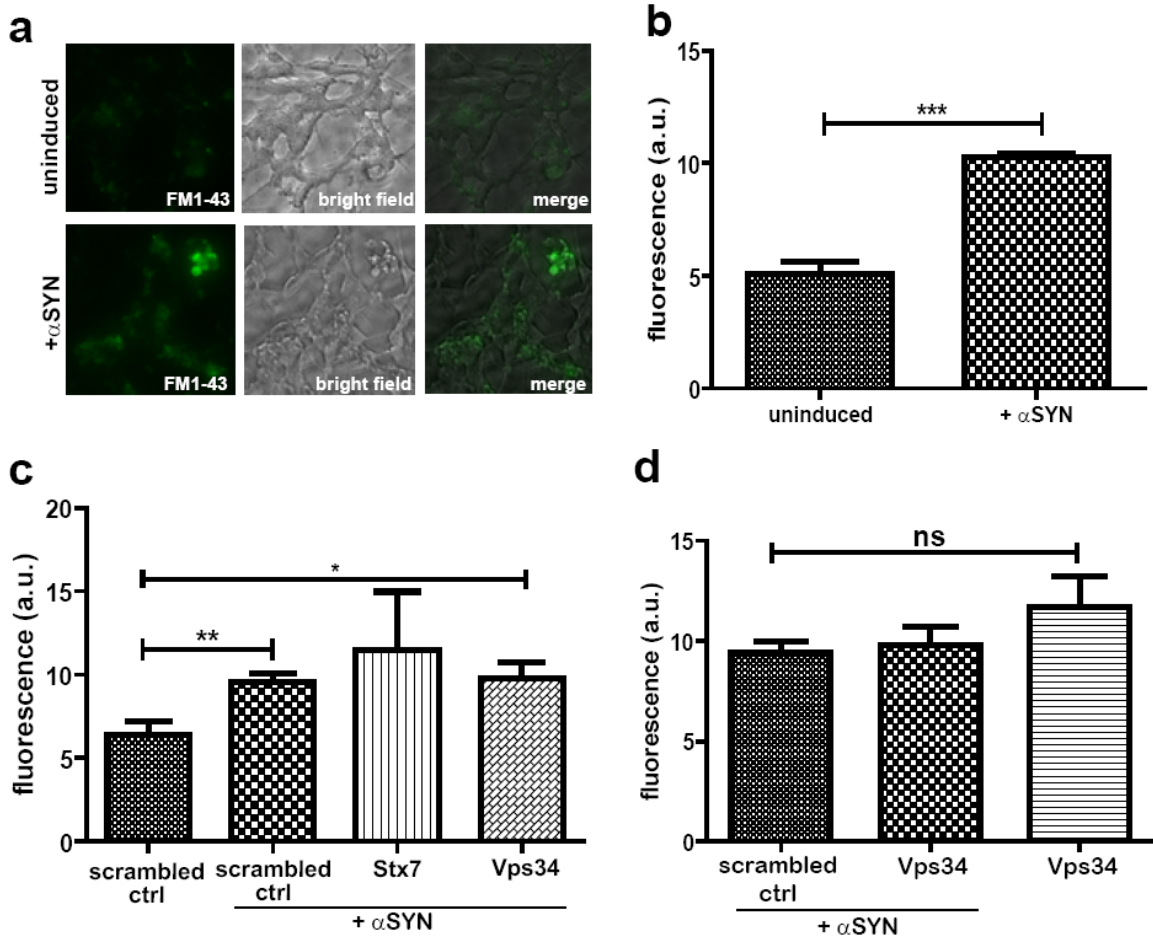


Figure 8. α SYN-induced exocytosis impairment does not correlate with modulation of toxicity by genetic modifiers. (a) Retention of FM1-43 in differentiated SH-SY5Y cells with or without α SYN overexpression following KCl depolarization. (b) Quantification of FM1-43 fluorescence intensity. (c) Retention of FM1-43 in SH-SY5Y cells transfected with shRNA against Stx7 and Vps34 with or without α SYN overexpression 6 days post differentiation. * $P < 0.05$ ** $P < 0.01$ *** $P < 0.001$, Student's t-test. Mean \pm SEM, $n = 3$ experiments, 4 fields per experiment. (d) Quantification of FM1-43 fluorescence intensity in day 6 post-differentiation SH-SY5Y cells with or without α SYN-overexpression transfected with scrambled or Vps34 shRNA.

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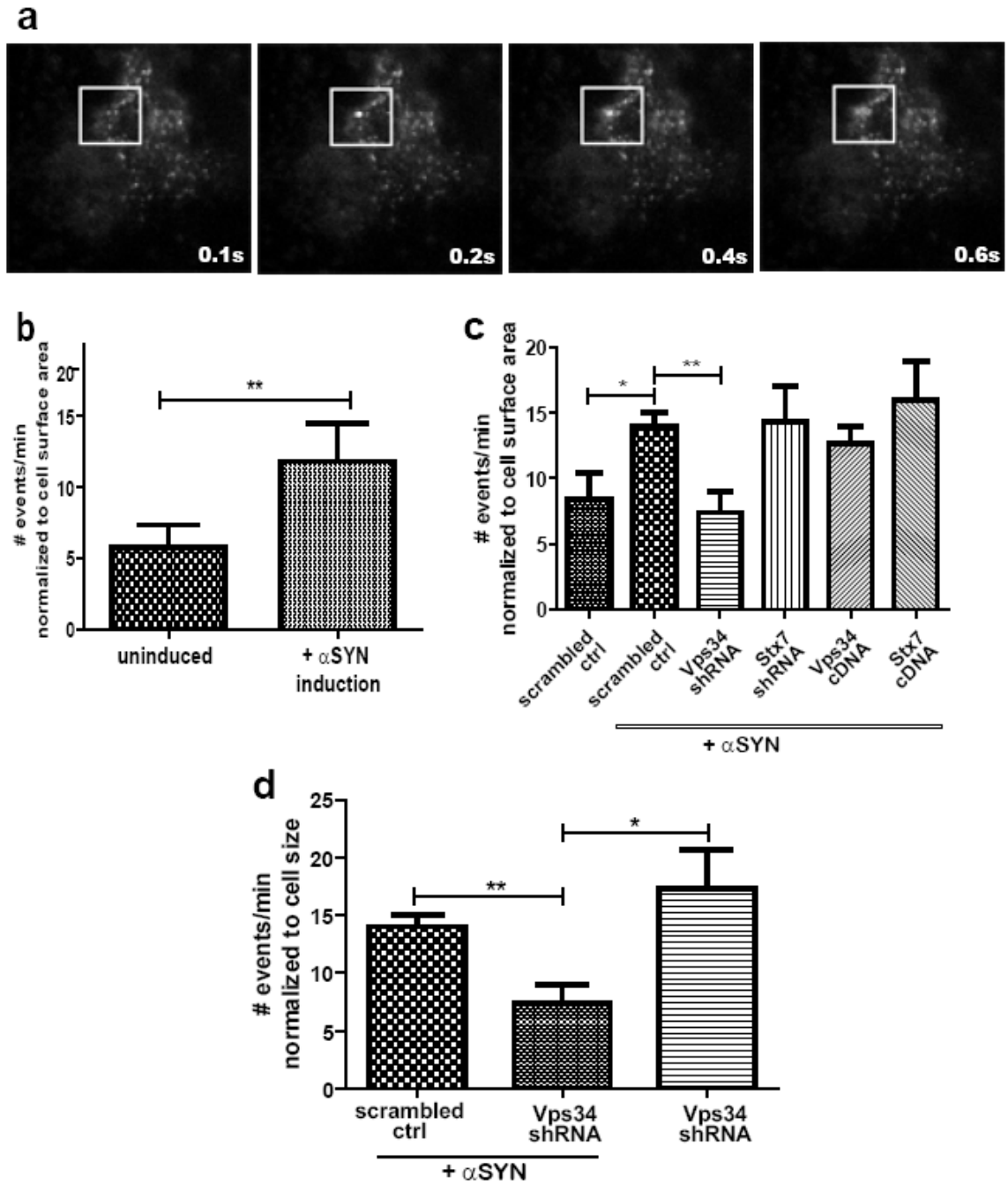


Figure 9. Overexpression of α SYN induces increased transferrin receptor (TfR) recycling in differentiated SH-SY5Y cells. (a) Rapid TIR-FM image series of differentiated SH-SY5Y cell expressing TfR. Boxed area show representative TfR

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exocytic insertion event in the plasma membrane. (b) Quantification of TfR exocytic insertion events per minute normalized to cell surface area. **P<0.01, Student's t-test. Mean \pm SEM, n > 12 cells per condition. (c) Quantification of TfR exocytic insertion events per minute normalized to cell surface area in α SYN-induced cells transfected with shRNA against or overexpression constructs for Stx7 and Vps34 6 days after differentiation. *P<0.05 **P<0.01, Student's t-test. Mean \pm SEM, average n = 8 cells per condition. (d) Quantification of TfR exocytic insertion events per minute normalized to cell surface area in cells transfected with shRNA against Vps34 in cells with or without α SYN induction. *P<0.05, **P<0.01, Student's t-test. Mean \pm SEM, average n = 8 cells per condition.

CHAPTER 4 – CONCLUSIONS AND FUTURE DIRECTIONS

CHAPTER 4 – CONCLUSIONS AND FUTURE DIRECTIONS

Our initial genetic and cell biological analyses in yeast suggest that α SYN disrupts the endosomal trafficking of transmembrane proteins destined for intravacuolar degradation. Based on the observation that loss-of-function alleles (*Vps24 Δ* , *Vps28 Δ* , *Vps60 Δ*) of genes encoding distinct subunits of endosomal sorting (ESCRT) complexes required for transport exacerbate α SYN-induced growth defects in yeast, we hypothesized that α SYN pathogenesis in neuronal cells is driven, at least in part, by a similar endosomal trafficking defect. Indeed, we found evidence of endo-exocytic trafficking abnormalities in differentiated neuroblastoma cells that could be the direct result of, or possibly arose as a compensatory mechanism for, toxic α SYN accumulation. In validation of our yeast studies, we also showed that human orthologs of the ESCRT genes and others also involved in the endosomal protein trafficking pathways (*Vps34*, *Vps45*, *Vps52*, *Stx7*) are able to modulate α SYN-induced toxicity through complementary shRNA knock down and overexpression experiments.

Although the degeneration of dopaminergic neurons in PD appear to be specific to their biology, there may be a more basic biological explanation underlying PD and α SYN pathogenesis. The proper trafficking of proteins and membranes is especially critical in highly polarized cells like neurons, which have morphologically segregated compartments of the axon and dendrites for specialized functions. A general trafficking impairment that disrupts the fine-tuned balance of neurons would thus have devastating consequences. Dopaminergic neurons, which are the primary target cells in PD would be especially sensitive to disruptions in vesicle trafficking as dopamine is a neurotransmitter

CHAPTER 4 – CONCLUSIONS AND FUTURE DIRECTIONS

prone to producing reactive oxygen species in the cytoplasm of the cell unless sequestered into vesicles.

The accumulation of vesicles, similar to our observations in yeast, have long been observed in neurons before Lewy body formation in early stages of the disease (Hayashida et al., 1993), and in close proximity to Lewy bodies in later stages of the disease (Watanabe et al., 1977). Furthermore, the consequences of a malfunctioning protein trafficking system have been characterized in various neurological diseases. Mutations in the charged multivesicular body protein 2B (CHMP2B), a subunit of the human ESCRT-III complex together with Vps24, are linked to autosomal dominant forms of frontotemporal dementia (Skibinski et al., 2005). Further, Almeida et al. (2006) documented defects in multivesicular body sorting in a neuronal model of β -amyloidopathy. Similarly, deletion of the lipid kinase Vps34, which produces the PI3P responsible for targeting ESCRT-I complex to endosomes (Katzmann et al., 2003), gives rise to rapid neurodegeneration in mice (Zhou et al., 2010). Mice lacking in Vac14, a regulator of PI(3,5)P₂ synthesis also experience drastic loss of midbrain and peripheral sensory neurons (Zhang et al., 2007). In addition, mutations in SNARE proteins have been implicated in neurological disorders, such as schizophrenia and the CEDNIK syndrome (Saito et al., 2001; Sprecher et al., 2005).

A basic understanding of the pathogenic mechanism of α SYN may lead to the identification of novel drug targets and even drugs. Our studies illustrate the novel findings that trafficking at the early endosome is critical to α SYN toxicity, and that we

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can modulate α SYN toxicity by altering levels of genetic modifiers regulating endosomal trafficking. Validation of these results *in vivo* would have tremendous implications for the treatment of PD and would provide potential pharmacologic targets for early therapeutic intervention of PD.

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Chemicals and antibodies

The reagents were from Sigma unless specified. The mouse monoclonal GM130 antibody was from BD Biosciences. The mcherry antibody was from Clontech. The p42/44 map kinase antibody was from Cell Signaling Technology. The mouse monoclonal alpha-SYNuclein antibody was from BD Biosciences. AlexaFluor® 488-, 555-, and 647-conjugated goat anti-mouse secondary antibodies, and HRP-conjugated secondary anti-mouse and anti-rabbit antibodies were from Jackson ImmunoResearch.

Plasmids

Plasmids p426GPD α SYN(WT)GFP, p426GAL α SYN(WT)GFP, pGS416 (*GFP-SNC1*), pGSSO416 (*GFP-SNC1-SSO1*), pGNS416 (*GFP-NYVI-SSO1*), pPEP416 (*GFP-PEP12*), pPHM5 (*GFP-PHM5*) and pSNA3416 (*SNA3-GFP*) have been described .

Plasmid pSTE2416 was created by replacing the *SNA3* gene from plasmid pSNA3416 with the *STE2* gene as a *HindIII-AgeI* digested product of PCR amplification.

Plasmid p8xmycSNC1416 (*8xMYC-SNC1*) was created by replacing the *GFP* gene from plasmid pGS416 by the *8xMYC* sequence as a *HindIII-EcoRI* digested product of PCR amplification. Plasmid p8xmycSNC1406 was then created by subcloning the *TP11pr-8xMYC-SNC1* fusion from plasmid p8xmycSNC1416 into the *XhoI* and *BamHI* sites of the pRS406 integrating vector . p8xmycSNC1406 was linearized with *EcoRV* for integration.

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Plasmid pmCheSSO416 (*mCherry-SNCA-SSO1*) was created by replacing the GFP tag from plasmid pGSSO416 with the mCherry gene from plasmid pmCheV5ATG8406 as an *XhoI-EcoRI* fragment. Plasmid pmCheSSO415 was created by then created by subcloning the *TP11pr-mCherry-SNCA-SSO1* fusion from plasmid pmCheSSO416 into the *XhoI* and *SacI* sites of the plasmid p415TEF .

Plasmid p423GPD α SYN(WT)GFP was created by subcloning the *SNCA(WT)-GFP* fusion from plasmid p426GAL α SYN(WT)GFP into the *SpeI* and *XhoI* sites of plasmid p423GPD .

Plasmid p423GPD α SYN(WT) was created by subcloning *SNCA(WT)* from plasmid p426GPD α SYN(WT)GFP into the *SacI* and *XhoI* sites of p423GPD .

Plasmids p426GAL α SYN(S129A)GFP and p426GAL α SYN(S129E)GFP were created by recombining PCR-amplified *SNCA(S129A)* and *SNCA(S129E)* (kindly provided by Dr. Robert Edwards, UCSF) into *BamHI*-linearized p426GAL α SYN(WT)GFP. Plasmids pRS304 α SYN(WT)GFP, pRS304 α SYN(S129A)GFP, pRS304 α SYN(S129E)GFP, pRS306 α SYN(WT)GFP, pRS306 α SYN(S129A)GFP, pRS306 α SYN(S129E)GFP, were then created by subcloning the *GAL1pr-SNCA(WT, S129A and S129E)-GFP* fusions from the p426GAL-derived plasmids into the *SacI* and *KpnI* sites of the integrating vectors pRS304 and pRS306 . Plasmids pRS304(MCS-) and pRS306(MCS-), lacking the multiple cloning site, were created by digesting pRS304 and pRS306 with *SacI* and *KpnI*,

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blunting the ends with DNA Polymerase I, Large (Klenow) Fragment (New England Biolabs) and re-circularizing the plasmids. pRS304 and pRS306-derived plasmids were linearized with *EcoRV* for integration into the W303-1A strain.

Plasmids pRS405TRP1 α SYN(WT)GFP, pRS405TRP1 α SYN(S129A)GFP, pRS405TRP1 α SYN(S129E)GFP were generated by sequential insertion of the *GAL1pr-SNCA*(WT, S129A and S129E)-*GFP* fusions from the p426GAL-derived plasmids into the *SacI* and *KpnI* sites of the integrating vector pRS405 followed by insertion of the first and the last 300bp of the *TRP1* ORF in inverted order (3'5') separated by a *XmaI* site into the *SacI* site of plasmid pRS405 for gamma integration into the *TRP1* locus. Plasmid pRS405TRP13'5' was generated by removing the *GAL1pr-SNCA*(WT, S129A and S129E)-*GFP* insert within the *SpeI* and *XhoI* sites, blunting the ends with DNA Polymerase I, Large (Klenow) Fragment (New England Biolabs) and re-circularizing the plasmids.

Plasmids pRS406PDR1 α SYN(WT)GFP, pRS406PDR1 α SYN(S129A)GFP, and pRS406PDR1 α SYN(S129E)GFP were generated by sequential insertion of the *GAL1pr-SNCA*(WT, S129A and S129E)-*GFP* fusions from the p426GAL-derived plasmids into the *SacI* and *KpnI* sites of the integrating vector pRS406 followed by insertion of the first and the last 300bp of the *PDR1* ORF in inverted order (3'5') separated by a *MfeI* site into the *SacI* site of plasmid pRS406 for gamma integration into the *PDR1* locus. Plasmid pRS406PDR13'5' was generated by removing the *GAL1pr-SNCA*(WT, S129A and S129E)-*GFP* insert within the *AgeI* and *XhoI* sites, blunting the ends with DNA

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Polymerase I, Large (Klenow) Fragment (New England Biolabs) and re-circularizing the plasmids.

pRS405 and pRS406-derived plasmids were linearized with *XmaI* and *MfeI*, respectively, for integration into the Y5563 strain.

Plasmids p425GALYPT1 and p425GALYCK1 were created by subcloning *YPT1* and *YCK1* from the Yeast ORF collection (Open Biosystems) into p425GAL (Addgene) using Gateway Technology (Invitrogen).

Plasmid p415YCK1 was created by cloning *YCK1* with its endogenous promoter into plasmid p415TEF as a *SacI-BamHI* digested product of PCR-amplification from yeast genomic DNA.

Yeast strains and manipulation

The strains used in this study are summarized in Chapter 2, table 1.

To generate strain VSY1, the *GAL1pr-SNCA(WT)-GFP* fusion was PCR-amplified from plasmid p426GAL α SYN(WT)GFP and the *MX4-NatR* cassette was PCR-amplified from plasmid p4339 (kindly provided by Dr. Charles Boone, University of Toronto). Primer sequences were designed to enable the merging of both fragments in a third PCR reaction and the site-directed integration of the resulting *GAL1pr-SNCA(WT)-GFP-NatR* fusion at the *ADE2* locus by homologous recombination in the BY4741 strain .

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To generate strain VSY2, the *GAL1pr-SNCA(WT)-GFP* fusion was PCR-amplified from plasmid p426GAL α SYN(WT)GFP and the *URA3-MX6* cassette was PCR-amplified from plasmid p4348 (kindly provided by Dr. Charles Boone, University of Toronto). Primer sequences were designed to enable the merging of both fragments in a third PCR-reaction and the site-directed integration of the resulting *GAL1pr-SNCA(WT)-GFP-URA3* fusion at the *TRP1* locus by homologous recombination in the Y5563 strain .

To generate strain VSY4, strains VSY1 and VSY2 were crossed. Diploid cells were selected on SD–Ura + G418 (Invitrogen)/ClonNAT (Werner BioAgents) plates and sporulated. Spores were germinated and haploid cells of both mating types were selected in SD – Arg/Lys/Ura + canavanine (Sigma-Aldrich)/thialysine (Sigma-Aldrich)/G418/clonNAT plates. *MAT \square* cells were selected by their inability to grow on SD–His plates and the mating type was subsequently confirmed by mating test.

Strains VSY53-61 were obtained from a cross between strain VSY4 and the corresponding deletion strains.

Strains *pdr1 Δ* , *yck1 Δ* , *yck2 Δ* , *tlg2 Δ* and *spo14 Δ* were retrieved from the Yeast *MATa* Genome Deletion Collection (Open Biosystems).

Strain VSY64 was generated by disruption of the *PDR1* gene from strain VSY4 with the *kanMX4* cassette obtained by PCR-amplification of genomic DNA from the strain *pdr1 Δ* .

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Strain VSY65 was generated by disruption of the *kanMX4* cassette from strain VSY57 with the *LEU2* cassette obtained by PCR-amplification from plasmid pRS415.

Strain VSY66 was generated by disruption of the *PDR1* gene from strain VSY65 with the *kanMX4* cassette obtained by PCR-amplification of genomic DNA from the strain *pdr1Δ*.

Strain FRY346 was generated by integration of *EcoRV*-linearized p8xmycSNC1406 plasmid in the BY4741 strain.

Strains VSY67 to VSY74 were generated by consecutive integration of *EcoRV*-linearized pRS306-derived and pRS304-derived plasmids in the W303-1A strain.

Strains VSY75-78 were generated by disruption of the *YCK1* gene from strains VSY71-78 with the *kanMX4* cassette obtained by PCR-amplification of genomic DNA from the strain *yck1Δ*.

Strains VSY79-86 were generated by consecutive integration of *XmaI* linearized pRS405-derived plasmids followed by integration of *MfeI*-linearized pRS406-derived plasmids in the Y5563 strain.

Strains BY4741 and FRY346 were transformed with the indicated plasmids using the one-step protocol and cultured in SYNthetic complete medium without the corresponding nutrients for auxotrophic selection and with the indicated carbon sources.

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The integrated strains were transformed using the standard protocol and cultured in rich (YEP) medium with the indicated carbon sources.

Yeast growth curves

The indicated strains were inoculated in triplicate in 100 μ l of raffinose-containing medium in 96-well plates and grown for 48 h to stationary phase. Cultures were then diluted 100-fold in raffinose and galactose-containing media and incubated at 30°C. The OD₆₀₀ was recorded at the indicated times. Growth rates were determined as the slope of the growth curves during logarithmic phase.

Pharmacologic inhibition of CKI activity

For the CKI inhibitor studies, strains *pdr1* Δ (0c α SYN in *pdr1* Δ), VSY64 (2c α SYN in *pdr1* Δ), and VSY65 (2c α SYN in *pdr1* Δ *yck1* Δ) were grown in raffinose-containing medium to stationary phase, diluted to OD₆₀₀ = 0.1 in raffinose and galactose-containing media and dispensed in 100 μ l aliquots to 96-well plates. Aliquots were treated in triplicate with the indicated concentrations of D4476 (Calbiochem, CA) or vehicle DMSO alone.

Phosphorylation assays

For the time-course experiment, strain VSY4 (2c α SYN in WT) was grown to logarithmic phase (OD₆₀₀ ~ 0.8) in raffinose-containing medium and α SYN expression was induced by adding 0.2% galactose. Eight ml aliquots were collected at the indicated times. For protein extraction, cells were collected by centrifugation, washed with water, and resuspended in 200 μ l of extraction buffer [200 mM Tris pH 8.0, 150 mM

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ammonium sulfate, 10% glycerol, 1 mM EDTA, 1 μ M microcystin LR, 200 μ M activated Na_3VO_4 , and 1x complete protease inhibitor cocktail (Roche)] and 100 μ l of acid-washed glass beads (425–600 μ m) (Sigma-Aldrich). Cells were lysed by vortexing two times for 5 min at 4°C. Supernatants were separated from cell debris and beads by centrifugation at 5,000 rpm for 5 min and then cleared by centrifugation at 13,000 rpm for 30 min. The soluble fractions (supernatant) were separated by SDS-PAGE and proteins analyzed by immuno-blot with mouse anti- α SYN (1:20,000) (BD Transduction Laboratories) and anti-S129 phospho-specific antibodies (1:20,000) (JH22.11A5, Elan Pharmaceuticals).

For comparison of α SYN phosphorylation levels in different deletion backgrounds, strains VSY4, VSY57, VSY58 and VSY60 were grown to logarithmic phase ($\text{OD}_{600} \sim 0.8$) in raffinose-containing medium and α SYN expression was induced by adding 0.2% galactose for 1 h. Samples were treated as described before and soluble fractions were analyzed by western blot. Band densities were quantified with ImageQuant 5.2 (Molecular Dynamics).

To assess α SYN phosphorylation in *YCK1* overexpressing cells, the indicated strains were grown for 12 h to logarithmic phase in raffinose-containing medium and induced with 2% galactose. Ten ml aliquots were collected at 5.5 h and 11 h. When indicated, cultures were treated with 500 nM microcystin and 200 μ M cell-permeable Na_3VO_4 for 15 min prior to cell harvesting. Samples were analyzed as described before.

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Analysis of α SYN levels in yeast

Strains VSY67-74 and VSY79-86 were grown to logarithmic phase in raffinose-containing medium and induced with 2% galactose for 8 h. Samples were processed and analyzed by western immuno-blot as described before.

Analysis of α SYN, Rab5, Rab4, EEA1 and CK1 δ cellular levels

Brain homogenates were solubilized in lysis buffer (1% Triton X-100, 10% glycerol, 50 mM HEPES, pH 7.4, 140 mM NaCl, 1 mM EDTA, 1 mM Na₃VO₄, 20 mM β -glycerophosphate, and proteinase inhibitor cocktails), and separated into cytosolic and particulate fractions by centrifugation. Twenty mg of the particulate fractions were resolved by SDS-PAGE and blotted onto membranes before be decorated with rabbit polyclonal anti- α SYN (Chemicon), mouse monoclonal anti-Rab5 (BD Transduction Laboratories), mouse anti-human EEA1 (BD Transduction Laboratories), mouse anti-human Rab4 (BD Transduction Laboratories), goat anti-CK1 δ (C-18) (Santa Cruz Biotechnology), and mouse monoclonal anti-actin (Chemicon).

Mouse models

For this study, 12 heterozygous transgenic (tg) 6 month old mice expressing human α SYN under the regulatory control of the platelet-derived growth factor- β (PDGF β) promoter (Line D) and 12 littermate non transgenic (non-tg) age-matched controls were used. These animals were selected because they display abnormal accumulation of detergent-insoluble α SYN, develop cytoplasmic α SYN-immunoreactive inclusion-like structures in the brain, and display neurodegenerative and motor deficits that mimic

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certain aspects of DLB/PD. Comparisons of the patterns of α SYN and Rab5 distribution were performed with 6 to 6 months old mice that mimic AD-like pathology by expressing the human mutant amyloid precursor protein (APP) (line 41) under the thyl promoter .

Human cases and neuropathological evaluation

This study examined a total of 18 subjects (Table II), including 8 cases of dementia with Lewy bodies (DLB/PD), 6 cases of Alzheimer's disease (AD) and 4 non-demented controls. Autopsy material was obtained from patients studied neurologically and psychometrically at the Alzheimer Disease Research Center/University of California, San Diego (ADRC/UCSD). For each case, paraffin sections from 10% buffered formalin-fixed neocortical, limbic system and sub-cortical material stained with haematoxylin and eosin (H&E) and thioflavin-S were used for routine neuropathological analysis that included Braak stage. The diagnosis of DLB/PD was based on the clinical presentation of dementia followed by parkinsonism and the pathological findings of Lewy bodies (LBs) in the locus coeruleus, substantia nigra (SN), or nucleus basalis of Meynert, as well as in cortical and subcortical regions. LBs were detected using H&E anti ubiquitin and anti α SYN antibodies as recommended by the Consortium on DLB criteria for a pathologic diagnosis of DLB/PD. In addition to the presence of LBs, the great majority of these cases display sufficient plaques and tangles to be classified as Braak stages III-IV. Specifically, DLB/PD cases had abundant plaques in the neocortex and limbic system but fewer tangles compared to AD cases.

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Fluorescence microscopy of yeast

For the S129 mutagenesis study, strains VSY67-74 were grown to stationary phase at 30°C in raffinose-containing medium and diluted 100-fold in galactose-containing medium. Cells were induced for 16 h, mounted and sealed as described.

For the trafficking studies, strain BY4741 cotransformed with plasmids p423GPD α SYN(WT) or p423GPF and pGS416 (*GFP-SNC1*), pGSSO416 (*GFP-SNC1-SSO1*), pGNS416 (*GFP-NYV1-SSO1*), pPEP416 (*GFP-PEP12*), pPHM5 (*GFP-PHM5*), pSNA3416 (*SNA3-GFP*) or pSTE2416 (*GFP-STE2*), was grown for 12 h to logarithmic phase at 30°C in glucose-containing medium and mounted as described. Strains BY4741, *yck1* Δ , VSY4 and VSY57 transformed with plasmid pmCheSSO416 (*mCherry-SNC1-SSO1*) were grown for 12 h to logarithmic phase at 30°C in galactose-containing medium and mounted as described.

For FM 4-64 labeling, the indicated strains were grown for 12 h in medium containing glucose [deletion and temperature-sensitive mutant strains transformed with plasmid pGSSO416 (*GFP-SNC1-SSO1*)] or galactose (strains VSY71-74) at 30°C (deletion strains and VSY71-74) or room temperature (temperature sensitive strains). A total of 0.16 culture ODs were centrifuged and resuspended in 40 μ l of medium containing 40 μ M FM 4-64 to a final OD₆₀₀ of 4.0. Cells were pulsed with the dye for 15 min, washed with 1 ml of H₂O, resuspended in 0.5 ml of unlabeled medium and incubated for 1 h to let the dye internalize. The deletion and VSY71-74 strains and were labeled at 30°C whereas the temperature sensitive strains were pre-incubated at 37°C or room temperature for 30

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min prior to the FM 4-64 pulse and kept at the same temperature throughout all the steps for imaging.

For the rescue studies, strain BY4741 cotransformed with plasmids p423GPD α SYN(WT) or p423GPF alone, and pGSSO416 (*GFP-SNC1-SSO1*), was transformed with plasmids p425GALYPT1, p425GALYCK1 or left untransformed (No plasmid). Cells were grown in glucose-containing medium at 30°C to stationary phase and diluted down 20-fold in galactose-containing medium. Cultures were induced for 16 h and prepared for imaging as described.

For the mutagenesis, trafficking, rescue and FM 4-64 studies, cells were imaged with a Nikon Plan Apo VC 100x (N.A. 1.4) objective on a spinning disk confocal microscope (Nikon) and images were acquired with a Cascade II digital camera (Photometrics) using Micro-Manager 1.3 (University of California, San Francisco).

Immunoelectron microscopy of yeast

For single labeling, strain BY4741 transformed with the plasmid p426GAL α SYN(WT)GFP was grown at 30°C in glucose-containing medium to early logarithmic phase, washed with water, resuspended in galactose-containing medium, and incubated for 6 h or 12 h. For double labeling, the strain FRY346 transformed with plasmid p423GPD α SYN(WT)GFP was grown for 12 h at 30°C in glucose-containing medium to logarithmic phase. In both cases, cells were fixed with 2% glutaraldehyde-0.2% para-formaldehyde and prepared for the Tokuyasu cryosectioning procedure

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according to a protocol optimized for *S. cerevisiae*. Ultrathin sections were incubated first with antibodies recognizing the tags and subsequently with protein A-gold conjugates . After standard staining with uranyl and embedding in methylcellulose, sections were visualized in a JEOL 1010 electron microscope (JEOL) and images were recorded on Kodak 4489 sheet films.

For single labeling, a polyclonal anti-GFP antiserum was used (Abcam). For double labeling, a monoclonal anti-myc antibody (Santa Cruz Biotechnology) and the same anti-GFP antiserum were used. Untransformed cells were treated in the same way and used as background controls.

Immunofluorescence of mammalian cells

For the co-localization studies, sections from the temporal cortex of DLB/PD and control cases and from α SYN tg and non-tg mice were used. Free-floating 40 μ m thick vibratome sections were washed with Tris buffered saline (TBS, pH 7.4), pre-treated in 3% H₂O₂, and blocked with 10% serum (Vector), 3% bovine serum albumin (Sigma-Aldrich), and 0.2% gelatin in TBS-Tx.

Double-immunofluorescence analyses were performed utilizing the Tyramide Signal Amplification™-Direct (Red) system (NEN Life Sciences). Specificity of this system was tested by deleting each primary antibody. For the Rab5 studies, sections were double-labeled with monoclonal antibodies against α SYN (1:20,000) (Cell Signaling) and Rab5 (1:75) (Vector), and detected with Tyramide Red and fluorescein isothiocyanate

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(FITC)-conjugated secondary antibodies (1:75) (Vector), respectively. For the CKI α studies, sections were double-labeled with the polyclonal antibodies against α SYN (1:200) (Chemicon) and CKI δ (C-18) (Santa Cruz Biotechnology), and detected with FITC and Tyramid Red-conjugated secondary antibodies (1:75) (Vector), respectively. Sections were imaged with a Zeiss 63X (N.A. 1.4) objective on an Axiovert 35 microscope (Zeiss) with an attached MRC1024 laser scanning confocal microscope (LSCM) system (BioRad). All sections were processed simultaneously under the same conditions and experiments were performed twice for reproducibility.

Construction of RNA interference plasmid & mcherry-tagged proteins

The pSilencer plasmid (gift from Dr. L. Gan, Gladstone Institute of Neurological Disease, San Francisco, CA) was used to construct the RNAi plasmid. Each shRNA insert was designed as a synthetic duplex with 18-22-nucleotide oligonucleotides corresponding to gene-specific sequences of each genetic modifier between an inverted motif that contains the six-nucleotide spacer and five Ts and cloned into the pSilencer plasmid with *EcoRI* and *XhoI*. Four shRNA constructs were generated per gene and sequenced for accuracy. The shRNA constructs that best suppressed gene expressions were used in subsequent experiments. The following nucleotides were used:

Cog6 forward: TTGTACGCAAGAGAACTTTGAC, reverse:

GTCAAAGTTCTCTTGCGTACAA;

Rabgef1 forward: GCAGCAAGCACATCTTCAATGC, reverse:

GCATTGAAGATGTGCTTGCTG;

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Stx1a forward: AGAACTCATGTCCGACATAAA, reverse:

TTTATGTCGGACATGAGTTCT;

Stx7 forward: TGATGATTCATGAACAAGG, reverse: CCTTGTTTCATGAATCATCAC;

Stx12 forward: TTTTCCTTTTCAGATACCCTTC, reverse:

GAAGGGTATCTGAAAAGGAAAA;

Stx16 forward: TTGTCACACCAATCGCTGCTTCTCGA, reverse:

TCGAGAAGCAGCGATTGGTGTGACAA;

Vps24 forward: CTTCTGATCGTCCATGCTTTC, reverse:

GAAGAAAGCATGGACGATCAGGAAG;

Vps28 forward: GTGAAGTTGTACAAGAACG, reverse: CGTTCTTGTACAACCTTCA;

Vps34 forward: TCAACATTGGGTCTTCCAGGACAGC, reverse:

GCTGTCCTGGAAGACCCAATGTTGA;

Vps45 forward: ATACCGCGTGTGATTTATT, reverse: AATAAATCACACGCGGTA;

Vps52 forward: CTAGATAAGAATCCAGGTG, reverse: CACCTGGATTCTTATCTAG;

scrambled forward: TATAAATTACGTAGT, reverse: ACACTACGTAATTTATACACC

Full-length cDNA stx7, Vps24, Vps28, Vps34 and Vps45 plasmids were from Openbiosystems and sub-cloned into pcDNA3.1(-) vector from Invitrogen *NotI* and *XbaI* or *NotI* and *XhoI* with mCherry cloned in the *KpnI* site.

Cell Culture and transfection

SH-SY5Y cells stably transfected with inducible α SYN (gift from Dr. L. Stefanis, Department of Neurology, University of Athens medical school, Athens, Greece) were

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cultured in RPMI 1640 (Invitrogen, UCSF Cell Culture Facility), 10% fetal bovine serum (FBS) (Gibco) and 250 $\mu\text{g}/\text{mL}$ G418 (Invitrogen) and 50 $\mu\text{g}/\text{mL}$ Hygromycin B (UCSF Cell Culture Facility). αSYN expression was switched off with 2 $\mu\text{g}/\text{mL}$ doxycycline (UCSF Cell Culture Facility). Cells were differentiated with 20 μM all-trans retinoic acid (Invitrogen). Transient transfections on SH-SY5Y cells were carried out using lipofectamine 2000 (Invitrogen).

For primary neuronal survival studies primary cortical neurons were prepared from embryonic day 20-21 timed pregnant rats (Charles River Laboratories), cultured in Neurobasal-A with B27 (Invitrogen) for 5 days and transfected with lipofectamine2000. For the analysis of neuronal survival, images were taken at 12-24 hr intervals using an automated microscope with image acquisition and analysis using Metamorph and custom-designed programs. Transfected neurons were selected for analysis based on fluorescence intensity and morphology, including the presence of extended processes at the start of the experiment. Neuronal death was determined by the changes in neuronal morphology that included cell body fragmentation and the ultimate loss of the venus signal. Survival time was determined as the last time point at which the neuron was seen alive. For statistical analysis, StatView software was used to construct Kaplan-Meier curves from the survival data. Survival functions were fit to these curves and used to derive cumulative hazard (or risk of death) curves. Differences in cumulative risk of death curves were analyzed for statistical significance with the log-rank test, and each of the experiments was performed independently 3 times.

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Toxicity assays

In the case of the LIVE/DEAD assay, cell cultures were exposed to components of the LIVE/DEAD kit (Molecular Probes) for 30 min at room temperature. Fluorescence intensity corresponding to viable and non-viable cells in three separate wells were then assayed using a fluorescent plate reader. In the case of the LDH assay, culture media was replaced by RPMI 1640 containing 1% FBS 24 hours prior to the start of the assay. Cell culture media was collected and exposed to the components of the LDH assay kit (Roche) and absorbance corresponding to cell death was assayed in three separate wells using a fluorescent plate reader. All experiments were repeated in triplicate and reported as mean \pm SE.

Cell lysis and immunoblotting

Cells were washed twice with ice-cold PBS and lysed with NP-40 buffer (50mM Tris, pH7.6, 150mM NaCl, 1% Triton X-100, 2mM EDTA, protease inhibitors) on ice for 20 min before centrifugation at 14,000x g for 30 min. Protein concentrations of supernatant were determined using the Bradford method (Bio-Rad). Protein samples were resolved on pre-cast SDS-PAGE gels in Bis-Tris glycine buffer (Invitrogen) and transferred to nitrocellulose membrane. Blots were blocked in 5% non-fat dry milk in PBS with 0.1% Tween 20 (PBST) for 30 min. The blots were then incubated with primary antibodies overnight at 4°C or 1 hour at room temperature. The blots were then washed three times with PBST and incubated with HRP-conjugated secondary antibodies for 1 hour at room temperature. The blots were washed with PBST for at least 1 hour and developed with the ECL-Plus chemiluminescence kit (Amersham).

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Immunocytochemistry

Cells were plated onto poly-D-lysine coated glass coverslips and cultured according to experiment requirements. The cells were fixed with 4% paraformaldehyde (PFA) for 10 min at room temperature and washed 3 times with wash buffer (PBS with 5% FBS and 0.1% Triton 100). The cells were then blocked in wash buffer for 10 min and stained with GM-130 antibody diluted in wash buffer (1:200) for 1 hour at room temperature. After rinsing with wash buffer three times, cells were incubated with AlexaFluor® 488 conjugated secondary antibodies diluted in wash buffer (1:200) for 1 hour at room temperature. The coverslips were then washed three times with wash buffer and once with PBS then mounted with vectashield with DAPI (Vecta Labs). The images were acquired by confocal microscopy (Nikon Eclipse Ti-E Motorized Inverted Microscope) with a 60X Plan-Apochromat oil immersion objective.

Exocytosis and transferrin receptor recycling assays

To monitor release of FM1-43 as a measure of exocytosis, differentiated SH-SY5Y cells were incubated with 15 μ M FM1-43 and depolarized with high KCl media (Hank's balanced salts medium with Ca^{2+} and Mg^{2+} plus 90 mM KCl and 63 mM NaCl) for 90s at room temperature. Unbound probe was removed by washing the cells with fresh saline solution for 10 min. Cells were washed twice with Hanks' balanced salts medium and re-incubated with depolarizing solution for 90 s at room temperature. FM1-43 retention is observed only cells with impaired exocytosis. The cells were then washed with Hanks' balanced salts medium, fixed with 4% paraformaldehyde for 10 min at room temperature and imaged by the MC02 Nikon Eclipse TE300 inverted microscope with the

METHODS

40X Plan-Fluor objective.

To monitor transferring receptor recycling, SH-SY5Y cells were plated on poly-D-lysine coated dishes (Mat-tek) and transfected with a plasmid expressing GFP-tagged transferrin receptor (gift from Dr. G. Yudowski, UCSF, San Francisco). Cells were imaged in OptiMEM (UCSF Cell Culture Facility) without added serum and imaged using a Nikon TE-2000E inverted microscope with a 6 x 1.45 NA TIRF objective, equipped for through-the-objective TIRF illumination using a 488-nm argon laser focused on the periphery of the back focal plane as previously described (30). Data is presented as mean number of events/cell normalized to size of the cell with error bars representing SE of the mean.

Statistical analyses

Statistical analysis was performed using Prism 5 (GraphPad Software). Student's t test were run for pair wise comparisons between groups at a single condition, and ANOVA for repetitive measurements were run for pair wise comparisons between groups throughout multiple treatments or times. Significance P-values were *P< 0.05; **P<0.01; ***P<0.001.

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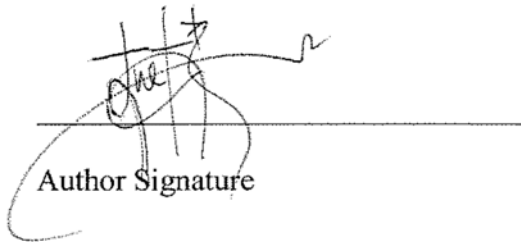
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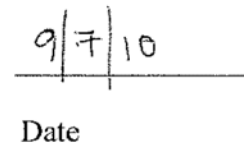
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Date