

REVIEW ARTICLE

Role of Lysosomal Genes for Parkinson's Pathogenesis: Insights from Molecular Mechanism to Therapeutic Strategies

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Abstract: Current review aims to clarify the role of lysosomal genes in the pathogenesis of Parkinson's Disease (PD), directing on the molecular mechanisms underlying lysosomal dysfunction and its involvement to α -synuclein accumulation. To deliberate PD-related genes including *GBA1*, *LRRK2*, *VPS35*, *PRKN*, *PINK1*, *TMEM175*, *ATP13A2*, *ATP10B*, and *DJI*, highlighting their contribution in lysosomal damage. It investigates the disorder of lysosomal enzymes such as cathepsins, glucocerebrosidase, galactocerebrosidase, and acid sphingomyelinase, and the consequent impairment of the autophagic-lysosomal pathway, which helps pathological α -synuclein accumulation. Therapeutic approaches targeting lysosomal dysfunction and α -synuclein pathology are reviewed, including pharmacological chaperones, immunization strategies, enzyme replacement therapies, and small-molecule oligomer modulators. While recent clinical trials expose certain limitations, combinatorial treatment strategies show potential to improve therapeutic efficacy. Lysosomal pathways are critical contributors to PD pathogenesis and denote promising targets for intervention. Integrating mechanistic understandings with developing therapies underlines the importance of targeting lysosomal dysfunction to mitigate α -synuclein aggregation and advance PD treatment.

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1. INTRODUCTION

Parkinson's Disease (PD) is a neurological disorder caused by irreversible impairment of dopaminergic neurons in the substantia nigra part of the brain. Early-Onset Parkinson's Disease (EOPD) accounts for almost 10% of cases, taking place in younger people, while only about 1% of those over 60 years are affected [1, 2]. Monogenic forms, resulting from mutations in high-risk genes, account for 5-10% of cases, although 15-25% of patients report a family history. Pathological mutations in genes associated with the genetic form of PD have been identified in several genes, notably *GBA1*, *LRRK2*, *VPS35*, *PRKN*, *PINK1*, *TMEM175*, *ATP13A2*, *ATP10B*, and *DJI* [3-5]. PD is a multifaceted condition resulting from a combination of genes, environment, and personal habits [6]. One of the key features of PD is the presence of Lewy bodies, which are composed of aggregated α -synuclein and a number of associated proteins. The presence of Lewy bodies in PD highlights the role of lysosomes and their dysfunction in the evolution of the disease [7, 8].

Symptomatic management can be obtained through methods such as replacement therapy using dopamine. However, such methods do not have an impact on the progression of the condition. Approaches under investigation include pharmacological chaperones, enzyme replacement therapies targeting *GBA1*-related lysosomal enzyme dysfunction, immunotherapies to reduce pathological α -synuclein, small-molecule modulators to avert toxic protein aggregation, and gene therapy [9, 10].

Further cellular pathways implicated in lysosomal dysfunction in PD include dysregulation of the mTOR-AMPK-ULK1 axis, which influences autophagy, PERK-eIF2 α -CHOP-mediated endoplasmic reticulum (ER) stress, dropping proteostasis [11], neuroinflammatory signaling via TLR4/NF- κ B impairing α -synuclein aggregation, and mitochondrial-lysosomal crosstalk through the PINK1/Parkin pathway involving mitophagy failure to dopaminergic neuron loss [12]. Understanding these integrated pathways may reveal new biomarkers and therapeutic targets, thereby enhancing understanding of PD pathology. This review aims to bridge mechanistic insights into lysosomal dysfunction with the translational developing of these novel therapies.

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2. PHYSIOLOGICAL FUNCTION OF THE LYSOSOMAL SYSTEM IN PD

Lysosomes are very important organelles that play significant roles in critical cellular processes such as autophagy and endocytosis, by which pathogens and other toxic substrates and degradation products are cleared [13]. Their degradative capacity depends on more than 60 hydrolytic enzymes, including lipid-degrading enzymes, proteases, phosphatases, glycosidases, nucleases, and sulfatases, which require a tightly regulated acidic environment (pH ~4.6-5.0) for optimal activity. These enzymes are synthesized in the endoplasmic reticulum and are tagged with mannose-6-phosphate, facilitating their recognition and transport *via* the mannose-6-phosphate receptor [14, 15]. Among the proteins, lysosomal integral membrane protein 2 mediates the transport of glucocerebrosidase into the lysosome. Approximately 50 associated membrane proteins maintain lysosomal homeostasis by regulating lysosomal pH, metabolic signal transport, and hydrolysis product, substrate, and ion transport [16].

As illustrated in Fig. (1), besides catalyzing secondary lysosomal transport, functions such as maintaining lysosomal pH, supplying substrates, distributing metabolites *via* exocytosis, and interacting with the cell membrane all

contribute to lysosomal function. The buildup of toxic substrates, cell debris, pathogens, and ruptured proteins disrupts cellular function and may contribute to cell death [15]. Chaperone-mediated autophagy is another cellular process that entails the transport and delivery of substrates to lysosomes [17]. The control of protein and signaling pathways involved in autophagosomes and autolysosomes is important in efficient autophagy [18-20].

Ineffective lysosomal protein degradation compromises the processing of neurodegeneration-related proteins like α -synuclein aggregates and other toxic substances [21]. As such, the episodic aggregate buildup could culminate in the induction of a pathogenic cascade that targets a molecule other than the defective enzyme. The pathogenic cascades include mitochondrial pathology, disrupted membrane integrity, impaired vesicle formation and transport, impaired autophagy, disrupted calcium balance, and accumulation of the RCS [22]. The complex lysosomal impairment has thus established its pivotal implication in the pathophysiology of the disease.

3. LYSOSOMAL SIGNALING PATHWAYS IN PD

The mTOR-AMPK signaling pathway modulates the initiation of autophagosomes and lysosome formation through transcription factors such as transcription factor EB

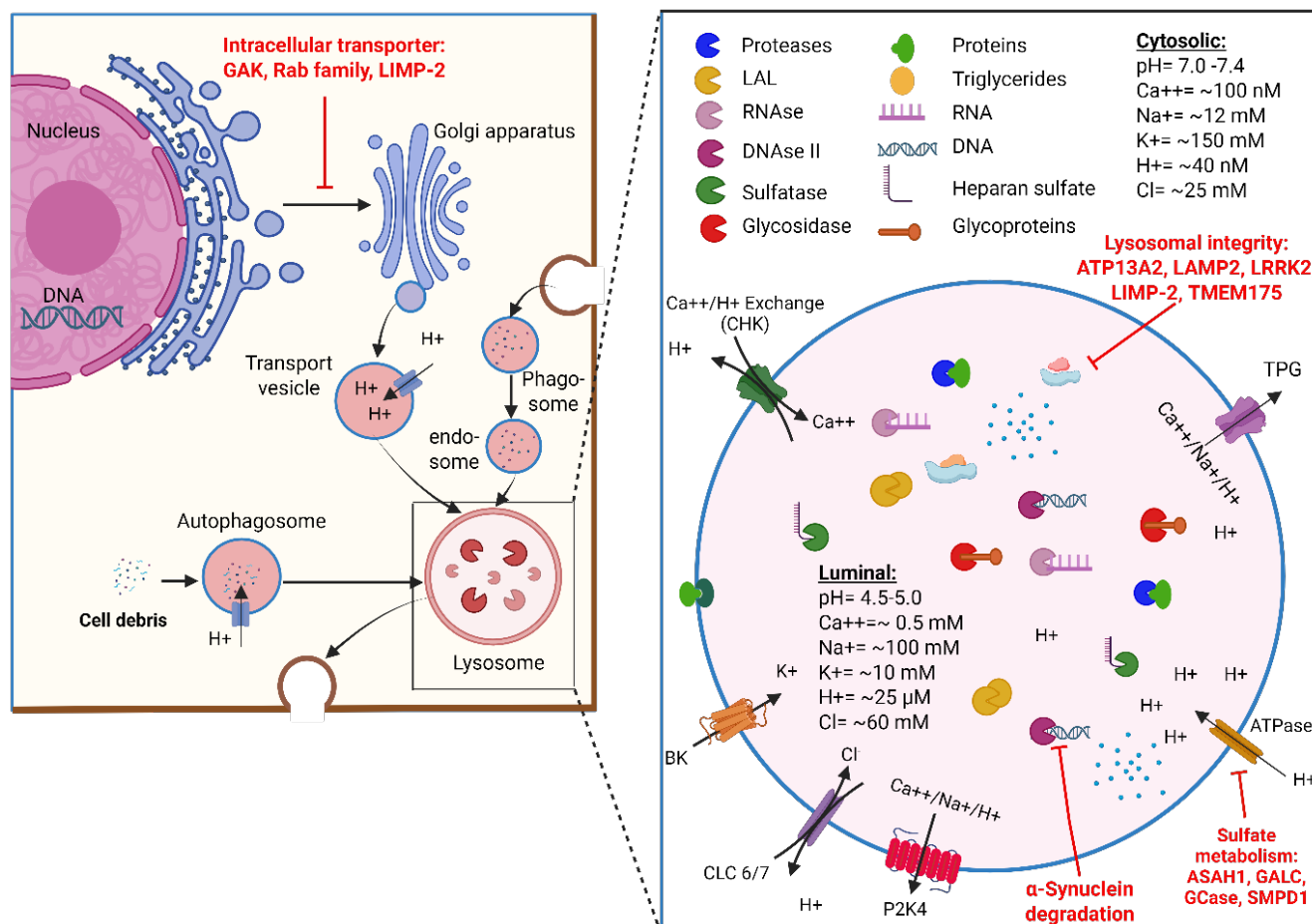


Fig. (1). Impression of lysosomal formation and function, highlighting corresponding PD-associated pathways and selected genetic variants. (A higher resolution / colour version of this figure is available in the electronic copy of the article).

Table 1. Molecular pathways linked to lysosomal dysfunction and PD pathogenesis.

Pathway	Key Components	Mechanistic Role in PD	References
mTOR/AMPK–TFEB signaling	mTORC1, AMPK, ULK1, TFEB	Controls autophagy initiation and lysosomal biogenesis; changed mTOR activity suppresses autophagic flux in PD	[23]
Mitochondrial lysosomal crosstalk	PINK1, PRKN, ATP13A2	Manages mitophagy and energy metabolism; defective crosstalk leads to mitochondrial ROS and dopaminergic neuron damage	[24]
ER-stress/Unfolded Protein Response	PERK, IRE1 α , ATF6, CHOP	Misfolded protein accumulation triggers unfolded protein response; chronic ER stress contributes to α -synuclein aggregation.	[25]
Neuroinflammatory (NF- κ B/TLR)	TLR4, MyD88, NF- κ B, TNF- α , IL-1 β	Microglial activation and cytokine release impair α -synuclein propagation and neuronal damage.	[26]
Oxidative stress and Nrf2	Nrf2, Keap1, HO-1, SOD2	Oxidative imbalance damages proteins and lipids; Nrf2 activation encourages antioxidant defense.	[27]

and transcription factor enhancer 3 [23]. Additionally, the activation of the mammalian Target Of Rapamycin Complex 1 (mTORC1) by the nutrient-deprived or oxidative-stressed state is negatively modulated through the activation of the protein kinase associated with the regulation of the mammalian target of rapamycin complex 1-activated protein kinase (AMP-activated protein kinase or AMPK), which promotes the nuclear translocation of the transcription factor EB protein. This is because the mammalian target of rapamycin complex 1 is positively modulated through the endogenous suppression of the transcriptional activity of the transcription factor EB protein [24]. The endoplasmic reticulum (ER) stress response pathways, specifically the “sensor” pathways of the IRE1 α and Protein Kinase RNA-like ER Kinase (PERK), modulate the regulation of Ca²⁺ transport and autophagic removal (Table 1) [25]. Moreover, aberrant regulation of nuclear factor kappa B (NF- κ B) and pro-inflammatory gene pathways sustains the elevated activity of inflammatory processes that compromise lysosomal integrity. It creates a vicious inflammatory cycle that propagates α -synuclein-mediated neuronal toxicity [26]. Taken together, these interconnected metabolic and inflammatory pathways suggest that lysosomal dysfunction in PD results from a complex network of overlapping mechanisms rather than isolated defects [27].

4. LYSOSOMAL GENE MUTATIONS ASSOCIATED WITH PD

Genetic disruption of lysosomal function thus appears as a central pathogenic axis in PD. Mutations in lysosome-associated genes disrupt substrate degradation, vesicular trafficking, lipid homeostasis, and autophagic clearance, and converge on α -synuclein accumulation and neuronal vulnerability. Table (2) summarizes key lysosomal genes implicated in PD. Each gene is reviewed below in a uniform format covering physiological function, mutation-specific mechanisms, clinical relevance, and therapeutic implications [28-38].

4.1. *GBA1*

The gene *GBA1* encodes lysosomal acid β -glucocerebrosidase, an enzyme that hydrolyzes glucosylcer-

amide into glucose and ceramide to maintain sphingolipid homeostasis in the lysosome [39]. Pathogenic mutations in *GBA1* (e.g., *N370S*, *L444P*, *D496H*) and mild/benign mutations (e.g., *E326K*, *T369M*) impair the folding efficiency and intracellular targeting of glucocerebrosidase, thereby inducing the accumulation of glucosylceramide in cells [40, 41]. The lipid imbalance promotes the stabilization of soluble α -synuclein oligomers and hinders chaperone-mediated autophagy; in turn, it creates a pathogenic cycle between glucocerebrosidase activity reduction and α -synuclein aggregation [42, 43]. *GBA1*-associated PD is defined by an earlier age at onset, faster disease progression, the preponderance of non-motor symptoms, and a higher incidence of cognitive disability than idiopathic PD. Pharmaceutical chaperones to improve glucocerebrosidase protein folding and secretion, substrate reduction therapy targeting glucosylceramide production, and gene therapies to normalize enzyme levels are used in its management [44].

4.2. *LRRK2*

LRRK2 encodes a multidomain kinase that controls vesicular trafficking, endolysosomal dynamics, and autophagosome maturation. Gain-of-function mutations (e.g., *G2019S*, *R1441C/G/H*) increase kinase activity, disorderly lysosomal positioning, and Rab-mediated vesicle trafficking [45, 46]. These changes impair autophagic flux independently of canonical mTOR signaling, leading to ineffective α -synuclein clearance. *LRRK2*-associated PD often phenotypically resembles idiopathic PD but displays mutable penetrance and age at onset [47, 48]. Brain-penetrant *LRRK2* kinase inhibitors and antisense oligonucleotides are under clinical development to normalize lysosomal aggregation and autophagic effectiveness [49, 50].

4.3. *TMEM175*

TMEM175 encodes a lysosomal potassium channel that is important for maintaining membrane potential, pH stability, and enzymatic activity. Risk variants such as *p.M393T* decrease potassium conductance, destabilize lysosomal pH, and, secondarily, diminish glucocerebrosidase activity [51]. This makes a tolerant environment for α -synuclein aggrega-

Table 2. Lysosomal gene mutation involved in PD.

Gene	Encoded Protein	Location	Proposed Mechanisms	References
<i>GBA1</i>	Glucosidase	Lysosomes	Lysosomal dysfunction, α -syn aggregation	[28, 29]
<i>LRRK2</i>	LRRK2	Cytoplasm, organelles	Hyperactive kinase disrupts trafficking, autophagy	[30]
<i>VPS35</i>	VPS35	Endosomes	Retromer dysfunction, mitochondrial stress	[31]
<i>PRKN</i>	Parkin	Cytoplasm/mitochondria	Impaired mitophagy, oxidative stress	[32]
<i>PINK1</i>	PINK1	Mitochondria	Mitophagy failure, mitochondrial dysfunction	[33]
<i>TMEM175</i>	TMEM175	Lysosomes	Lysosomal ion imbalance, α -syn accumulation	[34, 35]
<i>ATP13A2</i>	ATP13A2	Lysosomes	Impaired autophagy, lysosomal stress	[36]
<i>ATP10B</i>	ATP10B	Lysosomes	Lipid imbalance, α -synuclein toxicity	[37]
<i>DJ1</i>	DJ-1	Cytoplasm/mitochondria	Loss of oxidative stress defense	[38]

tion due to compromised proteolytic capacity [52]. *TMEM175* variants modulate PD susceptibility across diverse populations, highlighting lysosomal ion homeostasis as a disease modifier. Repair of lysosomal ionic balance through channel modulators represents an emerging therapeutic idea [53, 54].

4.4. *ATP13A2*

ATP13A2 encodes a lysosomal P5-type ATPase intricate in polyamine transport, metal ion homeostasis, and membrane integrity [55]. Loss-of-function mutations damage lysosomal acidification and polyamine export, promoting oxidative stress and imperfect autophagosome clearance [56]. *ATP13A2* mutations cause early-onset, fast progressive PD with prominent cognitive decline and severe lysosomal pathology. Potential strategies include restoring polyamine balance, enhancing lysosomal biogenesis, and gene replacement methods [57, 58].

4.5. *VPS35*

VPS35 is a main component of the retromer complex, mediating endosome-to-Golgi trafficking of lysosomal enzymes and autophagy-related proteins [59]. The *D620N* mutation disturbs retromer stability, leading to malfunctioning hydrolase recycling, reduced autophagosome formation, and increased α -synuclein burden. *VPS35*-associated PD typically presents as a late-onset disease with autosomal-dominant inheritance. Retromer-stabilizing pharmacological chaperones and gene therapy methods are being discovered to reestablish trafficking reliability [60].

4.6. *ATP10B*

ATP10B encodes a lysosomal phospholipid flippase accountable for translocating glucosylceramide and phosphatidylcholine across the lysosomal membrane [61]. *ATP10B* deficiency disrupts lipid asymmetry, impairs lysosomal

acidification, and impairs autophagic degradation, indirectly enhancing α -synuclein aggregation [62]. Rare *ATP10B* variants contribute to PD susceptibility in both familial and sporadic cases. Interventions aimed at correcting lipid imbalance or dipping substrate load denote rational therapeutic methods [63].

4.7. *PRKN*

PRKN encodes Parkin, an E3 ubiquitin ligase critical for tagging injured mitochondria for mitophagic removal [64]. Damage to Parkin function impairs effective mitophagy, leading to the accumulation of dysfunctional mitochondria, amplified oxidative stress, and neuronal injury [65, 66]. *PRKN*-associated PD typically manifests in adolescence or early adulthood, progresses slowly, and often lacks Lewy body pathology. Methods focus on enhancing mitophagy, stabilizing mitochondrial function, and gene replacement strategies [67, 68].

4.8. *PINK1*

PINK1 encodes a mitochondrial kinase that senses membrane depolarization and triggers Parkin-dependent mitophagy [69, 70]. *PINK1* loss-of-function mutations prevent recruitment of autophagy receptors, damaging mitochondrial quality control and promoting oxidative damage [71, 72]. *PINK1*-associated PD is characterized by early onset and marked mitochondrial involvement. Mitophagy enhancers and mitochondrial bioenergetic stabilizers are under investigation [73].

4.9. *DJ-1*

DJ-1 is a redox-sensitive chaperone complex in oxidative stress sensing, protein stabilization, and mitochondrial defense [74]. Loss of *DJ-1* redox activity increases susceptibility to oxidative stress and, indirectly, disrupts autophagic degradation pathways [75, 76]. *DJ-1* mutations cause EOPD with heightened oxidative vulnerability. Antioxidant

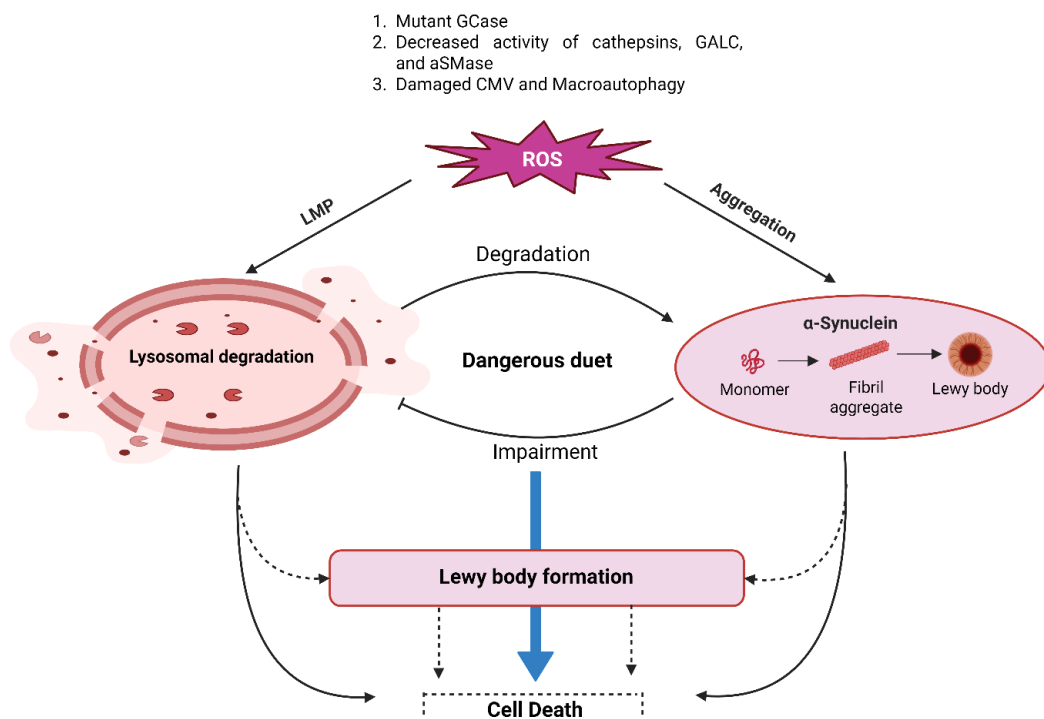


Fig. (2). Lysosomal dysfunction in α -synuclein pathology. Mutant GCase or GCase knockdown leads to α -synuclein accumulation. (A higher resolution / colour version of this figure is available in the electronic copy of the article).

strategies, Nrf2 pathway activation, and gene therapy methods are being explored [77, 78].

5. THE PATHOPHYSIOLOGY OF A-SYNUCLEIN IS INFLUENCED BY LYSOSOMAL MUTAGENIC DYSFUNCTION

Lysosomal hydrolases (e.g., cathepsins [CTSD, CTSL, CTSB]) promote the accumulation of species prone to aggregation [79]. Deficiencies of other lysosomal hydrolases, including galactocerebrosidase and acid sphingomyelinase, increase ceramide excesses and thereby increase the toxicity of α -synuclein [80-82]. Together, these observations emphasize the role of α -synuclein pathology as a causative agent and the extent to which lysosomal dysfunction contributes to it, as shown in Fig. (2) [83].

5.1. The Pathology of α -synuclein and Glucocerebrosidase

Lower Cer levels may impair lysosomal degradation of α -synuclein because Cer binds to and activates cathepsin D. Decreased Cer levels have been observed in brain regions such as the anterior cingulate. Glucocerebrosidase activity influences the propensity of α -synuclein to aggregate by altering lipid membrane composition [84].

5.2. Galactocerebrosidase, Acid Sphingomyelinase, and α -synuclein Pathology

Besides acid sphingomyelinase and galactocerebrosidase, two lysosomal enzymes that generate Cer, dysregulation of these enzymes is implicated in PD and α -synucleinopathies. Acid sphingomyelinase catalyzes sphingomyelin breakdown

into Cer and phosphorylcholine; its blood levels decline 3.5-5.8 years before PD onset. Galactosylceramidase hydrolyzes galactosylceramide and galactosylsphingosine, with elevated cortical galactosylsphingosine levels found in PD patients compared to controls. Moreover, galactosylsphingosine dose-dependently enhances α -synuclein aggregation [85, 86].

5.3. ALP Dysfunction and Pathology of α -synuclein

Inhibition of the ALP decreases hydrolase activity, smoothing α -synuclein aggregate accumulation and intercellular propagation. For example, bafilomycin A1-mediated ALP obstruction causes α -synuclein aggregates to accumulate in primary cortical neurons and non-neuronal cells [87].

6. THERAPEUTIC STRATEGIES TARGETING LYSOSOMAL DYSFUNCTION IN PD

Advances in the molecular understanding of lysosomal dysfunction in PD have allowed the development of therapeutic approaches aimed at restoring proteostasis, lipid balance, vesicular trafficking, and autophagic-mitochondrial crosstalk. Rather than targeting individual genes in isolation, most current methods converge on shared pathogenic mechanisms, including impaired lysosomal enzyme activity, malfunctioning autophagy, disrupted ion and lipid homeostasis, and secondary α -synuclein accumulation. It synthesizes therapeutic efforts by mechanistic class, highlighting translational progress and limitations (Table 3).

6.1. Therapeutic Targeting of *GBA1*

The *GBA1* is a primary target for treating *GBA1*-associated PD and GD. Pharmacological chaperones

Table 3. Ongoing and completed therapeutic strategies targeting lysosomal dysfunction in PD disease.

Target / Strategy	Drugs	Clinical Phase	Mechanism of Actions	Outcome	References
<i>GBA1</i>	Ambroxol	Phase II (NCT02914366)	BBB-penetrant pharmacological chaperone enhancing glucocerebrosidase activity.	Increased enzyme activity observed in early clinical studies	[90]
	Isogomine	Phase I (NCT01353585)	ER chaperone stabilizing glucocerebrosidase folding and trafficking	Improved enzyme stability and lysosomal delivery	[90]
	LTI-291	Phase I (NCT03939522)	Non-inhibitory activator of β -glucocerebrosidase	Currently under clinical evaluation	[91]
	S-181	Preclinical	Small-molecule non-inhibitory glucocerebrosidase activator	Demonstrated enzymatic activation in preclinical models	[91]
	Eliglustat	Approved for GD1 (NCT00358150)	Substrate reduction therapy; non-BBB permeable	Effective in systemic Gaucher disease; limited CNS benefit	[92]
	Miglustat	Approved for GD1 (NCT00074985)	Inhibits glucosylceramide synthesis	Reduces systemic substrate burden with minimal CNS efficacy	[93]
<i>LRRK2</i>	DNL151 (BIIB122)	Phase II (NCT04556630)	LRRK2 kinase inhibition reduces Rab phosphorylation	Favorable safety and efficacy signals in PD trials	[97]
	DNL201	Phase I (NCT03710707)	Brain-penetrant LRRK2 kinase inhibitor	Positive pharmacodynamic and safety outcomes	[97]
	MLi-2	Preclinical	Selective LRRK2 kinase inhibition	Neuroprotective effects in PD models	[98, 108]
	PF-06447475	Preclinical	LRRK2 kinase inhibition	Improved lysosomal and autophagic function	[99]
	GNE-7915	Preclinical	Reversible LRRK2 kinase inhibitor	Restoration of lysosomal homeostasis	[99]
<i>ATP13A2</i>	PBT2	Phase II (NCT00462701)	Metal chelation reduces oxidative stress	Neuroprotection observed in experimental models	[104]
	Clioquinol	Phase I/II (NCT01273141)	Chelation of zinc and manganese	Attenuation of oxidative neuronal damage	[104]
<i>TFEB</i>	Trehalose	Preclinical	TFEB activation promoting lysosomal biogenesis	Enhanced α -synuclein clearance in PD models	[105]
<i>VPS35</i>	R55	Preclinical	Retromer stabilization improving intracellular trafficking	Mitochondrial rescue in PD models	[107]
	R33	Preclinical	Pharmacological chaperone correcting VPS35 mutation effects	Improved retromer complex stability	[107]
<i>PRKN</i>	Nicotinamide Riboside	Phase II (NCT03432871)	Enhances mitochondrial biogenesis and mitophagy	Improved mitochondrial function	[113]
	Urolithin A	Phase I/II (NCT04160312)	Induction of mitophagy	Positive bioenergetic outcomes	[113]
	KH176	Phase II (NCT03562494)	Redox modulation supporting mitochondrial integrity	Promoted neuronal survival	[114]
	EPI-589	Phase II (NCT02462630)	Redox-balancing neuroprotective agent	Improved mitochondrial health	[114]
<i>PINK1</i>	Niclosamide	Phase I (NCT02521870)	PINK1-independent mitophagy activation	Enhanced mitochondrial clearance	[116]
<i>DJ-1 pathway</i>	Sulforaphane	Preclinical	Augments DJ-1-mediated antioxidant defenses	Reduced ROS-mediated neurotoxicity	[120]
	Dimethyl fumarate	Phase II (NCT04200911)	Nrf2 activation compensating for DJ-1 dysfunction	Enhanced antioxidant gene expression	[122]

enhance correct folding and lysosomal trafficking of mutant enzymes, thereby increasing residual enzymatic activity [88, 89]. For example, a brain-penetrant chaperone, Ambroxol, has demonstrated increased glucocerebrosidase activity and reduced α -synuclein burden in patient-derived cells and early clinical studies [90]. Non-inhibitory chaperones such as LTI-291 and S-181 aim to avoid competitive substrate interference and are undergoing clinical evaluation [91].

Substrate reduction therapies (SRTs) prevent the synthesis of glucosylceramide, thereby reducing the lysosomal lipid burden. While eliglustat and miglustat are effective in systemic Gaucher disease, their limited blood-brain barrier (BBB) penetration limits their utility in PD [92, 93]. CNS-penetrant SRTs remain an active area of examination, particularly for conditions involving *ATP10B*- and *GBA1*-related lipid dysregulation [94].

6.2. Therapeutic Targeting of *LRRK2*

Therapeutic methods targeting *LRRK2*, particularly for pathogenic mutations such as *G2019S*, which increase kinase activity and disrupt cellular homeostasis, are the main focus in PD treatment [95]. Numerous small-molecule inhibitors, kinase blockers, and antisense oligonucleotides have been developed to control their activity [96]. Denali Therapeutics and Biogen developed brain-penetrant inhibitors DNL201 and DNL151 (BIIB122), which control lysosomal and mitochondrial dysfunction by reducing *LRRK2* kinase activity and phosphorylation of Rab proteins. Phase I and II studies have shown positive safety and pharmacodynamics [97]. MLI-2 is another selective inhibitor that determines strong *LRRK2* inhibition and neuroprotection in preclinical trials [98]. Pfizer's PF-06447 and Genentech's GNE-7915 also suppress *LRRK2* selectively and reversibly, dipping the phosphorylation of *LRRK2* substrates and enhancing lysosomal function [99].

6.3. Therapeutic Targeting of *TMEM175*

TMEM175, a lysosomal potassium channel linked to PD and lysosomal function, is progressively related to neurodegenerative research. It preserves the lysosomal membrane potential, pH stability, and degradative capacity [100]. Direct pharmacological modulators are in the primary stages of research, with no approved drugs or advanced inhibitors. Structure-based drug design and high-throughput screening have identified small compounds that modulate *TMEM175*, encouraging ongoing efforts to develop channel agonists or potentiators to reestablish function of PD [101].

6.4. Therapeutic Targeting of *ATP13A2*

ATP13A2, also known as PARK9, is a protein that, when disturbed, contributes to the pathogenesis of PD and Kufor-Rakeb Syndrome. *ATP13A2* plays important roles in lysosomal homeostasis, metal ion transport, and autophagic clearance [102]. Current therapeutic strategies aim to reestablish *ATP13A2* activity. To date, direct modulation of *ATP13A2* has been minimally studied [103]. Metal ion chelation therapy with PBT2 or clioquinol decreases the accumulation of intracellular metals, reduces oxidative stress, and provides some neuroprotective effects in models

derived from *ATP13A2*-deficient mice [104]. Trehalose, 2-Hydroxypropyl- β -cyclodextrin, and rapamycin are TFEB activators that upregulate the expression of lysosomal genes and increase lysosomal clearance [105].

6.5. Therapeutic Targeting of *VPS35*

VPS35 (*Vacuolar Protein Sorting 35*), an important retromer complex component, is involved in PD, with the *D620N* mutation disrupting lysosomal trafficking, mitochondrial dynamics, and endosomal sorting. This mutation decreases autophagy and causes mitochondrial fragmentation and α -synuclein accumulation, contributing to neurodegeneration [106]. Pharmacological chaperones R55 and R33 stabilize the retromer, develop cargo recognition, adapt trafficking, mitigate α -synuclein pathology, and enhance mitochondrial function in models [107]. *LRRK2* inhibitors, such as DNL151 and MLI-2, which lower Rab protein phosphorylation and normalize lysosomal and mitochondrial function, are under clinical study for *LRRK2* and *VPS35*-linked PD [108].

6.6. Therapeutic Targeting of *ATP10B*

Variants in *ATP10B*, a lysosomal P4-type ATPase responsible for lipid movement, that impair function increase the risk for developing PD [109]. No drugs are currently approved that directly affect *ATP10B*, but therapies are being developed with the intent to correct lipid metabolic balance, reduce the substrate burden, or remedy the loss of the protein (*ATP10B*) itself [110]. Other potential therapies that promote the use of lysosomal contents *via* autophagy and enhance lysosomal gene expression and increase α -synuclein clearance in the absence of *ATP10B* deficiency include rapamycin, trehalose, and transfected expression vectors [111].

6.7. Therapeutic Targeting of *PRKN*

PRKN (Parkin) plays a crucial role in mitochondrial housekeeping and the autophagic clearance of damaged mitochondria, a process known as mitophagy [112]. No approved drugs directly reestablish Parkin function. Indirect methods include mitophagy activators such as nicotinamide riboside (NR), urolithin A, and actinonin, which improve mitochondrial biogenesis and autophagy, mitigate stress, and recover existence in models [113]. Redox modulators KH176, Sonlicromanol, and EPI-589 aim to decrease oxidative stress and restore cellular redox balance, contributing to neuroprotection. Gene therapy using AAV vectors to deliver functional *PRKN* and mRNA-based treatments for transient Parkin expression is under development [114].

6.8. Therapeutic Targeting of *PINK1*

PINK1, a mitochondrial kinase that controls mitophagy, accumulates on injured mitochondria to recruit Parkin, initiating clearance. *PINK1* mutations disrupt this pathway, leading to mitochondrial damage and neurodegeneration [115]. No FDA-approved *PINK1* targeted drugs exist. Therapeutic directions include mitophagy activators bypassing *PINK1*, such as niclosamide, CCCP, and urolithin

A, and NAD⁺ boosters like nicotinamide riboside to improve mitochondrial biogenesis [116]. Kinase modulators that stabilise or enhance *PINK1* activity are in development. Redox modulators EPI-589 and KH176 are explored for falling oxidative stress in *PINK1*-mutant neurons [117].

6.9. Therapeutic Targeting of *DJ-1*

DJ-1 (*PARK7*), involved in oxidative stress response, mitochondrial function, and neuroprotection, is related to early-onset PD [118]. Recently, no approved *DJ-1*-targeted drugs have existed [119]. Small molecular compounds, including isatin and sulforaphane, activate or stabilise *DJ-1*, enhancing antioxidant protective barricades [120]. AAV vectors carrying the wild-type *DJ-1* gene have been demonstrated to restore function and protect neurons from damage in models of neurodegeneration. mRNA-based approaches that target the *DJ-1* protein are also under investigation [121]. Moreover, pharmacologic activation of the Nrf2 pathway with dimethyl fumarate or bardoxolone methyl (a synthetic triterpenoid) has been shown to improve outcomes in patients with *DJ-1* deficiency [122].

6.10. Blood-Brain Barrier (BBB) Delivery Challenges

Discuss the significant obstacle posed by the BBB in delivering AAV vectors and Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) components well to the central nervous system. Highlight current strategies to overcome this, such as engineering AAV capsids for improved BBB penetration, intrathecal or intracerebroventricular administration routes, and the limitations these approaches present in terms of efficiency, safety, and scalability [123].

6.11. Translational Limitations

Emphasise the gap between preclinical success and clinical application, including differences in disease models, immune responses to viral vectors, off-target effects of gene editing, and long-term safety concerns. Address the challenges of scaling doses from animal models to humans, as well as the regulatory hurdles gene therapies must overcome.

6.12. Realistic Interpretation of Gene Therapy and CRISPR Approaches

Deliver a balanced view on the current stage of these technologies, acknowledging that while AAV-mediated wild-type *VPS35* gene therapy and CRISPR-based editing targeting the *D620N* mutation are hopeful, they remain experimental. Discourse potential risks such as immunogenicity, insertional mutagenesis, and incomplete editing efficacy. Stress the need for rigorous clinical trials to establish efficacy and safety before these therapies can be considered practical treatment options [123].

7. INTEGRATION OF FAMILIAL AND SPORADIC PD MECHANISMS: LYSOSOMAL DYSFUNCTION AND MITOPHAGY

Idiopathic PD arises from various genetic and environmental factors. Familial PD is linked to mutations in

genes such as *GBA1*, *LRRK2*, *ATP13A2*, *PRKN*, and *PINK1*, which disrupt lysosomal or mitochondrial homeostasis. *GBA1* mutations decrease glucocerebrosidase activity, causing accumulation of glucocerebrosides and α -synuclein aggregates, while hyperactivation of glucocerebrosidase alters vesicle trafficking within the endo-lysosomal system, damaging autophagy [124]. Mutations in *PINK1* and *PRKN* damage mitophagy and the clearance of damaged mitochondria. Sporadic PD shares these mechanisms, compounded by aging, oxidative stress, and toxic exposures, leading to similar lysosomal and mitophagy dysfunctions [125]. Both forms exhibit overlapping transcriptional and translational profiles, including common regulation of autophagy mediators (*LAMP2*, *TFEB*) and mitochondrial genes (*DJ-1*, *PINK1*). Contempt genetic differences, lysosomal dysfunction, and mitophagy failure are common drivers of dopaminergic neurodegeneration [126].

CONCLUSIONS AND FUTURE PERSPECTIVES

Lysosomal dysfunction plays an essential and multifaceted role in the pathogenesis of PD, influencing key pathological features, including α -synuclein aggregation, impaired autophagy, disrupted lipid homeostasis, and mitochondrial dysfunction. Genetic mutations in lysosomal genes, including *GBA1*, *LRRK2*, *TMEM175*, *ATP13A2*, *VPS35*, *ATP10B*, *PRKN*, *PINK1*, and *DJ-1*, highlight the close interaction between lysosomal pathways and neurodegeneration. Therapeutic approaches targeting these pathways, ranging from pharmacological chaperones and substrate-reduction therapies that manage symptoms. Still, significant translational challenges remain, particularly regarding BBB delivery, safety, and long-term efficacy of advanced therapies such as AAV-mediated gene delivery and CRISPR-based editing. Continued research to improve these mechanistic understandings and overcome translational challenges is important for developing effective, disease-modifying treatments for PD.

STUDY LIMITATIONS

This review assesses the effects of lysosomal dysfunction and genetic mutations in PD, allowing for various limitations. It points out possible discrimination by only including confident studies and using preclinical models and small clinical studies, which makes it less useful in reality. The review also examines the difficulties of PD, which is caused by a number of genetic and environmental factors. This type is difficult to understand, as lysosomal dysfunction is involved. Furthermore, some of the therapeutic strategies studied are still in early clinical stages and lack sufficient long-term safety and efficacy data.

AUTHORS' CONTRIBUTIONS

The authors confirm contribution to the paper as follows: study conception and design: VCB., AKG; data collection: MKS. analysis and interpretation of results: AK., SKT. AKP. draft manuscript: VCB. SK. All authors reviewed the results and approved the final version of the manuscript.

LIST OF ABBREVIATIONS

AAV	=	Adeno-Associated Virus
ALP	=	Alkaline Phosphatase
AMPK	=	AMP-activated Protein Kinase
BBB	=	Blood-Brain Barrier
CM	=	Chaperone-mediated Autophagy
CRISPR	=	Clustered Regularly Interspaced Short Palindromic Repeats
EOPD	=	Early-Onset Parkinson's Disease
ER	=	Endoplasmic Reticulum
mTORC1	=	Mammalian Target of Rapamycin Complex 1
NF- κ B	=	Nuclear Factor Kappa B
NR	=	Nicotinamide Riboside
PD	=	Parkinson's Disease
PERK	=	Protein Kinase RNA-like ER Kinase
RCS	=	Reactive Carbonyl Species
SRTs	=	Substrate Reduction Therapies

CONSENT FOR PUBLICATION

Not applicable.

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CONFLICT OF INTEREST

The authors declare no conflict of interest, financial or otherwise.

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