



# Endosomal Trafficking in Alzheimer's Disease, Parkinson's Disease, and Neuronal Ceroid Lipofuscinosis

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**ABSTRACT** Neuronal ceroid lipofuscinosis (NCL) is one of the most prevalent neurodegenerative disorders of early life, Parkinson's disease (PD) is the most common neurodegenerative disorder of midlife, while Alzheimer's disease (AD) is the most common neurodegenerative disorder of late life. While they are phenotypically distinct, recent studies suggest that they share a biological pathway, retromer-dependent endosomal trafficking. A retromer is a multimodular protein assembly critical for sorting and trafficking cargo out of the endosome. As a lysosomal storage disease, all 13 of NCL's causative genes affect endolysosomal function, and at least four have been directly linked to retromer. PD has several known causative genes, with one directly linked to retromer and others causing endolysosomal dysfunction. AD has over 25 causative genes/risk factors, with several of them linked to retromer or endosomal trafficking dysfunction. In this article, we summarize the emerging evidence on the association of genes causing NCL with retromer function and endosomal trafficking, review the recent evidence linking NCL genes to AD, and discuss how NCL, AD, and PD converge on a shared molecular pathway. We also discuss this pathway's role in microglia and neurons, cell populations which are critical to proper brain homeostasis and whose dysfunction plays a key role in neurodegeneration.

**KEYWORDS** Alzheimer's disease (AD), endocytic pathway, endosomal trafficking, genetic and cell biology findings on Alzheimer's disease, microglia, NCL genes, Parkinson's disease, retromer defects, retromer proteins (Vps35, Vps26, Vos29), retromer viral vectors for AD gene therapy

**A**lzheimer's disease (AD) is a neurodegenerative disease that progressively destroys memory and thinking skills and disrupts behavior, ultimately leading to complete dependency and death. It is the most common type of dementia among individuals 65 or older (1). Currently, more than 5.5 million Americans are living with AD, and this number is expected to triple by the year 2050 (2). While the majority of cases occur beyond age 65, 5 to 10% of cases show an early-onset form, with clinical onset between 30 and 50 years of age (3). Key pathological hallmarks are extracellular diffuse and neuritic amyloid plaques composed of abnormally folded A $\beta$ 40 and A $\beta$ 42 and intraneuronal accumulation of neurofibrillary tangles (NFT) composed of hyperphosphorylated tau protein (p-tau), often accompanied by neuropil threads, dystrophic neurites, associated astrogliosis, microglial activation, and cerebral amyloid angiopathy (4). These changes commonly show a specific spatial/temporal profile initiating in entorhinal cortex and then spreading to other areas of the brain (5).

Ten percent of these early-onset AD cases are explained by known mutations in the

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presenilin 1 (PSEN1), presenilin 2 (PSEN2), and amyloid precursor protein (APP) genes (3). The apolipoprotein E gene (*APOE*) poses the strongest risk factor for the late-onset form (6, 7). In addition, large-scale genomic studies conducted over the past 10 years have identified over 25 genes modulating AD susceptibility (8, 9). Notably, these genes cluster predominantly in specific molecular pathways, in particular lipid metabolism, inflammation/immune response, endocytosis, and intracellular trafficking (8–10).

The second most prevalent neurodegenerative disease, Parkinson's disease (PD), affects 1% to 2% of the population and is characterized by resting tremor, rigidity, and bradykinesia, along with memory impairments and other behavior changes (11, 12). PD pathology, characterized in particular by progressive loss of dopaminergic (DA) neurons in the substantia nigra, usually initiates in the basal ganglia, with involvement of cerebellum, thalamus, hypothalamus, and limbic system (13–16). Several genes have been associated with PD (*LRRK2*, *GBA*, *PRKN*, *SNCA*, *MAPT*, *EIF4G1*, *DNAJC13*, *CHCHD2*, *PINK1*, and *PARK7*). Notably, some of these have been implicated in endolysosomal dysfunction (11–13, 17–21).

A master conductor of endosomal sorting and trafficking is the retromer complex (22). Retromer recognizes specific transmembrane proteins and exports them to their appropriate destinations within the cell. It facilitates this transport by forming tubules. Protein cargo from the endosomes can be exported to three possible destinations: retrograde transport to the *trans*-Golgi network (TGN), recycling to the plasma membrane, and sorting to the lysosomes for degradation. The former two are controlled by retromer (22–24). The retromer complex is composed of multiple modules, with the two central components being the cargo recognition module (CRM) and the tubulation module (SNX-BAR). The CRM consists of three largely globular proteins, VPS35, VPS26, and VPS29, named after the vacuolar protein-sorting genes in yeast. The tubulation module comprises heterodimers of the BAR domain-containing sorting nexins SNX1/SNX2 and SNX5/SNX6 (23, 25–27).

Retromer and endolysosomal dysfunction have been firmly established in the etiology of both AD and PD (28–38). The first evidence for an association with AD came from a model-guided microarray study showing a reduction of VPS26 and VPS35 in brain regions affected by the disease (39), followed by the identification of *SORL1* (a retromer cargo receptor) (40) as a risk gene for AD and demonstrating that *SORL1* is critical for trafficking of APP away from amyloidogenic pathways and recycling it back to the cell surface (41, 42). A series of subsequent genetic studies firmly confirmed *SORL1* in both early- and late-onset AD (41, 43–45) and have linked several additional retromer core proteins to AD; among these are SNX1, SNX3, and rab7a (26, 46). In line with this notion, there is evidence of endolysosomal dysfunction starting early in entorhinal cortex and hippocampus in AD brains with enlargement of endosomes (39, 47–49). The strongest genetic risk factor for sporadic AD, APOE4, is also associated with enlargement of endosomes and their dysfunction in an age-dependent manner (50–53). In early-onset PD, mutations in *PRKN* (parkin) lead to autosomal recessive early-onset PD (54), with loss of parkin function, increased formation of intraluminal vesicles coupled with enhanced release of exosomes, decreased endosomal tubulation, and membrane association of vesicle protein sorting 35 (VPS35) and sorting nexin 1 (SNX1), as well as decreased mannose 6 phosphate receptor (M6PR), in line with impairment of retromer pathway in parkin-deficient cells. In addition, a rare mutation in the retromer gene *VPS35* (*D620N*) is associated with risk of PD (28–36), supporting a role of retromer-dependent trafficking and endolysosomal function.

In addition to these AD-associated retromer genes and proteins, over the past few years an additional set of genes has been linked to retromer function and AD. Among these were a small number of experimental, cell biology, and animal studies reporting genes implicated in neuronal ceroid lipofuscinosis (NCL) (55), a genetically determined lysosomal storage disorder. It has been demonstrated that retromer is essential in the delivery of certain hydrolytic enzymes to lysosomes, and its deficiency leads to the accumulation of dysfunctional autolysosomes (56, 57).

## CLINICAL AND MORPHOLOGICAL CHARACTERISTICS OF NCL

NCL is morphologically characterized by cellular lipopigment inclusions, neuronal loss, and progressive neurodegeneration (58). The childhood forms present clinically as progressive mental and motor deterioration and loss of vision with shortened life expectancy, while the rare adult-onset forms are dominated by dementia. To date, 13 genetically distinct forms of NCL have been identified (Table 1), all characterized by the accumulation of abnormal lipofuscin-like material in the lysosomes of nerve cells, associated with progressive and selective destruction of neurons, particularly in the cerebral and cerebellar cortex and in the retina (58–61). Historically, NCL has been classified into four distinctive forms, based on the clinical manifestation, morphologic features, and age of onset: infantile (INCL), late-infantile (LINCL), juvenile (JNLC), and adult type NCL (ANLC) (59).

## NEURONAL CEROID LIPOFUSCINOSIS AND RETROMER

Of the 13 genes causing NCL, four have been linked to retromer function: *CLN1*, *CLN3*, *CLN5*, and *CLN10* (cathepsin D, or CTSD) (55, 61–66). These NCL variants cause pathological changes that seem to share an endolysosomal dysfunctional pathway. *CLN10* disease presents as congenital or early infantile neuronal ceroid lipofuscinosis disease and is caused by mutations in *CTSD*, encoding cathepsin D (67–69). Cathepsin D is a lysosomal protease that is highly expressed in the brain (70). CTSD shows pepsin-like activity and has an important role in protein turnover and activation of hormones and growth factors through proteolysis. Retromer plays a vital role in CTSD processing. Procathepsin D is transported by cation-independent mannose 6-phosphate receptor (CI-M6PR) or sortilin to the endosome, where it is processed to the mature cathepsin D (71–74). Retromer, in turn, mediates trafficking of sortilin and CI-M6PR out of the endosomal-lysosomal system and prevents their degradation (72–75). Alterations in CTSD protein and mRNA levels have been demonstrated in AD (71, 76–78), and CTSD deficiency has been shown to promote tau neurotoxicity, likely through a mechanistic defect in endosomal-lysosomal trafficking (76, 79–81).

Juvenile *CLN3* disease is characterized by early vision loss at around 6 years of age with cognitive decline followed by seizures, psychosis, and motor dysfunction (82–84). The *CLN3* gene encodes a palmitoyl-protein delta-9 desaturase protein, which also modulates lysosomal transport and function (85, 86). *CLN3* protein has been implicated in retrograde transport of cargo from the endosome to the Golgi compartment by modulating SNARE phosphorylation and assembly (87–89), and a recent investigation by Yasa and Lefrancois established that *CLN3* protein plays a key role in facilitating the interaction between Rab7A, retromer, and sortilin (63). Rab7A belongs to the family of Rab GTPases proteins that is active at endosomal membranes and has been involved in endosome-to-TGN trafficking, retromer recruitment, autophagosome-lysosome fusion, lysosomal positioning, and degradation of endocytic cargo (62, 78, 90–92). In the absence of wild-type *CLN3*, CI-M6PR and sortilin receptors are degraded, which in turn leads to impaired CTSD processing (63).

The *CLN5* gene is implicated in late infantile NCL, a type of NCL that affects children between ages 2 and 4 and has a very high mortality. In the mouse brain, *CLN5* is expressed in cortical neurons, hippocampal pyramidal neurons, hypothalamus, and cerebellum (93); the highest levels, however, have been detected in microglial cells (55, 94). *CLN5* protein undergoes posttranslational modifications that include glycosylation and cleavage (95, 96). The depletion of *CLN5* leads to lysosomal degradation of the retromer receptors sortilin and CI-M6PR (62). In the absence of *CLN5*, Rab7 is not activated, VPS26 is not recruited to endosomes, and sortilin and CI-M6PR receptors are degraded in lysosomes (62). Glycosylation defects result in ER mislocalization of *CLN5*, which results in a loss of function and ER stress (55, 97). *CLN5* is usually localized to the endolysosomal compartment, and it is also secreted into the extracellular space (55, 95, 98, 99).

Using whole-exome sequencing, we recently identified a rare missense variant of *CLN5* (rs199609750; c.A959G; population frequency, 7.418e–05) that segregates with

**TABLE 1** Genes and proteins implicated in NCL and their association with retromer function and/or Alzheimer's disease<sup>a</sup>

Gene	Protein	Protein function(s) (reference[s])	NCL clinical phenotype(s)	AD association(s) (reference[s])	Retromer or endosomal trafficking association(s) (reference[s])
<i>CLN1</i>	Palmitoyl protein thioesterase 1 (PPT1)	Removes palmitic acid from S-acylated proteins (137, 138)	Infantile, juvenile, adult	Metabolic clearance of A $\beta$ in early stages of AD (105); disruption of protein palmitoylation/depalmitoylation balance is associated with AD (106–108)	Transported to lysosomes by mannose 6-phosphate receptor (64–66)
<i>CLN2</i>	Tripeptidyl-peptidase 1 (TPP1)	Lysosomal serine protease; also has endopeptidase activity (139–142)	Late infantile	Destabilizes A $\beta$ fibrils in lysosomes through multiple proteolytic cleavages within the $\beta$ -sheet domain (115)	
<i>CLN3</i>	CLN3 (transmembrane protein)	Protein function has not been completely unraveled; has multiple lysosomal targeting signals; activates Rab7; implicated in a complex interaction of cytoskeleton with endocytic membrane trafficking (82)	Juvenile		Retrograde transport of cargo from endosome to Golgi compartment by modulating SNARE phosphorylation and assembly (87–89); also mediates Rab7A–PLEKHM1 interaction (63)
<i>CLN4 (DNA/C5)</i>	Cysteine-string protein alpha (CSP $\alpha$ )	Active at synapses; regulates exocytosis and other proteins involved in secretion dynamics (143–146)	Adult		
<i>CLN5</i>	CLN5	Secreted glycoprotein that might act as glycoside hydrolase in amoeba and may interact with CLN10 and CLN3 (147, 148); may also have a role in embryonic development of interneurons (149), in mitochondrial function (150), and in autophagy (151)	Late infantile, juvenile	Rare missense variant mutation of <i>CLN5</i> gene segregated with AD status in multiplex families (55)	Recruitment of Rab7A and retromer to the endosomal membrane (62); AD variant leads to altered processing of cathepsin D and APP (55)
<i>CLN6</i>	CLN6	Transmembrane protein of unknown function, localized at the endoplasmic reticulum (152)	Late infantile, adult		
<i>CLN7</i>	MFSD8	Unknown function	Late infantile, juvenile		
<i>CLN8</i>	CLN8	Unknown function	Late infantile		
<i>CLN10</i>	CLN10/cathepsin D (CTSD)	Aspartyl endopeptidase; major roles in endocytic, autophagic, and apoptotic degradation of proteins; highly expressed in brain tissue (70, 71)	Congenital late infantile, juvenile, adult	Changes in CTSD levels have been associated with AD (71, 76–78); CTSD deficiency associated with Tau toxicity in animal models (76, 79, 80)	Trafficked via sortilin or CI-M6PR to the endosomal-lysosomal system (71–74)
<i>CLN11</i>	Progranulin/prospherilin/acrogranin (GRN)	Exact mechanism is unknown; has been proposed to act as neurotrophic factor and may be involved in biogenesis and function of lysosomes (153); also may play a role in microglial innate immunity in the CNS (124, 125, 153)	Adult	Associated with A $\beta$ plaques, neurofibrillary tangles, tau phosphorylation, and increased CSF tau (118–121); also modulates lysosomal activity in neurons and glia leading to AD pathology (122, 123)	

(Continued on next page)

**TABLE 1** (Continued)

Gene	Protein	Protein function(s) (reference[s])	NCL clinical phenotype(s)	AD association(s) (reference[s])	Retromer or endosomal trafficking association(s) (reference[s])
<i>CLN12</i>	CLN12/ATPase (p-type)/13A2/KRPPD/PARK9/HSA9947/RP-37C10.4	Unknown function	Juvenile		
<i>CLN13</i>	Cathepsin F (CTSF)	Cysteine protease (58, 129)	Adult	Autosomal recessive CTSF gene variant was found in a clinically diagnosed early-onset AD family (130); a family with clinically suspected Kufs disease was shown to carry a novel <i>PSEN1</i> mutation (131); a homozygous mutation in CTSF was found in an early-onset AD case (73); biallelic mutations of CTSF have been linked to Kufs disease type B (28)	Associated with endosomal regulation and lysosomal trafficking through lysosomal integral membrane protein type 2 (LIMP-2) cleavage (129)
<i>CLN14</i>	Potassium channel tetramerization domain-containing protein 7 (KCTD7)	Unknown function	Infantile, late infantile		

<sup>a</sup>NCL, neuronal ceroid lipofuscinosis; AD, Alzheimer's disease; A $\beta$ , amyloid beta;  $\beta$ , beta; SNARE, 4 alpha helix protein phosphorylation complex; Rab7A, Ras-nucleotide GTP-related protein; PLEKHM1, pleckstrin homology domain-containing family M member 1; CSF, cerebrospinal fluid. *PSEN1* gene, encodes presenilin-1 protein; ER, endoplasmic reticulum; CNS, central nervous system.

AD in multiplex families. Employing a combination of molecular biology, biochemistry, and immunofluorescence experiments, we validated that this *CLN5* AD variant is glycosylation deficient, which causes the expressed protein to be partially trapped in the ER, reduces its normal delivery to the endolysosomal system, and reduces its secretion. We also demonstrated that an effective deficiency in endosomal *CLN5* caused by the missense variant results in a shift in the relative levels of procathepsin D, an established phenotype of retromer dysfunction (29, 71, 78, 100), and a reduction in the full-length APP. These studies further strengthen the findings from Mamo et al., who described the recruitment of retromer to the endosomal membrane by *CLN5* and degradation of retromer trafficked receptors in lysosomes in the setting of *CLN5* depletion, establishing that *CLN5* deficiency translates into retromer's dysfunction (62). Since *CLN5* is heavily enriched in microglia (94, 101), a cell type linked to AD, we postulate that the identified c.A959G missense mutant mediates its AD-associated toxicity by affecting retromer function in microglia. Microglia are activated upon tissue damage and are critical for brain homeostasis. The identification of *CLN5* as a microglial gene associated with AD is in line with the implication of the microglial gene *TREM2* as an AD susceptibility gene (102). Notably, retromer deficiency has been found in the microglia of AD brains (103), but the mechanisms underlying this deficiency are still unclear.

*CLN1* disease primarily presents as infantile but has a broad age of onset, extending all the way into adulthood (104). The *CLN1* gene codes for palmitoyl-protein thioesterase 1 (PPT1), expressed in both neurons and microglia (105). PPT1 is a depalmitoylation enzyme, and, as such, a disruption of the protein palmitoylation/depalmitoylation balance is associated with AD (106–108). PPT1 has been implicated in endosomal trafficking (109, 110) and synaptic maintenance (110–112). In addition, PPT1 levels in the cell potentially can be influenced by retromer activity, since there is evidence that it is transported to lysosomes by the mannose 6-phosphate receptor (64–66). A study employing a proteomic approach in an APP<sup>NL-F</sup> mouse model of AD found that PPT1 is upregulated and colocalizes with A $\beta$  in this model. The authors conclude that PPT1 might have a role in A $\beta$  clearance in the early stages of the disease, indicating that the upregulated expression of PPT1 is a compensatory mechanism resulting from elevated A $\beta$  levels in early AD (105).

## RECENT DEVELOPMENTS

A series of recent observations from human, animal, and cell biological studies provide additional evidence for an overlapping molecular etiology of AD and NCL. While it remains to be established if and how some or all of these links converge on the retromer pathway, the observed findings provide critical additional support for a shared molecular etiology of both syndromes.

AD pathology is characterized by the presence of A $\beta$  protein oligomers, amyloid plaques (composed of insoluble fibrils), tau tangles, and neuroinflammation (113, 114). A recent study reported that microglial TPP1 protein (encoded by the *CLN2* gene) binds, digests, and causes destabilization of A $\beta$  fibrils in the lysosomes through multiple proteolytic cleavages within the  $\beta$ -sheet domain (115).

The *CLN11* gene (alias *PGRN* or *GRN*), encoding progranulin (PGRN), has been linked to various neurodegenerative diseases, including NCL, frontotemporal lobar degeneration (FTLD), and AD (116, 117). Increased expression of *PGRN* has been documented in AD. *PGRN* is associated with A $\beta$  plaques, neurofibrillary tangles, tau phosphorylation, and increased CSF tau levels (118–121). A microglial specific knockdown of *PGRN* results in malfunctioning phagocytic activity (116). A recent comprehensive review on *PGRN* discusses its role in lysosomal function in both neurons and microglia and argues that mutations in *PGRN* modulate lysosomal activity in both of these cell types, which in turn leads to AD pathology (122, 123). A global *PGRN* (i.e., *CLN11*) deletion can lead to an increase in lysosomal size and numbers in microglia, cd68 positivity, complement activation, and increased synaptic pruning (124). Microglial specific deletion of *PGRN*,



however, does not result in neuroinflammation, indicative of the fact that normal levels of neuronal PGRN play a significant role in preventing pathology in these mice (125).

Finally, *CLN13* (or *CTSF* gene) encodes cathepsin F protein, a soluble lysosomal cysteine protease (58). Mutations in the *CTSF* gene can cause Kufs disease type B, an adult form of NCL (126), where patients commonly present with epileptic seizures, ataxia, behavioral impairments, and dementia (127, 128). *CTSF* protein function has been linked to endosomal regulation and lysosomal trafficking through lysosomal integral membrane protein type 2 (LIMP-2) cleavage (129). Notably, an exome sequencing study in a consanguineous family with clinically diagnosed early-onset AD that previously tested negative for *PSEN1*, *PSEN2*, *APP*, *TAU*, *PGRN*, and *PRNP* mutations found an autosomal recessive *CTSF* gene variant (cG1243A:p Gly415Arg) (130). Vice versa, in a separate report, four members of a family with clinically suspected Kufs disease were shown to carry a novel *PSEN1* mutation (p.Leu381Phe). Carriers in this family developed dementia in their early 30s and showed neuropathological features of both Kufs and AD (131). These findings support the notion that NCL and AD are linked etiologically and clinically.

## CONCLUSIONS

Several genes associated with NCL have now been linked to AD, and with *PSEN1* and *PRGRN* variants also being observed in families and individuals clinically presenting with NCL, evidence is mounting that these two syndromes overlap both etiologically and clinically.

The fact that at least 4 NCL genes have now been linked to endosomal trafficking, and that the major genomic studies on AD clearly identified endosomal trafficking as one of three major etiological pathways in AD (8–10, 22), strongly suggests a dysfunctional endolysosomal trafficking system as the shared molecular hub on which both disorders converge. Within the endolysosomal system, some of the molecular overlap seems to converge on retromer, suggesting that improving efficacy of the retromer trafficking pathway would decrease pathology in both syndromes. Additionally, brain transcriptome sequencing (RNA-seq) studies from the laboratory of B. Barres show that RNAs of most of the NCL-causing proteins discussed here are highly enriched in mouse microglia/macrophages (101, 132), whereas in humans these RNAs are enriched in mature astrocytes and microglia/macrophages, with the exception of *CLN13*, which has a considerable presence in human neurons as well (101, 132). These data, coupled with recent findings that retromer depletion in neurons leads to massive activation of microglia and astrocytes in mouse brains and that the astrogliosis can be partially rescued with retromer repletion using AAV (133), further support an interaction between NCL genes, endolysosomal trafficking, neurons, and glia. The fact that some of the genes associated with PD also have been implicated in endolysosomal dysfunction and retromer function (12, 13, 17, 20, 21, 28–36) further emphasizes the importance of the endolysosomal system and retromer in neurodegenerative disease, and it suggests that there is also at least a partial etiologic overlap with this disorder. Notably, particularly in Alzheimer's disease, the range of age of onset associated with disease-associated variants functioning in the endolysosomal pathway, for example, *SORL1* (44), is significant, and enlargement of endosomes can be observed early in the disease process long before the onset of clinical symptoms (10), indicating that endolysosomal dysfunction in AD and PD can begin across a wide age range, likely even in early life.

Experimental, animal, and human studies are needed that comprehensively disentangle the molecular etiologies of NCL and AD, delineate their clinical subtypes, meticulously characterize their molecular and clinical overlap and association with retromer function, and delineate their etiologic overlap with other neurodegenerative disorders associated with retromer dysfunction, including PD. Studies on retromer enhancing pharmacological chaperones and retromer gene therapies have demonstrated that retromer function can be enhanced (133–136). While these studies have focused on adult-onset neurodegeneration (AD and PD), they provide proof of principle

and indicate that therapies targeting the retromer pathway also can benefit patients with NCL subtypes associated with retromer dysfunction.

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