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Exploring new pathways of neurodegeneration in ALS: the role of mitochondria quality control

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Abstract

Neuronal cells are highly dependent on mitochondria, and mitochondrial dysfunction is associated with neurodegenerative diseases. As perturbed mitochondrial function renders neurons extremely sensitive to a wide variety of insults, such as oxidative stress and bioenergetic defects, mitochondrial defects can profoundly affect neuronal fate. Several studies have linked ALS with mitochondrial dysfunction, stemming from observations of mitochondrial abnormalities, both in patients and in cellular and mouse models of familial forms of ALS. Mitochondrial changes have been thoroughly investigated in mutants of superoxide dismutase 1 (SOD1), one of the most common causes of familial ALS, for which excellent cellular and animal models are available, but recently evidence is emerging also in other forms of ALS, both familial and sporadic. Mitochondrial defects in ALS involve many critical physiopathological processes, from defective bioenergetics to abnormal calcium homeostasis, to altered morphology and impaired trafficking. In this review, we summarize established evidence of mitochondrial dysfunction in ALS, especially in SOD1 mutant models of familial ALS. The main focus of the review is on defective mitochondrial quality control (MQC) in ALS. MQC operates at multiple levels to clear damaged proteins through proteostasis and to eliminate irreparably damaged organelles through mitophagy. However, since ALS motor neurons progressively accumulate damaged mitochondria, it is plausible that the MQC is ineffective or overwhelmed by excessive workload imposed by the chronic and extensive mitochondrial damage.

Keywords

ALS; mitochondria; mitophagy; SOD1; parkin; p62

Introduction

Amyotrophic Lateral Sclerosis (ALS) is the most prevalent, adult-onset, motor neuron disease, characterized by the degeneration of upper and lower motor neurons, progressive

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muscle weakness and atrophy, leading to muscle paralysis. (Cleveland and Rothstein, 2001; Sabatelli et al., 2013). The incidence is 2 in 100,000 individuals per year (Hirtz et al., 2007). Patients die of respiratory failure in 2 to 5 years, after clinical symptoms develop. There is no cure for ALS, and only one drug, Riluzole, has been approved for treatment (Bensimon et al., 1994; Lacomblez et al., 1996; Pandya et al., 2013). Unfortunately, Riluzole only prolongs average patients' survival by a few months. This dramatic lack of effective treatments prompts the need for a better understanding of disease pathogenesis to identify appropriate therapeutic targets and to develop disease biomarkers, which could help stratifying patients and select appropriate therapies.

Approximately, 90% of the patients develop ALS with unknown etiology, classified as sporadic ALS (sALS), while the remaining 10% are familial ALS cases (fALS) due to genetic defects, which are directly linked to the pathogenesis of the disease. An increasing number of genes are being linked to ALS (Andersen and Al-Chalabi, 2011; Renton et al., 2014). Superoxide dismutase 1 (*SOD1*) was the first gene discovered as causative for fALS in 1993 (Rosen, 1993) and since then more than 160 pathogenic mutations in SOD1 have been described (Andersen, 2006; Moreira et al., 2013). Mutations in SOD1 account for 20% of the fALS cases, and they have rarely been described in idiopathic cases (Tortelli et al., 2013).

In the last decade, new breakthroughs in the genetics of ALS emerged from the discovery that mutations in several DNA/RNA binding proteins, such as TAR DNA-binding protein (TARDBP, TDP-43) (Sreedharan et al., 2008) and fused in sarcoma (FUS) (Kwiatkowski et al., 2009; Vance et al., 2009), are associated with fALS and frontotemporal dementia (FTD), pointing to new pathological mechanisms related to RNA metabolism (Lattante et al., 2013; Ling et al., 2013; van Blitterswijk and Landers, 2010). Other fALS genes, like valosin-containing protein (VCP)(Johnson et al., 2010), ubiquilin 2 (UBQLN2) (Deng et al., 2011), and sequestosome 1 (SQSTM1) (Fecto et al., 2011), highlighted the importance of proteostatic pathways in neuronal cells (Fecto and Siddique, 2012). Profilin 1 (PFN1) (Wu et al., 2012) and dynactin (DCTN1) (Puls et al., 2003) mutations in fALS indicate that also cytoskeletal and axonal transport abnormalities are involved in disease pathogenesis. Recently, the largest proportion of fALS cases (40%) have been linked to intronic hexanucleotide repeat expansions in C9ORF72 (DeJesus-Hernandez et al., 2011; Renton et al., 2011), a gene with still unknown function, opening a new field of research that connects ALS/FTD to DNA repeat expansion (Majounie et al., 2012).

Several molecular mechanisms have been proposed to explain the neuronal degeneration in ALS. It is noteworthy that many of them emerge from studies of mutant SOD1, owing to the fact that many cellular and animal models have been developed and studied. The proposed mechanisms include oxidative stress, toxic gain of function of misfolded and aggregated proteins, endoplasmic reticulum stress, mitochondrial dysfunction, and axonal disorganization, including organelle transport defects(Cozzolino and Carri, 2011; Ferraiuolo et al., 2011; Kawamata and Manfredi, 2010b; Magrane and Manfredi, 2009; Pasinelli and Brown, 2006).

In this review, we will summarize established evidence of the involvement of mitochondrial dysfunction in ALS, especially in SOD1 mutant models of fALS; we will then focus on mitochondrial quality control (MQC) mechanisms. Mutations in critical components of MQC have been associated with a number of neurodegenerative diseases, including parkin and PINK1 (Phosphatase and tensin homolog (PTEN)-induced putative kinase 1) links to familial Parkinson disease (PD) (Scarffe et al., 2014), but also in familial ALS/FLTD (Frontotemporal Lobar Degeneration). However, despite evidence that damaged mitochondria accumulate in ALS, the role of MQC has not been fully elucidated yet.

Mitochondrial damage and dysfunction in ALS

Mitochondria are essential organelles for a wide variety of cellular processes, including cell intermediate metabolism, calcium homeostasis, bioenergetics, and intrinsic cell death processes. Mitochondrial dysfunction has long been associated with neurodegenerative diseases, because of the dependence on mitochondrial function of neuronal cells (Schon and Przedborski, 2011). Many studies have linked SOD1-fALS with mitochondrial morphological abnormalities, both in patients' biopsies and postmortem tissues (Sasaki and Iwata, 1996; Sasaki and Iwata, 2007; Sasaki, 2010) and in cellular and mouse models of fALS (Magrane et al., 2009; Magrane et al., 2014; Vinsant et al., 2013a; Vinsant et al., 2013b).

Although SOD1 is considered to be a cytosolic enzyme, a fraction of the protein resides in mitochondria. The majority of the SOD1 in mitochondria resides in the intermembrane space (IMS) (Jaarsma et al., 2001; Mattiazzi et al., 2002). Although it is not entirely clear which role the enzyme could be performing in mammalian mitochondria, a protective antioxidant effect was suggested (Okado-Matsumoto and Fridovich, 2001). This concept is supported by studies performed in mice lacking SOD1, in which the expression of a wild type SOD1 targeted to the mitochondria was able to rescue motor neuron loss (Fischer et al., 2011).,

Mitochondria are targets of mutant SOD1 toxicity (Cozzolino et al., 2013; Hervias et al., 2006; Higgins et al., 2002; Martin, 2011). Mutant SOD1 mice develop progressive bioenergetic abnormalities in the CNS, characterized by decreased mitochondrial respiratory chain activity and impaired ATP production (Mattiazzi et al., 2002), and defective calcium uptake (Damiano et al., 2006; Kim et al., 2012; Parone et al., 2013). These mitochondrial deficits could directly contribute to disease pathogenesis, because they compromise fundamental functions in neuronal cells.

In mitochondria, mutant SOD1 misfolds and aggregates, causing oxidative stress (Carri and Cozzolino, 2011). Mitochondrial damage can also ensue from the aberrant interaction of mutant SOD1 with proteins of the outer membrane (OM), such as VDAC (Voltage-dependent anion channel) (Israelson et al., 2010) and Bcl2 (B-cell lymphoma 2) (Pasinelli et al., 2004; Pedrini et al., 2010), and from the accumulation of misfolded mutant SOD1 on the OM (Vande Velde et al., 2011), in the IMS (Kawamata and Manfredi, 2010a) and on the inner membrane (IM) (Vijayvergiya et al., 2005).

In mutant SOD1 neurons, early studies reported deficits in axonal transport (Williamson and Cleveland, 1999; Zhang et al., 1997) resulting in defective mitochondrial transport (De Vos et al., 2007). Direct interactions between some axonal motor complexes (essentially dynein, the major motor protein required for retrograde axonal transport) and mutant SOD1 (Ligon et al., 2005; Shi et al., 2010; Zhang et al., 2007) are required for the formation of mutant SOD1 aggregates and have been proposed as the cause for the disruption of axonal transport. Thus, either formation of mutant SOD1-containing aggregates or sequestration of essential components, such as the dynein motor complex,) for axonal transport, together with reduced binding of cargoes, probably as a consequence of altered mitochondrial outer membrane structure, result in a deficit on mitochondrial transport (Magrane et al., 2009; Marinkovic et al., 2012). In addition, mitochondrial fusion and fission are imbalanced in SOD1 mutant neurons (Magrane et al., 2012). As a result, mutant SOD1 motor neurons accumulate mitochondria with abnormal morphology (Vande Velde et al., 2011), ultrastructure (Gould et al., 2006), and bioenergetics (Damiano et al., 2006; Kawamata and Manfredi, 2010a; Mattiazzi et al., 2002). Evidence of progressive accumulation of abnormal mitochondria with impaired axonal transport was also found in vivo in both mutant SOD1 and TDP43 transgenic mice, starting early on in the course of the disease, before onset of symptoms and motor neuron death (Magrane et al., 2014). Moreover, mitochondrial structural and dynamics abnormalities have been linked to physical association of mutant TDP-43 with mitochondria in cultured cells (Wang et al., 2013b). Although it is still unknown in which mitochondrial compartment TDP-43 resides, the authors showed that interactions with mitofusin 2 (Mfn2) on the OM might play a pathogenic role. Indeed, it was recently shown that TDP-43 perturbs the ER (endoplasmic reticulum)-mitochondria contact sites (or MAMs), by disrupting the interaction between VAPB (vesicle-associated membrane protein-associated protein-B) and the mitochondrial protein tyrosine phosphatase-interacting protein 51 (PTPIP51), resulting in dysregulation of intracellular calcium homeostasis (Stoica et al., 2014). Thus, abnormal TDP-43 expression could interfere with mitochondrial function.

Accumulation of damaged mitochondria may actively cause neuronal toxicity by excessive free radical production, leakage of pro-apoptotic factors, and clogging of the proteostatic and autophagic machineries. The toxicity from damaged mitochondria could act synergistically with impaired bioenergetics, leading to synaptic dysfunction and neuronal degeneration. Intriguingly, genetic ablation of cyclophilin D, a positive regulator of calcium-dependent mitochondrial permeability transition, increased calcium capacity in the CNS mitochondria of SOD1 mutant mice and the number of surviving motor neurons cell bodies, while decreasing the amount of SOD1 inclusions. However, it did not improve muscle denervation (Parone et al., 2013), and in one study it decreased survival in female SOD1 mutant mice (Kim et al., 2012). These results suggest that simply increasing mitochondrial calcium capacity by eliminating a highly conserved modulator, such as cyclophilin D, is not a viable strategy to protect motor neuron function.

Mitochondrial quality control mechanisms (MQC) and their implications for

ALS

Different mechanisms have evolved to ensure proper mitochondrial homeostasis: new mitochondria are generated by highly regulated biogenesis and damaged mitochondria are subjected to quality control processes. Why ALS motor neurons are unable to repair or eliminate damaged mitochondria and maintain homeostasis is unclear. Mitochondrial quality control systems (MQC) operate at multiple levels to clear damaged proteins through proteostasis and to eliminate irreparably damaged organelles through selective removal of damaged mitochondrial components or selective removal of organelles through mitophagy (Ashrafi and Schwarz, 2013; Cherra et al., 2010). Figure 1 schematically summarizes the putative major steps of MCQ in cells that express mutant SOD1 or other similar mitochondrial stressors. The figure highlights the MCQ components that have been linked to ALS. Since mutant SOD1 motor neurons accumulate damaged mitochondria, it is plausible that their MQC is ineffective. This could be the result of mutant SOD1 interference with the MQC machinery or excessive load imposed on the MQC by constitutive and extensive mitochondrial damage.

Mitochondrial proteostasis protects against mitochondrial damage

Mitochondria with loss of membrane potential or subject to protein oxidation and misfolding become targets of MQC. There are three main, partially interconnected, pathways of MQC: protein degradation, vesicular degradation, and mitophagy.

The first line of defense to maintain a pool of healthy mitochondria consists in mitochondrial proteostasis. This mechanism ensures the proteolysis and subsequent degradation of misfolded, oxidized, and damaged proteins by proteases residing in different compartments of the mitochondria (Anand et al., 2013). Figure 2 illustrates schematically various components of the proteostatic machinery dedicated to tagging and removal of damaged proteins in mitochondria.

Mitochondria have internal proteases, such as the AAA-protease complex (ATPases Associated with diverse cellular Activities) of the IM (Gerdes et al., 2012) and the Lon protease of the matrix (Matsushima and Kaguni, 2012). Mitochondria are also endowed with their own unfolded protein response (UPR), which is activated when misfolded proteins accumulate in the matrix (Pellegrino et al., 2013) and in the IMS (Papa and Germain, 2011). Although there is no direct link between mitochondrial protein degradation and ALS yet, it could be hypothesized that the accumulation of misfolded and aggregated proteins in different sub-compartments of the mitochondria would activate proteolytic mechanisms. Excessive accumulation of misfolded and oxidized proteins may slow down the system and, in the worst-case scenario, block it.

Less studied, in terms of quality control mechanisms, are the mitochondrial processing peptidases (MPP), which play a crucial role in the import of proteins into mitochondria. However, defective mitochondrial protein import has been reported in spinal cord-purified

mitochondria from transgenic mutant SOD1 rats (Li et al., 2010), suggesting that there could be a dysfunction in the processing of the imported peptides.

Mitochondria rely on the cytosolic ubiquitin-proteasome system (UPS) to eliminate damaged proteins destined to the OM or before they engage in the mitochondrial import pathway (Karbowski and Neutzner, 2012; Radke et al., 2008). Ubiquitin ligases, such as Parkin, ubiquitinate oxidized or misfolded OM proteins (Heo and Rutter, 2011). Parkin recruitment to the OM of damaged mitochondria that have lost membrane potential has been ascribed to PINK1, following its incomplete processing and import across the OM of depolarized mitochondria (Matsuda et al., 2010; Narendra et al., 2008; Narendra et al., 2010b; Vives-Bauza et al., 2010). Parkin-mediated OM protein ubiquitination can recruit valosin-containing protein (VCP or p97/Cdc48) to mitochondria (Kim et al., 2013b). VCP is an AAA⁺-ATPase, whose segregase activity extracts ubiquitinated proteins from the OM, as well as other membranes and organelles, and targets them for proteasomal degradation (Xu et al., 2011; Ye et al., 2005). Mutations in VCP are associated with multisystem disorders (Watts et al., 2004), including IBMPFD (Inclusion body myopathy with early-onset Paget disease and frontotemporal dementia) and ALS (Nalbandian et al., 2011). VCP mutations cause mitochondrial structural changes in transgenic mice, and loss of VCP impairs the clearance of damaged mitochondria (Kim et al., 2013b). Selective VCP translocation to damaged mitochondria depends on Vms1 (VCP/Cdc48-associated Mitochondrial Stress responsive 1), a cytosolic protein that senses local mitochondrial stress (Heo et al., 2010; Heo et al., 2013) and binds VCP allowing its translocation to damaged mitochondria. Ubiquitination of OM proteins can be operated by the PINK1/Parkin system, but also by other ligases, such as the MITOchondrial ubiquitin Ligase MITOL (or MARCH5), an E3ubiquitin ligase resident in the OM (Nagashima et al., 2014), which ubiquitinates OM proteins involved in mitochondrial fusion (Mfn1 and Mfn2) (Park et al., 2010; Sugiura et al., 2013) and fission (Drp1) (Karbowski et al., 2007; Nakamura et al., 2006; Yonashiro et al., 2006). Interestingly, MITOL ubiquitinates and increases the turnover of mutant SOD1 on the OM (Yonashiro et al., 2009). Mitochondrial Ubiquitin Ligase Activator of NF-kB (MULAN) is another, less characterized, ubiquitin-ligase, which has also been implicated in the ubiquitination of Drp1 (Li et al., 2008b).

Degradation of oxidized components by mitochondrial-derived vesicles

It is unclear what drives the switch from proteostasis to mitophagy, but the extent of mitochondrial damage is likely a discriminating factor: when proteostasis cannot repair mitochondria, mitophagy ensues. In some cases, however, a newly discovered form of communication between mitochondria and lysosomes, involving limited sections of mitochondrial membranes (mitochondria-derived vesicles, MDV) containing oxidized proteins, could be sufficient to repair the damage, prevent full-blown mitophagy and maintain mitochondria with adequate membrane potential (Soubannier et al., 2012a).

Besides the continuous generation of MDV at basal levels, an increase in several pools of MDV (in terms of cargo selectivity) can be detected in response to increased levels of reactive oxygen species (ROS), in a Drp-1-independent fashion. The majority of MDVs reaches the lysosomes for degradation. However, this process is completely independent of

canonical macroautophagy, as cells non-competent for autophagy maintain basal levels of MDV formation and respond to ROS challenge by increasing the number of MDV that are released from mitochondria. In vitro reconstitution of MDVs further determined the content of these vesicles (Soubannier et al., 2012b), which is selective based upon the nature of the ROS source applied, and established that MDVs are enriched in oxidized mitochondrial proteins. Recently, it has been proposed that PINK1-parkin activity on mitochondria is indispensable for the formation of a subtype of MDVs (OM Tom20 negative and matrix proteins positive) as a fast response to intramitochondrial ROS insults (McLelland et al., 2014), preceding mitophagic degradation of the whole organelle. No direct evidences point to the participation of MDVs in the pathology of ALS yet, but a crosstalk between oxidized SOD1 and MDVs could be hypothesized as a mechanism for the elimination of oxidized cargo in lysosomes. This mechanism may emerge as a first line of defense, when the damage to mitochondria is moderate, to protect against accumulation of oxidized and misfolded SOD1. However, this pathway may become insufficient, and mitophagy could be required to degrade extremely damaged mitochondria

Mitophagy as a pathway to clear damaged mitochondria

The property which best describes mitophagy is specificity, as only those mitochondria that are properly tagged, in a controlled cascade of events, are degraded. Mitophagy plays a role in the selective clearance of mitochondria during development in certain cell types, but its involvement in the clearance of damaged mitochondria in neurons and in neurodegenerative diseases is still largely unknown.

As mentioned above, the molecular mechanism that couples the irreversible loss of mitochondrial membrane potential to mitophagy is the accumulation of PINK1 in the OM, phosphorylation of various targets and recruitment of the E3-ubiquitin ligase parkin. In some cases, parkin phosphorylation by PINK1 is necessary for its further activity (Birsa et al., 2014; Kondapalli et al., 2012).

Ubiquitination of mitochondrial proteins is part of the quality control system outlined above, but also one of the best-studied signals for the activation of mitophagy. Ubiquitination and degradation of Mfn1 and Mfn2 initiate mitochondrial fission (Poole et al., 2010; Tanaka et al., 2010; Ziviani et al., 2010), while degradation of the tubulin cargo adaptor Miro1 results in the arrest of mitochondrial transport (Wang et al., 2011). Fragmentation of the mitochondrial network and immobilization facilitate the engulfment of damaged mitochondria in autophagic vesicles. Ubiquitination of other OM proteins, such as VDAC1 (Geisler et al., 2010), can also trigger the initiation of mitophagy, since Parkin-mediated mitophagy can take place in the absence of mitofusins (Chan et al., 2011).

Mitophagy requires an ubiquitin-binding adaptor that recruits mitochondria to the autophagosome by binding to the lipidated form of LC3 (microtubule associated protein 1 light chain 3). p62/SQSTM1 is one of the adaptors, but others must exist, since mitophagy can occur in a p62-independent manner (Narendra et al., 2010a; Okatsu et al., 2010). Autophagosomes containing mitochondria are transported to lysosomes for the formation of autolysosomes, where mitochondrial components are degraded. In neurons, fully active

lysosomes are mostly localized in the soma, and autophagosomes containing mitochondria from axons and dendrites must be retro-transported to the soma. Thus, retrograde axonal transport and mitophagy are intimately interconnected processes. Recently, the presence of mature lysosomes was reported in the axons, where lysosomes are capable of fusion with autophagosomes. Retrograde transport of the autolysosomes to the soma is needed to achieve complete degradation of cargoes (Maday et al., 2012). Further studies from Ashrafi and colleges, described degradation of autophagosomes containing mitochondria, upon fusion with mature lysosomes, in the axon. It was suggested that immobilization of individual mitochondria and engulfment by autophagosomes follows PINK1/parkin-mediated Miro1 degradation and consequent mitochondrial arrest (Ashrafi et al., 2014). However, excessive and localized damage to mitochondria in distal axons, as it occurs in ALS, could result in sequestration and depletion of essential mitophagy components.

Mutant SOD1 impairs mitochondrial retrograde axonal transport (Magrane et al., 2014). Transport changes are accompanied by mitochondrial fragmentation (Vande Velde et al., 2011), especially in the distal portions of the motor axons (Magrane et al., 2012). These observations suggest that mitophagy takes place in mutant SOD1 neurons, since mitochondrial motility arrest (Wang et al., 2011) and increased fission (Twig et al., 2008) are associated with mitophagy. They may also suggest that mitophagy fluxes are delayed in ALS neurons. Therefore, delayed mitophagy fluxes in mutant SOD1 neurons could be due to both defective retrograde transport of autophagosomes and exhaustion of rate-limiting components.

The existence of the "canonical" PINK1/Parkin mitophagy pathway in neurons is somehow controversial (Grenier et al., 2013). Some investigators have detected PINK1 and Parkin recruitment after treatment with the potent uncoupler CCCP (Cai et al., 2012; Joselin et al., 2012; Koyano et al., 2013; Seibler et al., 2011), while others have not (Van Laar et al., 2011). In neurons, this event appears to be highly dependent on conditions, since the presence of antioxidants in the medium prevents mitophagy (Joselin et al., 2012), possibly by protecting mitochondria from oxidative damage. Mitophagy following PINK1-Parkin translocation requires longer time in neurons than in other cell types (Cai et al., 2012), and it involves only a subset of mitochondria, even when cells are treated with CCCP. This suggests that limited MQC may be taking place in neurons, with the goal of achieving a steady state of functional mitochondria through selective organellar degradation and recycling. This is of essence, since neurons cannot survive with exclusive glycolytic metabolism, and thus cannot dispense of their whole mitochondrial complement at once. It is plausible that in neurons both Parkin-dependent and independent MQC mechanisms coexist and that Parkin and other ubiquitin-ligases are involved in both proteostasis of OM proteins (i.e., mitochondrial repair) and mitophagy (mitochondrial 1elimination), depending on the severity of the damage. For example, MITOL or Mulan could compensate for loss of Parkin. In addition, cardiolipin exposure in the OM was found in neurons subjected to mitochondrial stress and has been proposed as an alternative mechanism for signaling mitophagy to the canonical PINK1/parkin (Chu et al., 2013). In this case, cardiolipin interacts directly with LC3 II and serves as a receptor for the fusion with the autophagosome.

Some reports have suggested interactions between key players in mitophagy and TDP-43. A decrease in RNA and protein levels of parkin was detected in cellular and animal models of TDP-43 and FUS depletion and in sALS spinal cord samples (Lagier-Tourenne et al., 2012; Polymenidou et al., 2011), which could eventually lead to increase vulnerability to mitochondrial dysfunction and cell death. Accordingly, parkin overexpression was capable of counteracting the deleterious effects of TDP-43 overexpression, through mechanisms involving ubiquitination and subsequent TDP-43 subcellular re-localization (Hebron et al., 2014; Hebron et al., 2013). This role of TDP-43 in cell survival was ascribed to its nuclear functions, without any implications of TDP-43 or FUS aggregates in the cytoplasm or in mitochondria. However, in ALS, disturbances in mitophagy mechanisms could also arise from excessive deposition of mutant and misfolded proteins, such as SOD1 and TDP43, on mitochondria, which might interfere with the normal PINK1/parkin pathway. In support of this hypothesis, it was demonstrated that overexpression of mutant TDP-43 results in a depletion of Parkin from the brain (Stribl et al., 2014).

Increased motor neuron-specific localization of the autophagic marker LC3 II has been reported in transgenic SOD1 mice (Li et al., 2008a; Morimoto et al., 2007). Others have reported the accumulation of autophagosomes and autophagolysosomes in human spinal cord ALS samples (Sasaki, 2011), together with p62 aggregates in degenerating motor neurons. Interestingly, many of the autolysosomes contained mitochondria, a clear indication of active mitophagy. Moreover, increased mitophagy was observed in NSC34 motor neuronal cell lines transfected with TDP-43 constructs (Hong et al., 2012). Altogether, biochemical and histological evidences point to an up regulation of macroautophagy in ALS, and mitophagy specifically.

Progressive accumulation of p62 occurs in the spinal cord of G93A mutant SOD1 transgenic mice (Gal et al., 2007) and LC3-positive vacuoles are increased in motor neurons (Li et al., 2008a). However, the interpretation of these data is complex, because mutant SOD1 can bind p62 and LC3 directly, indicating that SOD1 could interfere with the p62-LC3 complex (Gal et al., 2009). Although it is still unclear whether these markers indicate increased or impaired autophagy in SOD1-fALS the role of p62 in ALS is supported by several lines of evidence. Gal and coworkers found that p62 enables the sequestration of mutant SOD1 into cytoplasmic inclusions, independent of ubiquitination, and delivers these aggregates to autophagosomes, through direct interaction with LC3 (Gal et al., 2007; Gal et al., 2009). However, mitochondrial degradation was not specifically investigated, and autophagic degradation of SOD1 aggregates could be a process distinct from mitophagy.

A partner of p62 in the recognition of ubiquitinated mitochondria is HDAC6 (Histone Deacetylase 6) (Yan et al., 2013), a cytosolic member of the family of histone deacetylases (Hubbert et al., 2002). This protein works as an adaptor between ubiquitinated proteins and dynein motors, enabling the transport of cargoes retrogradely along microtubules to form the aggresome. Recently, it was proposed that HDAC6 contributes to the formation of large inclusions of SOD1 (Gal et al., 2013). Interactions between HDAC6 and ALS proteins, such as TDP43 and SOD1, have emerged as functionally relevant in ALS (Fiesel et al., 2010; Taes et al., 2013). HDAC6 also functions as a regulator of the fusion between autophagosomes and lysosomes, since it is capable of promoting the remodeling of F-actin

cytoskeleton, in a mechanism dependent of cortactin-recruitment (Lee et al., 2010). In this context, the retrograde transport of mitophagic vacuoles to reach the soma and fuse with the lysosomes is an essential step in mitophagy (Maday et al., 2012; Maday and Holzbaur, 2014) and mutant SOD1 impairs retrograde axonal transport in vivo and in vitro (Magrane et al., 2012; Magrane et al., 2014).

Dynein and dynactin form a complex that mediates interactions between cargoes and microtubules and is responsible for the retrograde transport. Perturbations in this complex result in motor neuron degeneration (Ikenaka et al., 2013). Mutations in the dynactin subunit p150 Glued have been linked to familial motor neuron disease (Levy et al., 2006). This raises the possibility that impairment of vesicular transport necessary for MQC is a pathological mechanism, especially in the context of the extremely large axons of the motor neurons, in which transport of autophagosome-engulfed mitochondria and components of the mitophagy machinery is essential for completing the mitophagy program and to ensure a proper turnover of damaged organelles.

Interestingly, genetic deletion of HDAC6 extended the survival of mutant SOD1 mice and maintained motor axon integrity. This protective effect was associated with increased 3-tubulin acetylation (Taes et al., 2013). Mitochondrial transport was not directly investigated in this study, but it is possible that increased 3-tubulin acetylation results in increased axonal transport and contributes to ameliorating the defect of mitochondrial dynamics in mutant SOD1 mice.

Therapeutic perspectives

Autophagy is emerging as a process that can be targeted for therapeutic interventions for neurological diseases. Pharmacological stimulation of autophagy was shown to be beneficial in a mouse model of mitochondrial encephalopathy (Johnson et al., 2013). In ALS, approaches to increase autophagy could lead to prospective therapeutic interventions aimed at potentiate the elimination of damaged components of the cell, such as dysfunctional mitochondria.

Several studies have investigated autophagy modulation in mutant SOD1 mice with varying outcomes. Down regulation of X-box-binding protein-1 (XBP-1) stimulated autophagy in mutant SOD1 mice, resulting in motor neuron protection and disease improvement (Hetz et al., 2009). Initial reports showed contradictory results upon treatment with general autophagy enhancers, such as lithium (Fornai et al., 2008; Pizzasegola et al., 2009) and rapamycin (Zhang et al., 2011), but several recent studies have demonstrated beneficial effects of enhancing autophagy in mutant SOD1 mice and other mouse models (Castillo et al., 2013; Kim et al., 2013a; Wang et al., 2012; Wang et al., 2013a; Zhang et al., 2013; Zhang et al., 2014). The therapies tested so far in ALS have been aimed at potentiating general macroautophagy mechanisms and not mitophagy or any other components of MQC pathways. A first step in this direction could be made by genetically targeting these pathways, especially in cellular and mouse models of ALS, where there is a clear mitochondrial involvement. Modulating the expression of genes that encode for components

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of the MQC could help determining the significance of maintaining appropriate mitochondrial homeostasis in ALS and could reveal unsuspected commonalities with different forms of neurodegeneration, such as familial Parkinson disease, where impairment of the MQC has been shown to play a determining role.

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Highlights

- Cells are endowed with mitochondria quality control (MQC) systems, such as proteostasis and mitophagy.
- Mitochondrial dysfunction and degeneration are associated with familial and sporadic forms of ALS.
- MQC systems fail to control mitochondrial damage in ALS motor neurons.
- This review discusses mitochondrial damage and the involvement of MQC in ALS.



Figure 1. Impaired pathways of mitochondria quality control (MQC) could be involved in ALS Mitochondrial homeostasis is maintained through repair or degradation of damaged mitochondria. In response to mitochondrial stress, as for example accumulation of mutant and misfolded fALS proteins (SOD1 and TDP-43), proteostasis mechanisms act to repair damaged mitochondria. In some instances, excessive overloading damage requires the complete elimination of mitochondria, in a process defined as mitophagy. The various steps (numbered 1–5 in this scheme) involved in these mechanisms require proteins such as VCP, p62 and p150Glued (in bold), which have been associated with fALS, suggesting that ineffective MQC participates in motor neuron degeneration.



Figure 2. Proteostasis and autophagy pathways in mitochondria

The elimination of misfolded or oxidized proteins in mitochondria proceeds through different mechanisms, depending on the nature of the protein and its localization in mitochondria. 1. Proteostasis: ubiquitin ligases, such as Parkin, MITOL, and Mulan are responsible for the proteasomal degradation of components of the OM; mitochondrial proteases (Lon, i-AAA, m-AAA) degrade proteins of the IM and the matrix. 2: MDV: Elimination of oxidized components can also occur through turnover of mitochondria-derived vesicles (MDVs). The accumulation of damaged proteins in the mitochondria could interfere with protein import, causing matrix protease (MPP) malfunction. 3. Mitophagy: if the damage is too extensive to be dealt with by proteostasis alone, mitophagy pathways could be activated for the elimination of whole organelles, mediated by ubiquitination of specific proteins of the OM and their interaction with the mitophagy adaptor p62 and autophagosomes, upon LC3 modification.