Vapb/Amyotrophic lateral sclerosis 8 knock-in mice display slowly progressive motor behavior defects accompanying ER stress and autophagic response

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Abstract

Missense mutations (P56S) in Vapb are associated with autosomal dominant motor neuron diseases: amyotrophic lateral sclerosis and lower motor neuron disease. Although transgenic mice overexpressing the mutant vesicle-associated membrane protein-associated protein B (VAPB) protein with neuron-specific promoters have provided some insight into the toxic properties of the mutant proteins, their role in pathogenesis remains unclear. To identify pathological defects in animals expressing the P56S mutant VAPB protein at physiological levels in the appropriate tissues, we have generated Vapb knock-in mice replacing wild-type Vapb gene with P56S mutant Vapb gene and analyzed the resulting pathological phenotypes. Heterozygous P56S Vapb knock-in mice show mild age-dependent defects in motor behaviors as characteristic features of the disease. The homozygous P56S Vapb knock-in mice show more severe defects compared with heterozygous mice reflecting the dominant and dose-dependent effects of P56S mutation. Significantly, the knock-in mice demonstrate accumulation of P56S VAPB protein and ubiquitinated proteins in cytoplasmic inclusions, selectively in motor neurons. The mutant mice demonstrate induction of ER stress and autophagic response in motor neurons before obvious onset of behavioral defects, suggesting that these cellular biological defects might contribute to the initiation of the disease. The P56S Vapb knock-in mice could be a valuable tool to gain a better understanding of the mechanisms by which the disease arises.

Introduction

Amyotrophic lateral sclerosis (ALS) is a fatal, typically late-onset neurodegenerative disorder associated with the dysfunction or death of motor neurons. Unfortunately, there is no primary therapy for this disease and its pathogenesis is poorly understood. The disease is most often sporadic, but about 10% of the patients inherit the disease (1). Currently, mutations in almost 20 genes including vesicle-associated membrane protein-associated protein B (VAPB, ALS8), Superoxide dismutase 1 (SOD1), TAR DNA binding protein 43 (TARDBP), Fused in Sarcoma (FUS), P62 (SQSTM1), Valosin-containing protein (VCP) and C9orf72 have been identified in familial forms of ALS (2–8). The existence of inherited ALS cases has provided excellent inroads towards unraveling the molecular pathology of the motor neuron diseases. Significantly, transgenic mice expressing mutant SOD1 have recapitulated the motor defects observed in ALS patients (9). Use of these mice has been...
crucial in characterizing familial and sporadic ALS disease mechanisms (10). However, therapeutic efficacy in these animals has been poorly predictive of human efficacy. Therefore, it is crucial to create model systems associated with other mutations in ALS and analyze the resulting phenotypes. ALSS8 is a slowly progressive and late-onset dominant form of ALS first identified in a large Brazilian family (11). The family shows clinical heterogeneity with different clinical courses, such as late-onset spinal muscular atrophy (SMA), slowly progressive ALS and typical severe ALS with rapid progression (11,12). They are all found to have the same mutation (P56S) in the VAPB gene (11). In addition, recently, other rare mutations in the VAPB gene were also found to cause ALS (13,14).

Human VAPB is evolutionarily conserved, with homologs in numerous species (15), including yeast scs2 and Drosophila vap. The Vap protein contains an amino (N)-terminal domain, called the major sperm protein (MSP) domain (16,17) and a transmembrane domain that anchors the protein in the endoplasmic reticulum (ER) (18). The N-terminal MSP domain of Vap is virtually identical in structure to the abundant MSP protein in C. elegans (19), where MSP functions as a secreted ligand (20,21). Indeed, the MSP domain of Vap is cleaved and secreted from neurons (22,23). The cleaved MSP acts as a ligand for growth cone guidance receptors expressed on muscle surfaces in C. elegans (23). Significantly, Vap proteins also have autonomous functions as they are ER-associated proteins. They have been shown to function in neurite extension (24), the development of the neuromuscular junctions (NMJs) (25), ER-to-Golgi protein trafficking (26,27) and calcium homeostasis in the mitochondria (28). However, it is not still now clear how these functions are relevant to the pathology in motor neuron disease.

Transgenic mice overexpressing P56S mutant human VAPB protein with neuron-specific and ubiquitous promoters have been generated (29–32). Although these mice have provided insights into the toxic property of the mutant proteins, only transgenic mice expressing P56S VAPB driven by Thy1.2 promoter showed motor behavior defects (30). Thus, the pathogenesis associated with the mutant VAPB protein remains unclear. Moreover, it has not been possible to undertake human pathological studies in ALS8/motor neuron disease associated with the mutant VAPB as the disease shows a late-onset ALS or SMA (average 50 years old) with a slowly progressive course (11,12).

Expressing the mutant proteins in the correct temporal and spatial expression patterns will help us dissect the mechanisms of cell-specific vulnerability and the effects of the pathological mutations. Here we report generation and characterization of Vapb knock-in mice replacing wild-type Vapb with the mutant (P56S) Vapb to faithfully create features of the human ALS8/SMA associated with P56S VAPB. Significantly, the Vapb knock-in mice exhibit late-onset motor behavior defects as observed in the patients associated with the P56S VAPB. The Vapb knock-in mice also display many cellular pathological features implicated in ALS, including accumulation of ubiquitinated proteins, ER stress and autophagic response before onset of obvious motor behavior defects. We propose that ER stress and autophagic response are key early pathogenic processes in the disease.

**Results**

**Generation of Vapb^{P56S} knock-in mice**

To elucidate the pathological mechanism underlying motor neuron diseases associated with P56S mutant VAPB, we established knock-in mice replacing the wild-type Vapb gene (Vapb^{WT}) with the P56S mutant Vapb (Vapb^{P56S}) gene by homologous recombination (Fig. 1A and Supplementary Material, Fig. S1). Crosses between heterozygous mice carrying the P56S mutation produced wild-type (Vapb^{WT}), heterozygous (Vapb^{WT/P56S}) and homozygous (Vapb^{P56S}) offspring with a Mendelian ratio, in expected proportions (data not shown).

To determine which Vapb gene in the targeted allele expresses Vapb transcript at comparable levels to those of Vapb^{WT} gene in the wild-type allele, we performed quantitative real-time polymerase chain reaction (qRT-PCR) and measured the levels of Vapb transcripts in the brain of Vapb^{WT}, Vapb^{WT/P56S} and Vapb^{P56S} mice. The qRT-PCR in Vapb^{WT/P56S} and Vapb^{P56S} mice generate almost equivalent levels of products to those in Vapb^{WT} mice (Fig. 1B). Average relative quantification (RQ) values, Vapb^{WT/P56S}/Vapb^{WT} = 1.15 and Vapb^{P56S}/Vapb^{WT} = 1.56, N = 3 mice, One way ANOVA, P > 0.05, suggesting that Vapb^{P56S} gene in the targeted allele is transcribed at comparable levels to those of Vapb gene in the wild-type allele.

To determine the effects of P56S mutation on VAPB protein, we extracted the proteins from the spinal cord of WT and P56S knock-in mice with 1% NP-40 and collected detergent-soluble and insoluble fractions. Immunoblotting with VAPB antibody (33) shows a specific 26 kDa band corresponding to the full-length VAPB protein in the detergent-soluble fraction extracted from Vapb^{WT} mice (Fig. 1C, lane 1, arrow). Compared with Vapb^{WT} mice, the levels of VAPB protein are decreased in the detergent-soluble fraction of Vapb^{WT/P56S} and, they are even further decreased in the Vapb^{P56S} mice (Fig. 1C, lane 2, 3). In contrast, the amounts of truncated forms of VAPB protein are increased in the detergent-insoluble fraction of Vapb^{WT/P56S} and Vapb^{P56S} mice (Fig. 1C, lanes 4–6, arrows), indicating that the P56S mutation causes the VAPB protein to have altered physico-chemical properties that lead to its detergent-insolubility. We observed decreased levels of full-length and increased levels of truncated VAPB protein in Vapb^{P56S} mice, compared with those in Vapb^{WT}, suggesting the dose-dependent effect of Vapb^{P56S} gene (compare lanes 2–3 and 5–6 in Fig. 1C). Interestingly, Vapb^{P56S} protein migrates in SDS-PAGE with different electrophoretic properties, compared with Vapb^{WT} protein (arrow lane 3 in Fig. 1C), suggesting that P56S mutation causes post-translational modification of VAPB. In summary, P56S mutation causes detergent-insolubility of VAPB protein and possibly post-translational modification.

The P56S mutant Vapb knock-in mice show progressive defects in motor behavior in a dose-dependent manner

Patients with P56S mutant VAPB gene show neurological signs compatible with the diagnosis of lower motor neuron diseases or atypical form of ALS with slow progression (11,12). We found that both Vapb^{WT/P56S} and Vapb^{P56S} mice are born and develop normally and have a life span similar to Vapb^{WT} mice. To determine whether the mice carrying the P56S mutation show defects in motor behaviors, we performed inverted grid and rotarod tests with a cohort of wild-type (Vapb^{WT}), heterozygous (Vapb^{WT/P56S}) and homozygous (Vapb^{P56S}) knock-in mice, tested from 7 to 15 months of age (Fig. 2). At 7 months of age, neither Vapb^{WT/P56S} nor Vapb^{P56S} mice show defects in the behavior tests compared with Vapb^{WT} mice. Importantly, Vapb^{WT/P56S} mice show mild defects in inverted grid at 11 months of age, and significant defects at 15 months of age. In contrast, Vapb^{P56S} knock-in mice show severe and significant defects in inverted grid even at 11 months of age (Fig. 2A). Consistently, Vapb^{WT/P56S} and Vapb^{P56S} also showed age-dependent deficits in the rotarod test at 15 months (Fig. 2B).
In contrast, no obvious differences were detected in body weight and open-field tests among \textit{VapbWT}, \textit{VapbWT/P56S} and \textit{VapbP56S} mice (Supplementary Material, Fig. S2). Hence, we have established that P56S knock-in mice exhibit slowly progressive defects in motor behavior analogous to those observed in human motor neuron disease associated with P56S VAPB.

The P56S mutant \textit{Vapb} knock-in mice show mild and chronic neurogenic defects in muscle pathology

Analysis of muscle biopsies from ALS8 patients show defects consistent with a neurogenic pattern including groups of small angulated fibers (11,12). To examine if the ALS8 knock-in mice show neurogenic defects, we performed histological analysis of the soleus muscles of \textit{VapbWT} and \textit{VapbP56S} mice that were used in the behavior tests shown in Figure 2. We find that the muscle cross-sections of \textit{VapbWT} mice show groups of uniformly sized muscle fibers (Fig. 2C). In contrast, the muscle sections of the \textit{VapbP56S} mice show small group of atrophic cells (arrows in Fig. 2D and E, quantification in Fig. 2G). We also found an increased number of internal nuclei in muscle fibers of \textit{VapbP56S} (arrow heads in Fig. 2D and F, quantification in Fig. 2G). We, however, did not observe significant differences in the staining of muscle cross-sections of \textit{VapbWT} and \textit{VapbP56S} mice with an early denervation marker, non-specific esterase [(34), Supplementary Material, Fig. S4]. Hence, histochemical analysis of muscle cross-sections shows chronic and mild neurogenic atrophies in the \textit{VapbP56S} mice.

The P56S mutant \textit{Vapb} knock-in mice show mild partial denervation of lower motor neurons

Mutant SOD1 transgenic mice and human ALS pathology have been characterized as dying back or slowly evolving distal to proximal axonal degeneration in the pathology (35–37). To determine if P56S mutant \textit{Vapb} knock-in mice show denervation or morphological defects in the NMJs, we examined the morphology of the NMJs of \textit{VapbWT}, \textit{VapbWT/P56S} and \textit{VapbP56S} mice. We performed immunostaining of soleus muscles of 16 months-old WT and ALS8 knock-in mice with a pre-synaptic (Synaptic vesicular protein 2, SV2) and post-synaptic marker [Acetylcholine receptors (AChRs) labeled with α-bungarotoxin] (Fig. 3A–C).
Chronic denervation accompanying re-innervation of NMJs leads to increased fragmentation of the NMJs (38–40). Interestingly, we observed significant differences in the morphology of the NMJs between WT and P56S Vapb knock-in mice. The VapbWT mice exhibit a typical pretzel-like appearance of post-synaptic area as observed in normal adult NMJs (Fig. 3A) (41). In contrast, VapbWT/P56S and VapbP56S mice show a fragmented appearance of post-synaptic areas (Fig. 3B and C). As shown in Figure 3D1, we found a significant increase in the total number of post-synaptic fragments per NM in VapbWT/P56S and VapbP56S mice (Number of fragments: vapbWT = 8.1 ± 0.6, VapbWT/P56S = 12.9 ± 1.0, VapbP56S = 17.9 ± 1.3, ***P < 0.01 for each pair), suggesting chronic denervation accompanied with re-innervation in the VapbWT/P56S and VapbP56S mice. We also examined other indications of denervation (Supplementary Material, Fig. S5, see Materials and Methods), including distribution of the post-synaptic area as defined by AChR staining (α-bungarotoxin labeling) and its coverage with pre-synaptic markers as defined by SV2 (Fig. 3D2) and the number of faintly clustered or ectopic AChR staining clusters (Fig. 3D3 and Fig. 3D4) (42). We observed a tendency towards an increased number of uncovered postsynapses (AChR) (Fig. 3D2) and ectopic AChR (Fig. 3D4) in the VapbWT/P56S and VapbP56S mice at 16 months of age. Hence, the VapbWT/P56S and VapbP56S mice show chronic denervation, although the denervation is likely to be very mild.

Figure 2. P56S mutation in the Vapb gene causes defects in motor behaviors and mild denervation changes in the muscle. (A and B) Inverted Grid (A) and Rotarod test (B) with a cohort of VapbWT (N = 7), VapbWT/P56S (N = 9) and VapbP56S (N = 8) mice at 7, 11 and 15 months of age. The latencies to fall of the mice were recorded for both tests. The latency to fall by inverted grid test in VapbWT/P56S and VapbP56S is significantly lower in a dose-dependent manner compared with VapbWT mice at 11 and 15 months of age. A significant decrease is notable in the latency to fall by rotarod test in VapbWT/P56S and VapbP56S compared with VapbWT mice at 15 months of age. Data are presented as average ± SEM, *P < 0.05, ***P < 0.01. (C–G) Hematoxylin and Eosin staining of soleus muscles of VapbWT and VapbP56S mice at 13 months of age. The muscle cross-sections of the wild-type mice show groups of uniformed size of muscle fibers (C). In contrast, the muscle sections of the Vapb-knock-in mice show small group atrophies (D and E) and an increased number of fibers with internal nuclei (D and F). The number of group atrophies observed per section and the percentage of fibers with internal nuclei were quantified (G). Data are presented as average ± SEM. N = 2 for each genotype. *P < 0.05.
Figure 3. The P56S mutant Vapb knock-in mice show mild partial denervation of lower motor neurons and morphological defects in the NMJs. (A–C) Representative pictures of NMJs observed on parallel myofibrils of soleus for VapbWT (A–A″), VapbWT/P56S (B–B″) and VapbP56S mice (C–C″). Staining with α-bungarotoxin and SV2 antibody. The NMJ in VapbWT displays a compact and pretzel-like appearance (A). NMJs in VapbWT/P56S and VapbP56S mice are both highly fragmented, and present an increased endplate area with numerous synaptic boutons (B and C). (D) Quantification of NMJs innervation phenotypes showing the number of post-synaptic fragments (D1), the fraction of NMJs showing AChR uncovered with SV2 (D2), faint clustered AChR (D3) and ectopic AChR (D4). See the criteria in materials and methods and Supplementary Material, Figure S5. Compared with VapbWT, VapbWT/P56S and VapbP56S mice show a significantly increased number of post-synaptic fragments (D1). Three female mice for each genotype and 30 NMJs of each mice were analyzed. (E–H) Histochemical analysis of spinal cord sections. Motor neurons in the ventral horn of the spinal cord from VapbWT (F) and VapbP56S (G) mice were stained with Cresyl Violet. The numbers of motor neurons in the sections were quantified (H, 10 sections/animal, N = 3 for each genotype). Decreased numbers of the motor neuron was not observed in VapbP56S mice.
The P56S mutant Vapb knock-in mice show morphological changes of the synaptic boutons in the NMJs

Drosophila Vap (dvap) is the structural homolog of human VAPB and regulates synaptic remodeling by affecting the size and number of boutons (synaptic varicosities) at NMJs (25,43). To determine the effect of P56S mutation on bouton number and morphology in adult mice, we performed analysis of the NMJs in the soleus muscles from 16-month old VapbWT, VapbP56S and VapbP56S mice (Fig. 3). We found a significant increase in the number of pre-synaptic boutons in VapbWT/P56S and VapbP56S when compared with VapbWT mice (Fig. 3E1). Number of boutons: VapbWT = 16.6 ± 1.0, VapbWT/P56S = 24.6 ± 1.6, VapbP56S = 29.3 ± 1.9, ***P < 0.01 for both pairs VapbWT/P56S and VapbWT/P56S/VapbWT.

In contrast, the size of synaptic boutons is not significantly different among VapbWT, VapbWT/P56S and VapbP56S mice (Fig. 3E2). We also observed an increased endplate area in the VapbWT/P56S and, significantly, in the VapbP56S mouse in a gene dosage-dependent manner (Fig. 3E3). Total endplate area: VapbWT = 393.7 ± 46.4 µm², VapbWT/P56S = 498.4 ± 50.7 µm², VapbP56S = 634.3 ± 71.9 µm², *P < 0.05 for VapbWT/P56S/VapbWT. Of note, Vapb null mutant mice have been shown to exhibit the same morphology of NMJs as VapbP56S mice even at 18 months of age (13). Taken together, the data suggests that P56S mutation causes morphological changes of the synaptic boutons in the NMJs of adult mice. Similar changes are also observed in flies expressing ALS8 mutant Vap (44).

VAPB protein is predominantly expressed in lower motor neurons

Human ALS8 patients affected with the P56S mutant VAPB gene show weakness and muscle atrophy associated with defects in lower motor neurons rather than upper motor neurons (12). To determine whether the distribution of VAPB protein might contribute to the selective vulnerability of motor neurons in ALS8, we examined expression of VAPB in the CNS and spinal cord in mice. To assess the specificity of VAPB antibody (33), we performed immunostaining of wild-type and mutant mice carrying the Vap locus (VapGT). The VapGT mice were generated from embryonic stem (ES) cells carrying a gene trapping vector inserted into the Vap locus (Supplementary Material, Fig. S3A) (45,46). We confirmed that VapGT mice are almost Vapb null with immunofluorescence and western blotting using VAPB antibody (Fig. 4A and B and Supplementary Material, Fig. S3B). Immunolabeling with VAPB antibody in WT and heterozygous VapbWT shows that VAPB protein is expressed predominantly in motor neurons (Fig. 4C and Data not shown), but not in sensory or other populations of neurons (Fig. 4D) within the spinal cord. VAPB was predominantly expressed in neuronal cell bodies and their dendrites (Fig. 4A and C), whereas VAPB shows little or no expression in glia cells (Fig. 4C). VAPB is also highly expressed in the motor neurons of the caudal brainstem (Fig. 4D), which is co-labeled with Choline Acetyltransferase antibody (data not shown). In contrast, VAPB is barely expressed in the cerebellum (Fig. 4F), the cerebrum (including cortical motor neurons labeled with CITP2) (Fig. 4G) and the hippocampus (Fig. 4H). In summary, the data indicate that VAPB is highly expressed in the lower motor neurons, which are the most vulnerable to dysfunction or degeneration in ALS8 or SMA.

The P56S mutation causes VAPB protein to be mislocalized into cytoplasmic inclusions

We, and others, have shown that the P56S mutation causes VAPB protein to be mislocalized into cytoplasmic inclusions when the mutant protein is overexpressed in flies and mice (22,29,30). However, the overexpression of proteins might cause or enhance defects in protein homeostasis, leading to the accumulation of the mutant protein. To determine the localization of P56S mutant VAPB protein when expressed at physiological levels, we performed immunostaining of motor neurons in the spinal cord of VapbWT, VapbWT/P56S and VapbP56S mice with VAPB antibody (33) at 6 months of age before defects in motor behaviors were observed (Fig. 2). As shown in Figure 5, VapbP56S mice exhibit a significant difference in the localization of VAPB protein compared with VapbWT mice. In the motor neurons of the spinal cord and brainstem of VapbWT mice, VAPB protein distributes diffusely in the cytoplasm (Fig. 5A). In contrast, VAPB protein accumulates into cytoplasmic inclusions in the VapbWT/P56S mice. Interestingly, VapbP56S mice show more widespread inclusions with no diffuse cytoplasmic distribution as observed in VapbWT mice (Fig. 5C). We found that VapbP56S mice show an increased number of cells presenting inclusions compared with VapbWT/P56S mice (Fig. 5D). VapbWT = 0% of cells with VAPB immunopositive inclusions, VapbWT/P56S = 70.9% ± 9.3 s.e.m, and VapbP56S = 100%. ANOVA then post-hoc Multiple student t-test, P < 0.01, N = 9, suggesting dose-dependent defects caused by VapbP56S gene. As we observe that VAPB is highly expressed in lower motor neurons, but not in other types of neurons, we do not observe VAPB inclusions in the other types of neurons in VapbWT/P56S and VapbP56S mice (data not shown). Taken together, the data show that VAPB protein accumulates into cytoplasmic inclusions selectively in lower motor neurons before the onset of behavior defects in VapbP56S knock-in mice.

The P56S mutant VAPB is translocated from the ER to the autophagosome

We, and others, have shown that VAPBWT is localized in the ER (22,47). To determine the intracellular location of VAPbP56S accumulations, we performed immunostaining of spinal cord sections from VapbWT and VapbP56S mice with anti-VAPB antibody and ER markers specific anti-Calreticulin (48) and KDEL antibodies (49). Consistent with the previous observations that VAPB is localized in the ER (47), VAPBWT colocalized with the ER markers, KDEL and Calreticulin in VapbWT mice (Fig. 6A, C and Data not shown). Significantly, in VapbP56S mice, the mutant VAPbP56S is excluded from the ER as it does not co-localize with KDEL and Calreticulin (Fig. 6B, D and Data not shown), suggesting that the mutant VAPbP56S is mislocalized and absent from the ER.

Ubiquitin immunoreactive inclusions in lower motor neurons represent a characteristic pathological feature of ALS (50). Importantly, the mutant VAPbP56S has been shown to be ubiquitinated and accumulated with ubiquitinated proteins in flies and mice when the mutant protein is overexpressed (22,29,30). However, VAPbP56S protein is barely extractable in non-ionic detergent and sequence detection system (SDS) buffer. Therefore, we
examined if VAPBP56S accumulates into ubiquitinated inclusions in the VapbP56S knock-in mice. We performed immunostaining of motor neurons of VapbWT and VapbP56S mice with VAPB and Ubiquitin (FK1) antibodies at 9 months of age. In VapbWT mice, ubiquitinated proteins labeled by the antibody are barely expressed in the motor neurons (Fig.6E′,E″), whereas ubiquitinated proteins accumulate in cytoplasmic inclusions in the VapbP56S mice (Fig.6F′,F″). Importantly, the mutant VAPBP56S is significantly colocalized with poly-ubiquitinated proteins (Fig.6F″), suggesting that VAPBP56S might be ubiquitinated or recruit ubiquitinated proteins.

Ubiquitinated proteins are processed by the proteasome system or degraded by the autophagic machinery or lysosome (51). To determine if mislocalized VAPBP56S is recruited into the autophagosome, we performed immunostaining of VapbWT and VapbP56S mice with P62 antibody. We found that the levels of P62 in VapbP56S mice are four times higher compared with VapbWT mice (Fig.6K and L), suggesting an increased autophagic response caused by P56S mutant VAPB. Hence, the data indicate that the P56S mutation causes VAPB protein to be mislocalized from ER to autophagosome and results in the autophagic response.

The P56S mutant VAPB causes ER stress

VAPB is localized in the ER and required for ER protein homeostasis (54,55). We observed that P56S mutant VAPB is barely localized in the ER (Fig. 6A–D), suggesting that P56S mutation might cause loss of VAPB function in the ER. We showed that loss of Vap induces ER stress in flies (55). To examine if the VapbP56S knock-in mice exhibit ER stress, we stained spinal cords of VapbWT and VapbP56S mice with ER stress markers, PDI (56) and GRP78/BiP (57) at 6 months and 9 months of age. PDI is expressed at low
levels in VapbWT mice (Fig. 7E), whereas PDI is significantly upregulated in the VapbP56S mice (Fig. 7F). We also find that VapbP56S mice show significant upregulation of BiP expression in the motor neurons at the age of 9 months (Fig. 7A–D), suggesting that P56S mutant VAPB causes ER stress in VapbP56S mice. The ER stress in VapbP56S mice is likely to be age dependent, as we do not observe upregulation of BiP in VapbP56S mice at 6 months of age (data not shown).
Figure 6. The P56S mutation causes VAPB protein mislocalization from the ER to the autophagosome. (A–D) Staining of motor neurons in the spinal cord of VapbWT (A–A″, C–C″) and VapbP56S mice (B–B″, D–D″) with anti-VAPB (A–D) and anti-KDEL (A–D″) at 8 months of age. (C) and (D) show higher magnification of (A) and (B), respectively. VAPBWT is colocalized with KDEL, the ER marker (C–C″), whereas VAPB P56S does not colocalize with the ER marker (arrows in D–D″). (E and F) Staining of motor neurons in the spinal cord of the VapbWT (E–E′) and VapbP56S mice (F–F′) with anti-VAPB (E and F) and anti-Ubiquitin (E′, F′) at 8 months of age. No significant Ubiquitin positive signals were observed in VapbWT mice (E′), whereas Ubiquitin positive inclusions were observed in the cytoplasm of motor neurons in VapbP56S mice (F′). VAPB-positive inclusions are almost completely overlapped with Ubiquitinated inclusions (F–F′). (G and H) Staining of motor neurons in the spinal cord of 9 months-old VapbWT (G) and VapbP56S (H) mice with antibodies against VAPB (G and H) and LC3 (G′ and H′), an autophagy marker. LC3 accumulated into cytoplasmic inclusions in the mutant mice (H′) and colocalizes with VAPB (H). LC3 is also upregulated in VapbP56S (H′), compared with VapbWT (G′). (I and J) Staining of motor neurons in the spinal cord of 8 months-old VapbWT (I) and VapbP56S (J) mice with antibodies against VAPB (I and J) and P62/SQSTM (I′ and J′), another autophagy marker. Almost all VAPB-positive inclusions are P62 positive (I′ and J′). Note that the levels of P62 are increased in VapbP56S (I′), compared with VapbWT (I). (K and L) Immunoblots of proteins extracted from spinal cord of 18 months-old VapbWT and VapbWT/P56S using anti-P62 and anti-Actin. The levels of P62 expression are quantified in (L). Intensities were normalized with Actin then a ratio was calculated using VapbWT as a reference so that the relative VapbWT intensity is set to 1. Error bars represent SEM of the intensities. The expression levels of P62 protein are significantly increased in VapbWT/P56S, compared with VapbWT (N = 3, Student’s t-test, *P < 0.05).
We find that VapbWT/P56S mice do not show BiP upregulation at 9 months of age, compared with VapbP56S mice (data not shown). To determine if heterozygous VapbWT/P56S mice show ER stress when aging, we performed immunoblotting of VapbWT and VapbWT/P56S mice with anti-BiP, an ER stress marker (A and D) and NeuN (A', D'). High magnification images of (A) and (B). The expression levels of BiP are upregulated in VapbP56S mice (B and D), but not in the VapbWT (A and C). (E and F) Staining of spinal cord motor neurons of 10 months-old VapbWT and VapbP56S mice with anti-PDI, another ER stress marker (E and F) and VAPB (E' and F'). PDI expression is significantly upregulated in VapbP56S mice (F) compared with VapbWT mice (E). (G and H) Immunoblots of proteins extracted from spinal cord of VapbWT and VapbWT/P56S 18 months-old mice with anti-phospho-eIF2α and anti-eIF2α. (H) Quantification of phosphorylation of eIF2α. p-eIF2α intensities were normalized with total eIF2α. A ratio was calculated using VapbWT as a reference so that the relative VapbWT intensity is set to 1. Error bars represent SEM of the intensities. The levels of p-eIF2α are significantly increased in VapbWT/P56S compared with those in VapbWT (N = 3 for each genotype, Student t-test, *P < 0.05).

Discussion

Previous studies have shown that transgenic mice overexpressing ALS mutant VAPB proteins with neuron-specific and ubiquitous promoters fail to show defects in motor behaviors (29,31,32,43). Among these ALS8 Vapb transgenic mice, only transgenic mice expressing ALS mutant Vap under the Thy1.2 promoter show motor behavior defects in aged mice. In this study, we have shown that the VapbP56S knock-in mice develop a slowly progressive motor neuron disease reminiscent of ALS8. Muscle weakness shown by grip test is apparent at 11 months of age. Patients associated with P56S mutation also display clinical signs associated with defects in lower motor neurons, with an average age of around 50 at onset (11). We do not observe loss of body weight in the VapbWT/P56S and VapbP56S knock-in mice. It is possible that body weight loss will not appear within the short life span of a mouse. Interestingly, these mice show cellular pathological defects specifically in motor neurons. The mutant mice demonstrate accumulation of ubiquitinated protein, induction of ER stress and autophagic response before showing motor deficits. Hence, having succeeded in developing a mouse model that invokes the correct temporal and spatial expression of the
VAPB protein to be less active in the ER, resulting in the ER stress. In the ALS8 knock-in mice, P56S mutation causes a gain of function in the NMJs, although there is a difference in certain situations in the ALS8 knock-in mice. We observed that the ALS8 knock-in mice show an increased number of synaptic boutons/varicosities in flies, hypomorphic and null mutations in Vap cause a severe decrease in numbers of varicosities and an increase in their size at the NMJs (25,43). Conversely, overexpression of drosophila Vap and human VAPB in Drosophila neurons induces a highly significant increase in the number of varicosities (43), similarity to what we observed in the ALS8 knock-in mice. The data suggests that ALS8 mutation might cause a gain of function in the NMJs, although there is a difference in neurotransmitter, receptors and molecular signals in Drosophila and mice NMJs (64). Notably, synaptic transmission is maintained in the vop null mutant flies and flies overexpressing human VAPB despite this structural alteration (43). Therefore, detailed studies are necessary to conclude how defects in morphology contribute to the pathology in ALS8.

A key observation in this study is that VAPB accumulates in the autophagosome in the motor neurons of the ALS8 knock-in mice, accompanying increased levels of P62/SQSTM1 and LC3 proteins. Significantly, other studies have implicated that defects in autophagic responses contribute to the pathology of ALS. Mutations in autophagy related genes including optineurin, P62/SQSTM1 and Tbk1 are found in familial forms of ALS (5,65). P62/SQSTM1 accumulates in motor neurons in ALS patients (66,67), indicating that autophagic responses might be implicated in the common and core pathology of ALS. Neuronal autophagy has been shown to have a protective role under normal conditions. Its loss in mice deficient for the genes essential for autophagy, ATG5 and ATG7, causes neurodegeneration characterized by the widespread accumulation of cytoplasmic inclusions positive for ubiquitinated proteins (68,69). Hence, in ALS8, accumulation of P62/SQSTM1 and LC3 might function as a protective event (51). Alternatively, upregulation of autophagic responses might induce detrimental defects in ALS8 as observed in other neurodegenerative diseases (70). Autophagic responses might also be a result of ER stress (70,71), leading to the core pathology of ALS8.

This knock-in mouse replicates numerous aspects of the human disease, from progressive motor defects to selective motor neuron cellular pathology. Not only will this model allow us to study the mechanism of these varied deficits in vivo, but it provides a more authentic means of testing interventional therapies. These mice could be used, for example, to test the efficacy of compounds that have proven effective in other model organisms on facets of the phenotypes of motor neuron diseases or ALS.

Materials and Methods

Animals

Generation of P56S Vapb knock-in mice: we introduced P56S mutation into the Vapb locus using homologous recombination in ES cells and screened the targeted ES cells by Southern analysis (Supplementary Material, Fig. S1B) (72). We generated chimeric mice by microinjection of correctly targeted ES cells into 129 Sv/Ev blastocysts and mated the chimeric mice to 129 Sv/Ev females. We confirmed germ line transmission of the targeted allele carrying the P56S mutation by Southern analysis (Supplementary Material, Fig. S1B), PCR and direct sequencing of the mutation in the Vapb gene. The primers used for PCR are 5’-gtctccctacgttagctgacccacaac-3’ and 5’-aattTGagcggctgctaga-3’.

Generation of C57Bl6 mice with targeted disruption of Vapb gene: ES cells carrying gene trap cassette in the Vapb gene were created at the Texas A&M Institute for Genomic Medicine as previously described (46). The procedures for injecting, selecting and growing mouse ES cells have been described (74). We generated chimeric mice by microinjection of correctly targeted ES cells into C57Bl/6 mice blastocysts and mated the chimeric mice to C57Bl/6 females. The heterozygous mice were crossed to C57Bl/6/Nctr strain bred to each other and the litter genotyped by PCR. The following primers were used for genotyping. VapbWT gene: 5’-cttgcaaatgtgcttaagc-3’ and 5’-cagatgtgattggaacctggaacgccaac-3’. VapbP56S gene: 5’-ctcttctatgactgtagctagc-3’ and 5’-cagatgtgattggaacctggaacgccaac-3’. A 440 and 380 bp fragments were amplified separately in wild-type and VapbP56S genotypes. All mice were bred and maintained at the Canadian Council on Animal Care (CCAC)-accredited animal facilities of the Montreal Neurological Institute according to the CCAC guidelines. Mice were housed in an enriched environment with continuous access to food and water, under constant temperature and humidity, on a 12-h light/dark cycle. Approval for the animal experimentation was granted by the Animal Care and Use Committee of the McGill University.

RNA expression

Quantification of mouse Vapb, Atf4, Atf6 and CHOP mRNA in mouse tissues was performed using The ViiA7 qPCR instrument (Life Technologies). Total RNA was isolated from mouse tissues using RNeasy kit (#74104, Qiagen, CA, USA) according to the manufacturer’s protocol and reverse-transcribed to cDNA using random primers and SuperScript® III reverse transcriptase (Invitrogen). Relative expression (RQ) was calculated using the SDS 2.2.2 software (Applied Biosystems). HPRT mRNA was used as a reference control. Primers used: gaaggtgatggaagagtgcag (Vapb Forward)—cccgaagtccttctttc (Vapb Reverse)—caacctgattatactcgttgaaga (CHOP Forward)—gacacctctctgaaacatct (CHOP Reverse).
Protein expression and extraction analysis
Proteins were extracted from the spinal cord in RIPA buffer (50 mM Tris–HCl pH 8.0, 150 mM NaCl, 1 mM EDTA, 1%NP40, 0.5% Sodium deoxycholate, 0.1% SDS) containing Complete (Roche) protease inhibitors and 1 mM PMSF. After homogenization, samples were spun at 20,000 g in a microcentrifuge, and supernatant was used for the soluble fraction. The insoluble pellet was dissolved in a buffer containing 8 M urea, 4% SDS, 0.125 M Tris–HCl (pH 6.8), 12 mM EDTA, 3% β-mercaptoethanol and 0.002% bromophenol blue; incubated at 65°C for 10 min; and subjected to SDS-PAGE. Western blot analysis was performed as previously described. Nitrocellulose blots were probed with rabbit polyclonal anti-Vap (1:5000) (33), guinea pig anti-p62/SQSTM (GP62-C, Progen, 1:2000), rabbit anti-phosphorylated eif2α (SAB4504388, Sigma, 1/1000), mouse anti-eif2α (L57A5, Cell Signaling Technology, 1/1000) and anti-β-Actin (GT5412, Genetex, 1/20,000) antibodies.

Immunofluorescence
Immunofluorescence staining was performed as previously described (75). The following antisera were used for immunofluorescence of brain and spinal cord: rabbit anti-hVAPB (1:5000) (33); mouse anti-PDI (1D3, Enzo Life Sciences, 1/100); mouse anti-LC3 (ab168803, Abcam, 1/50); mouse anti-CTIP2 (ab18465, Abcam, 1/500); mouse anti-BiP/GRP78 (FK1, BML-PW8805-0500, Enzo Life Science, 1/100); rabbit anti-mouse anti-choline acetyltransferase (ChAT, ab35948, Abcam, 1/100); rabbit anti-calreticulin (ADI-SPA-600, Enzo Life Science, 1:500); rat anti-KDEL (ab50601, Abcam 1/50); mouse anti-synaptic vesicular protein 2 (SV2, 1/500, Cedarlane Laboratories Ltd). Post-synaptic nicotinic AChRs were then labeled with Alexa-594-conjugated α-bungarotoxin (1/5000, 0.5 µg/ml, Invitrogen) for 30–45 min at room temperature. Antibodies were diluted in PBS containing 0.01% Triton X-100 and 2% normal donkey serum. Washing steps were done in PBS with 0.01% Triton X-100. Z-stacks were acquired with an LSM Zeiss 710 microscope. Morphological analysis was performed using ImageJ software. NMJ denervation was assessed by observing α-bungarotoxin/SV2 labeling coverage, incomplete coverage was noted as partial denervation. Faint clustered AChR corresponded to a faint α-bungarotoxin signal displaying a lack or organization. Ectopic AChRs were two AChR groups present on the same muscle fiber and separated by more than 5 µm (42). NMJs presenting more than five post-synaptic fragments were considered fragmented. A continuous patch of α-bungarotoxin staining was considered as one fragment. The number of synaptic boutons was assessed by counting distinct pre-synaptic SV2 labeled zones. Size of boutons was assessed by measuring the total surface of SV2 labeling (Threshold and Measuring tool in ImageJ) and dividing it by the number of boutons. Total endplate area was calculated by tracing a perimeter encompassing all post-synaptic clusters (40). Statistical analyses were done on JMP 11 software. All analyses were done with one-way ANOVA followed by a post-hoc Multiple student t-test when necessary. Data in figures are presented as average ± SEM (N = 3 female animals per genotype, n = 30 NMJs for each genotype).

Behavioral analysis
Rotarod test: A cohort of 24 female mice was tested at 7, 11 and 15 months old. The locomotor activity was assessed in a bank of eight Versamax Animal Activity Monitor chambers (Accuscan Model RS2USB v4.00, Columbus, OH, USA). On the first day, mice were trained for three trials of 120 s. Testing was conducted on the next three consecutive days; each mouse was administered three trials each with a maximum duration of 300 s. The start speed was 4 RPM and was increased to a maximum speed of 25 RPM. The time mice spent on the rod without falling was recorded. Behavioral scores were subjected to statistical analysis using ANOVA with repeated measures.

Inverted grid test: for each trial, the mouse was put on the grid (bars spaced 1.5 cm apart) in a vertical position, the grid was then reversed upside down at a height of 25 cm above a padded cushion. The latency until the animal fell from the grid was recorded, the cut-off time was 5 min.

Open-field test: mice were individually placed into a chamber and locomotor activity was then recorded for a period of 90 consecutive minutes. All activities were recorded by a Versamax data analyzer (Accuscan Model VMX 1.4B, Columbus, OH, USA) and quantified using the Versamax Software System (Version 4.00, Accuscan, Columbus, OH, USA). The distance moved (in cm), time moving, number of discrete movement bouts (periods of movement separated by a minimum of 1 s of inactivity), stereotype time (time in which the animal repeatedly broke the same photocell beams) and stereotypy bouts (periods of stereotypy separated by a minimum of 1 s) were recorded in 10 min intervals.

NMJ analysis
Soleus muscles were dissected as previously described (42). Nerve terminals were labeled overnight at 4°C with mouse IgG anti-synaptic vesicular protein 2 (SV2, 1/500, Developmental Studies Hybridoma Bank). The muscles were then washed and incubated for 1 h at room temperature in anti-mouse Alexa 488 (1/1000, Cedarlane Laboratories Ltd). Post-synaptic nicotinic AChRs were then labeled with Alexa-594-conjugated α-bungarotoxin (1/5000, 0.5 µg/ml, Invitrogen) for 30–45 min at room temperature. Antibodies were diluted in PBS containing 0.01% Triton X-100 and 2% normal donkey serum. Washing steps were done in PBS with 0.01% Triton X-100. Z-stacks were acquired with an LSM Zeiss 710 microscope. Morphological analysis was performed using ImageJ software. NMJ denervation was assessed by observing α-bungarotoxin/SV2 labeling coverage, incomplete coverage was noted as partial denervation. Faint clustered AChR corresponded to a faint α-bungarotoxin signal displaying a lack or organization. Ectopic AChRs were two AChR groups present on the same muscle fiber and separated by more than 5 µm (42). NMJs presenting more than five post-synaptic fragments were considered fragmented. A continuous patch of α-bungarotoxin staining was considered as one fragment. The number of synaptic boutons was assessed by counting distinct pre-synaptic SV2 labeled zones. Size of boutons was assessed by measuring the total surface of SV2 labeling (Threshold and Measuring tool in ImageJ) and dividing it by the number of boutons. Total endplate area was calculated by tracing a perimeter encompassing all post-synaptic clusters (40). Statistical analyses were done on JMP 11 software. All analyses were done with one-way ANOVA followed by a post-hoc Multiple student t-test when necessary. Data in figures are presented as average ± SEM (N = 3 female animals per genotype, n = 30 NMJs for each genotype).

Histochemistry
Muscle histology—Gastrocnemius and soleus muscles were dissected and frozen in liquid nitrogen-cooled isopentane. 10 µm transverse cryostat sections were prepared on Snowcoat X-tra slides (Surgipath) and processed following standard Hematoxylin–Eosin or esterase staining protocols.

Spinal motor neurons quantification—30 µm transverse cryostat sections of L5 segments of mice spinal cords were mounted onto Snowcoat X-tra slides (Surgipath) and stained with Cresyl Violet for Nissl staining. Motor neurons from 10 sections/animal (n = 3 animals per genotype) were quantified.

Supplementary Material
Supplementary Material is available at HMG online.

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References


