



Acyl-CoA synthetase 6 enriches the neuroprotective omega-3 fatty acid DHA in the brain

Regina F. Fernandez^a, Sora Q. Kim^b, Yingwei Zhao^b, Rachel M. Foguth^c, Marcus M. Weera^d, Jessica L. Counihan^e, Daniel K. Nomura^e, Julia A. Chester^d, Jason R. Cannon^c, and Jessica M. Ellis^{a,1}

^aDepartment of Physiology, East Carolina University, Greenville, NC 25878; ^bDepartment of Nutrition Science, Purdue University, West Lafayette, IN 47907; ^cSchool of Health Sciences, Purdue University, West Lafayette, IN 47907; ^dDepartment of Psychological Sciences, Purdue University, West Lafayette, IN 47907; and ^eDepartment of Nutritional Sciences and Toxicology, University of California, Berkeley, CA 94720

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Docosahexaenoic acid (DHA) is an omega-3 fatty acid that is highly abundant in the brain and confers protection against numerous neurological diseases, yet the fundamental mechanisms regulating the enrichment of DHA in the brain remain unknown. Here, we have discovered that a member of the long-chain acyl-CoA synthetase family, Acsl6, is required for the enrichment of DHA in the brain by generating an Acsl6-deficient mouse (Acsl6^{-/-}). Acsl6 is highly enriched in the brain and lipid profiling of Acsl6^{-/-} tissues reveals consistent reductions in DHA-containing lipids in tissues highly abundant with Acsl6. Acsl6^{-/-} mice demonstrate motor impairments, altered glutamate metabolism, and increased astrogliosis and microglia activation. In response to a neuroinflammatory lipopolysaccharide injection, Acsl6^{-/-} brains show similar increases in molecular and pathological indices of astrogliosis compared with controls. These data demonstrate that Acsl6 is a key mediator of neuroprotective DHA enrichment in the brain.

fatty acid metabolism | neurometabolism | docosahexaenoic acid | acyl-CoA synthetase | brain lipids

The omega-3 docosahexaenoic acid (DHA) and omega-6 arachidonic acid (AA) are the most abundant polyunsaturated fatty acids in the brain as the healthy brain contains ~15% DHA, three to four times higher than the amount of DHA in any other tissue, and ~13% AA (1–4). Importantly, low dietary intake of DHA, afflicting a majority of the US population (5), increases the risk of neurodegenerative diseases and related molecular events in rodents and humans (6–8). The neuroprotective properties of DHA are attributed to its ability to act as an antioxidant, increase membrane fluidity, and serve as the precursor for specialized proresolving mediators that attenuate inflammation and oxidative stress (9–12). Thus, low brain DHA results in neurodegenerative symptomatology, suggesting a role for brain DHA metabolism in the onset and progression of neurodegeneration. However, little is known about the fundamental regulatory mechanisms controlling brain fatty acid metabolism and incorporation into phospholipids.

Cellular fatty acid metabolism is initiated by the activation of free fatty acids to form acyl-CoA to trap fatty acids within cells and provide the substrate for nearly all fatty acid metabolic processes, including membrane phospholipid biosynthesis. The generation of acyl-CoAs is mediated by the Acyl-CoA synthetase (ACS) family of enzymes with diverse substrate preferences, regulatory mechanisms, binding partners, expression patterns across tissues, and subcellular localization (13–16). We and others have shown that these distinct properties allow the ACS family of enzymes to channel specific fatty acids toward directed metabolic fates (17–19). Of these ACS enzymes, ACSL6 is nearly exclusively expressed in the brain according to mRNA abundance, suggesting that it may play an important and unique role in regulating brain lipid metabolism (15, 20, 21). However, the role of Acsl6 in regulating brain lipid metabolism *in vivo* has remained unknown. We have generated an Acsl6-deficient mouse (Acsl6^{-/-}) and show that Acsl6-deficient mice exhibit reduced abundance of brain DHA, suggesting that Acsl6 is required for the incorporation and

enrichment of the omega-3 fatty acid DHA in the brain. In agreement with the neuroprotective effects of DHA, Acsl6^{-/-} mice exhibit motor dysfunction and increased astrogliosis. These data demonstrate that Acsl6 is critical for DHA metabolism in the central nervous system and that Acsl6-mediated lipid metabolism is critical for normal brain function and neuroprotection.

Results

Acsl6 Is Highly Enriched in the Central Nervous System. To confirm that Acsl6 protein, like its mRNA, is enriched in the central nervous system, an antibody was generated and used to demonstrate enrichment of ACSL6 protein in mouse brain, with minor expression detected in the spine, eye, and testis (Fig. 1A). Expression of Acsl6 was barely detected in all other tissues assayed (Fig. 1A). Acsl6 protein was abundant across brain regions but compared with hypothalamus, hippocampus, and cortex, Acsl6 was most abundant in the midbrain, medulla/pons, and cerebellum (Fig. 1B). Along the course of development, Acsl6 mRNA and protein was detectable at low levels in embryonic and early postnatal brain but increased at ~7 d of age and linearly up to day 28, remaining abundant up to 1 y of age, data that represents a combination of male and female mice (Fig. 1C and D). Thus, brain Acsl6 protein is induced 25-fold from fetus to

Significance

Neurodegenerative diseases are a leading cause of morbidity and mortality among older adults, the fastest-growing segment of the US population. Neurodegenerative disease risk is reduced by high dietary intake of the omega-3 fatty acid, docosahexaenoic acid (DHA), a highly abundant lipid in the brain. Yet the fundamental mechanisms regulating brain DHA enrichment remain unknown. Here, we have made a key discovery that Acyl-CoA synthetase 6 (Acsl6) is required to specifically enrich DHA in the brain. Of importance, mice lacking Acsl6 have impaired motor function and increased astrogliosis, demonstrating the critical need for Acsl6-mediated lipid metabolism in neurological health. This work provides critical insight into longstanding mysteries surrounding brain DHA metabolism and has broad-reaching health implications.

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¹To whom correspondence should be addressed. Email: ellisje18@ecu.edu.

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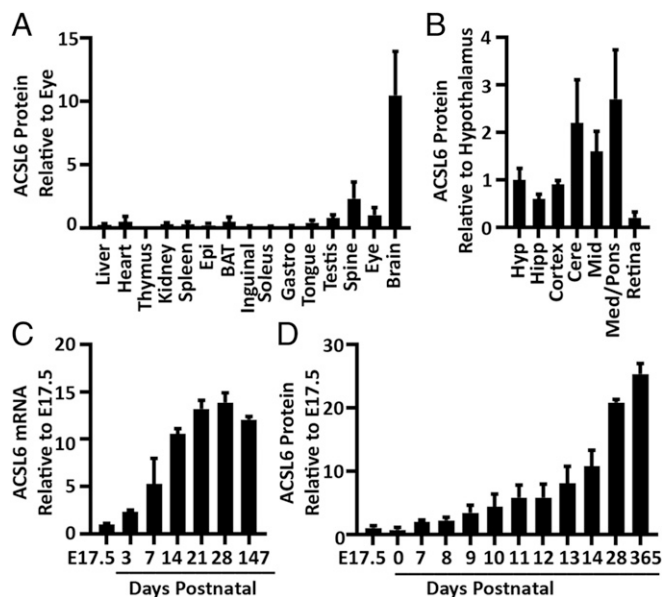


Fig. 1. Acs6 is highly enriched in the central nervous system. Quantification of Western blot for Acs6 normalized to HSP60 in mouse tissues (A), brain regions (B), and mRNA (C) and protein (D) in brain across development, $n = 3$. BAT, brown adipose tissue; Cere, cerebellum; Epi, epididymal white adipose tissue; Gastro, gastrocnemius; Hipp, hippocampus; Hyp, hypothalamus; Med/Pons, medulla oblongata and pons; Mid, midbrain. Data represent averages \pm SEM.

adult brain, later in development than several DHA-metabolizing enzymes (FABP5 and Mfsd2a) (22–24). These data suggest that mouse Acs6 is a developmental-induced central nervous system and testes-specific protein.

Generation of Acs6 Knockout Mice. To determine the role and importance of Acs6-mediated fatty acid metabolism and function, we generated an Acs6 conditionally deficient mouse strain (Acs6^{fllox/fllox}) and bred these mice to CMV-Cre expressing mice to generate a total body germ-line deletion of Acs6 (Acs6^{-/-}) (SI Appendix, Fig. S1A). Acs6^{-/-} mice were viable and born at expected Mendelian ratios (SI Appendix, Fig. S1B). The loss of Acs6 protein in Acs6^{-/-} was confirmed by Western blotting (Fig. 2A and B). The mRNA of other Acs1 isoforms were not induced to compensate for the loss of Acs6 (Fig. 2C). Initial rates of ACS activity were measured in total membrane fractions using radiolabeled fatty acid substrates, encompassing potential activity from all 25 ACS enzymes and assay conditions optimized using oleate (OA) as the substrate (SI Appendix, Table S1). The loss of Acs6 reduced total ACS activity for palmitate (PA) (C16:0) by 44%, OA (C18:1n9) by 41%, AA (20:4n6) by 36%, and DHA (22:6n3) by 37% in the midbrain (Fig. 2D), and similarly in the cortex (SI Appendix, Fig. S1C). Thus, the total ACS activity was reduced ~40% in Acs6^{-/-} brain. The loss of Acs6 did not alter body length, weight, or food intake compared with littermate controls (SI Appendix, Fig. S1D–F), nor did it alter brain weight, length, and width (SI Appendix, Fig. S1G and H) or cerebellar ultrastructure (SI Appendix, Fig. S1I) at 2 mo of age. Together, these data show that the loss of Acs6 does not impact viability and that Acs6 contributes to ~40% of total ACS activity in the brain.

To gain insight into how Acs6 affects neurometabolism more broadly, an unbiased metabolomics analysis was performed on control and Acs6^{-/-} hippocampus from 2-mo-old mice following an overnight fast. Acs6^{-/-} mice exhibit alterations in hippocampal tryptophan, glutathione, methionine, and cysteine that have potential implications for disruptions in antioxidant and neurotransmitter homeostasis (Fig. 2E). Several metabolites

related to glucose and energy metabolism were altered in the Acs6^{-/-} hippocampus including, lactate, glucose-6-phosphate, phosphoenolpyruvate, fumarate, and pantothenate (CoA synthesis) (Fig. 2F). Acs6^{-/-} hippocampal nucleotides, cytosine and uracil, and the nucleotide synthesis intermediate, CDP, were altered (Fig. 2G), which may reflect altered nucleic acid synthase or transcriptional activity.

Acs6 Deficiency Decreases Brain Omega-3 Docosahexaenoate-Containing and Increases Omega-6 Arachidonate-Containing Lipids.

To determine how the loss of Acs6 affects brain lipid composition, global unbiased lipidomic profiling of the cerebellum from 2-mo-old control and Acs6^{-/-} female mice was performed. The fatty acid profile of Acs6^{-/-} cerebellum, compared with controls, was marked by 22–71% reductions in phospholipids, lysophospholipids, monoacylglycerol, and diacylglycerol containing DHA and 25–61% increases in nearly every lipid species containing AA (Fig. 3). The pattern of reduced DHA and increased AA in Acs6^{-/-} cerebellum was also reflected in the free fatty acid and in the ether-linked and plasmalogen lipids (SI Appendix, Table S2). This level of reduced DHA, and increased AA, is similar to that seen after two generations of breeding rodents on an omega-3-deficient diet, suggesting that Acs6 is a major contributor to brain DHA enrichment (25). Phospholipids containing the monounsaturated fatty acid OA remained generally unchanged between genotypes. To determine if overnight fasting altered lipid composition in this genetic model, lipidomics was performed on cerebellum of control and Acs6^{-/-} mice challenged with overnight fasting to reveal similar genotypic alterations compared with the fed state (SI Appendix, Table S2). Together,

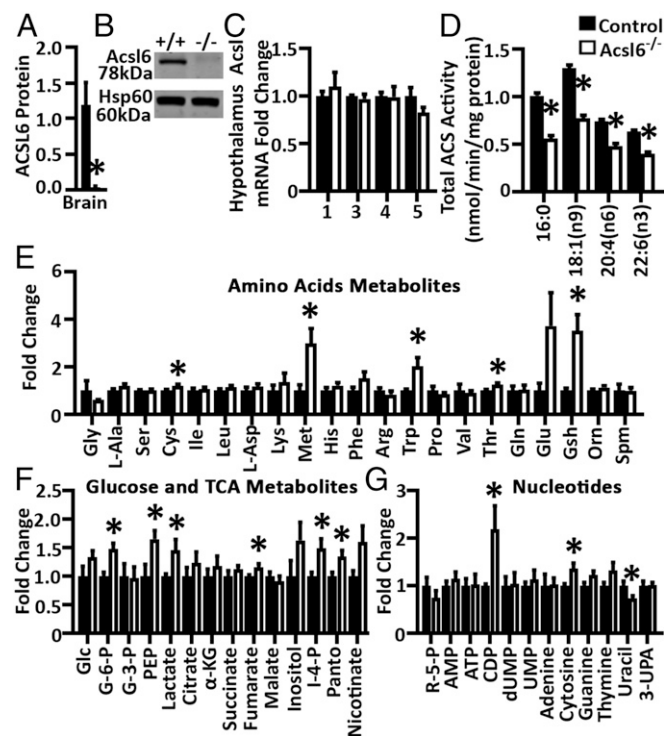


Fig. 2. Generation of Acs6 knockout mice. Quantification (A) and Western blot (B) image of Acs6 protein from control and Acs6^{-/-}, $n = 3$. (C) mRNA abundance of Acs1 isoforms 1, 3, 4, and 5 from control and Acs6^{-/-} hypothalamus, $n = 5$. (D) Initial rate of ACS activity for [¹⁴C]16:0, [¹⁴C]18:1n9, [¹⁴C]20:4n6, and [¹⁴C]22:6n3 from control and Acs6^{-/-} midbrain, $n = 5–6$. Amino acid (E), glucose and TCA (F), and nucleotide (G) metabolites in 2-mo-old female Acs6^{-/-} hippocampus relative to control, $n = 8$. Data represent averages \pm SEM; * $P \leq 0.05$ by Student's *t* test.

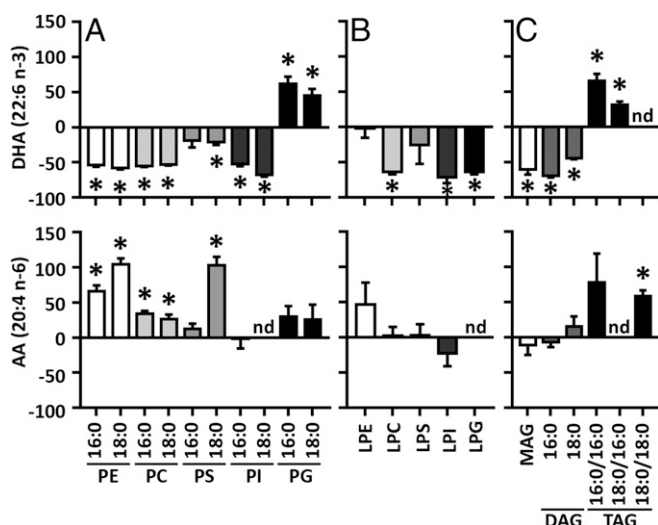


Fig. 3. *Acs16* deficiency decreases brain omega-3 docosahexaenoate-containing and increases omega-6 arachidonate-containing lipids. Lipid profile of phospholipids (A), lysophospholipids (B), MAG, DAG, and TAG (C) in 2-mo-old female cerebellum expressed as % change in the *Acs16*^{-/-} brains relative to the control samples, $n = 5-6$. Data represent averages \pm SEM; * $P \leq 0.05$ by Student's t test.

these data show that loss of *Acs16* reduced brain DHA content with a concomitant increase in the omega-6 fatty acid AA, suggesting that *Acs16* is critical for the incorporation of DHA into brain lipids.

To confirm *Acs16*-mediated DHA deficiency across brain regions and spine, lipidomics was performed in midbrain, hippocampus, cortex, and spine of 2-mo-old female control and *Acs16*^{-/-} mice. All *Acs16*^{-/-} brain regions and spine had consistent 24–40% reductions in predicted DHA-containing and 26–54% increases in

AA-containing phospholipids (Fig. 4 A–D), similar to the cerebellum (Fig. 3). To determine if *Acs16* deficiency altered peripheral lipid homeostasis, lipidomics was performed on liver (Fig. 4E) and soleus muscle (Fig. 4F) in control and *Acs16*^{-/-} mice to reveal no genotype effect on lipid content in these tissues. These data suggest that tissues expressing *Acs16* require it for DHA enrichment and that loss of *Acs16* does not impact whole-body lipid homeostasis.

To determine if *Acs16* deficiency-mediated impact on brain lipid metabolism was similar across sexes and with aging, lipidomics was performed on 6-mo-old male cerebellum (Fig. 4G) to demonstrate similar fatty acid profile compared with 2-mo-old female mice (Fig. 3). To determine the cell type-specific contribution of *Acs16*-mediated lipid metabolic control, an astrocyte-specific *Acs16* knockout mouse (*Acs16*^{G/-}) was generated resulting in a 57% reduction in *Acs16* protein in cerebellum (Fig. 4I). *Acs16*^{G/-} cerebellum lipidomic analysis revealed similar reductions in DHA compared with *Acs16*^{-/-} mice; however, AA was decreased, rather than increased, in *Acs16*^{G/-} (Fig. 4 G and H). These data suggest that approximately half of brain *Acs16* is expressed in astrocytes and that *Acs16* is critical for DHA enrichment independent of cell type.

Loss of *Acs16* Disrupts Motor Function. Because dietary DHA deficiency perturbs motor function in rodents (26) and *Acs16* loss results in brain and spine DHA deficiency, we assessed motor and neurosensory function in *Acs16*^{-/-} mice. *Acs16*^{-/-} performed poorly during a wire hang test compared with controls (Fig. 5A). Poor performance during a wire hang test could be due to reduced strength; however, the control and *Acs16*^{-/-} mice performed similarly in the neuromuscular grip strength assessment, suggesting no disruption in upper body strength (SI Appendix, Fig. S24). Rotarod tests were performed to assess motor coordination and showed a trend toward reduced performance by *Acs16*^{-/-} mice at 12 mo of age (Fig. 5B). Open field data showed no alterations in time spent in center

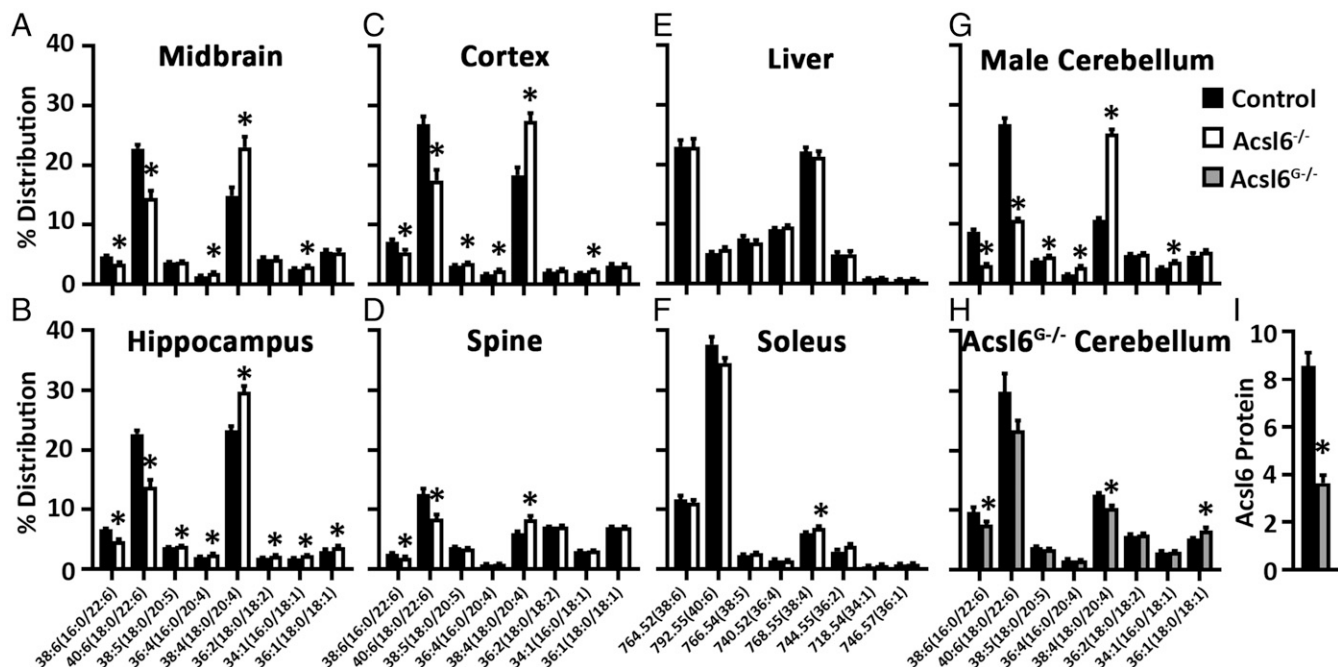


Fig. 4. *Acs16* deficiency decreases omega-3 docosahexaenoate across the central nervous system. Phosphatidylethanolamine profile in 2-mo-old female midbrain (A), hippocampus (B), cortex (C), spine (D), liver (E), soleus (F), 6-mo-old male cerebellum (G), and 4- to 7-mo-old male *Acs16*^{G/-} cerebellum (H) expressed as % ion intensity distribution in *Acs16*^{-/-} or *Acs16*^{G/-} relative to control, x axis represents carbon:unsaturated bonds, predicted fatty acid composition, or m/z , $n = 5-6$. (I) Western blot quantification of *Acs16* from control and *Acs16*^{G/-} cerebellum normalized to β -tubulin, $n = 5$. Data represent averages \pm SEM; * $P \leq 0.05$ by Student's t test.

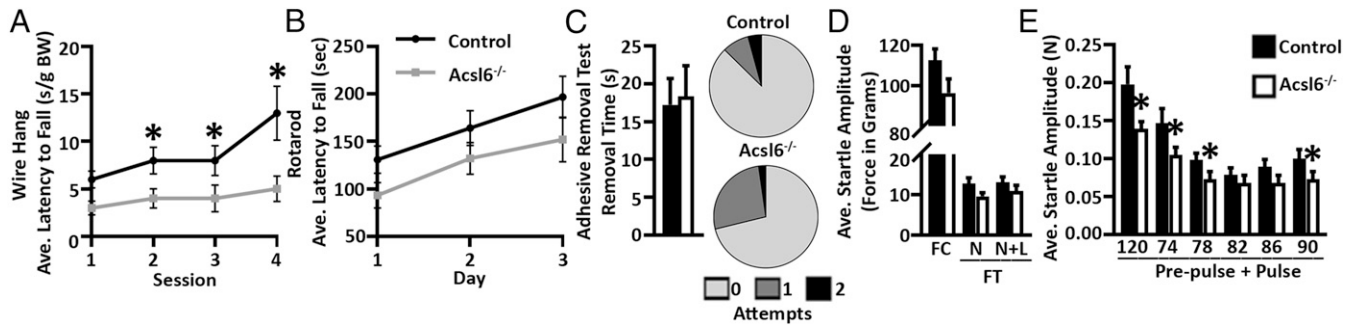


Fig. 5. Loss of *Acl6* disrupts motor control. (A) Control and *Acl6*^{-/-} 6-mo-old mice average latency to fall in the wire hang test normalized to body weight, *n* = 14–15. (B) Rotarod performance for 12-mo-old male control and *Acl6*^{-/-} mice during three consecutive days, *n* = 15–16. (C) Adhesive removal test removal time (Left) and number of failed attempts (Right) by 12-mo-old control and *Acl6*^{-/-} mice. (D) Average startle response during the fear conditioning session (FC) to a foot shock and during the fear testing session (FT) to a 100-dB tone (noise = N) and to noise + light stimulus in 6-mo-old control and *Acl6*^{-/-} mice, *n* = 28–30. (E) Average startle response to acoustic stimuli in 6-mo-old control and *Acl6*^{-/-} mice. Data represent averages ± SEM; **P* ≤ 0.05 by Student's *t* test.

versus periphery and no differences in locomotor activity, suggesting that *Acl6*^{-/-} mice do not have altered anxiety in the open field test (SI Appendix, Fig. S2B). Sensorimotor assessment by adhesive removal test showed similar time spent attempting to remove the sticker between *Acl6*^{-/-} and control, but the *Acl6*^{-/-} made more failed attempts to remove the adhesive compared with controls (Fig. 5C). The startle response of *Acl6*^{-/-} mice trended toward a reduction in response to an electrical impulse to the footpad and was significantly reduced in response to acoustic stimuli (Fig. 5D and E). However, fear potentiated startle and prepulse inhibition were not different between genotypes (SI Appendix, Fig. S2C and D). Together these data show impaired neurosensory and motor function in *Acl6*^{-/-} mice.

Acl6^{-/-} Mice Exhibit Potentiated Astroglia and Microglia Activity.

DHA has been shown to attenuate neuroinflammation in response to lipopolysaccharide (LPS) exposure in some, but not all, reports (27–31). To determine if *Acl6*-mediated DHA deficiency altered neuroinflammation in the brain and in response to LPS, control and *Acl6*^{-/-} male mice were given a single i.p. injection of LPS. No genotype effect was observed for immobility or hippocampal mRNA abundance of the inflammatory genes with or without LPS at 2 and 6 mo of age (Fig. 6A–C and SI Appendix, Fig. S2E). However, the mRNA abundance of the microglia markers, CD68 and CD11b, was increased in *Acl6*^{-/-} hippocampus, compared with saline-injected controls (Fig. 6D), and immunohistochemical staining of microglia by Iba1 in the substantia nigra showed morphology consistent with microglia activation, as demonstrated by the retracted processes and increased cell body size, in *Acl6*^{-/-} mice (Fig. 6E) (32). Motor-controlling dopaminergic neurons originate in the substantia nigra and extend to the striatum. Quantification of *Acl6*^{-/-} striatal terminal density of tyrosine hydroxylase-positive dopaminergic neurons increased, compared with controls (SI Appendix, Fig. S2F). Together these data suggest increased microglia activation and/or activity in *Acl6*^{-/-} mice.

LPS-induced inflammatory response includes altered glutamate homeostasis, oxidative stress, and astrocyte activation (33–35). The mRNA abundance of genes related to glutamate metabolism, oxidative stress, and astrocyte activation in hippocampus were increased in *Acl6*^{-/-} compared with controls (Fig. 7A–C). In agreement, immunohistochemistry in the cerebellum of *Acl6*^{-/-} mice compared with controls showed increased GFAP signal (Fig. 7D). Specifically, in cerebellar gray matter, GFAP immunoreactivity in the protoplasmic astrocytes surrounding Purkinje cells was increased in *Acl6*^{-/-}, compared with controls, with and without LPS (Fig. 7D). In cerebellar white matter where fibrous astrocytes reside, GFAP immunoreactivity was increased 7% and 9% in *Acl6*^{-/-}

mice compared with controls with or without LPS, respectively, suggesting increased reactivity of the *Acl6*-deficient astrocytes (Fig. 7D and E). Furthermore, the area occupied by GFAP⁺ cells in white matter was increased 45% in *Acl6*^{-/-} mice, compared with controls, suggesting increased number of astrocytes (Fig. 7F). Together, these data show that loss of *Acl6*-elevated glutamate and oxidative stress-related gene markers, and increased astrogliosis, an effect that remains elevated after a proinflammatory LPS challenge.

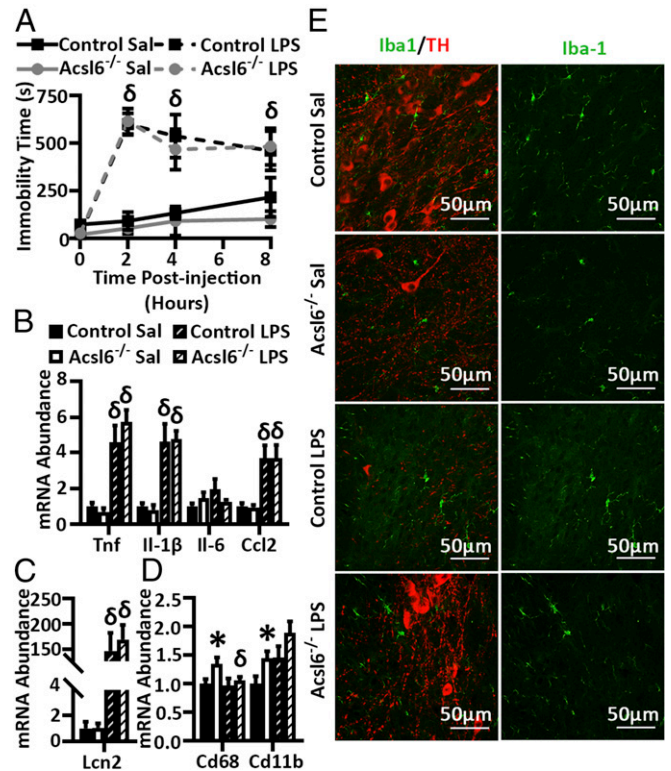


Fig. 6. *Acl6* deficiency increases microglia activity. Percent immobility and hippocampal mRNA abundance (A) of inflammatory (B and C) and microglial genes (D) in control and *Acl6*^{-/-} saline (Sal) or LPS treated 6-mo-old male mice, *n* = 7–8. (E) Representative images of Iba1 and tyrosine hydroxylase (TH) stained substantia nigra of control and *Acl6*^{-/-} mice injected with saline or LPS, *n* = 5. (Scale bars: 50 μm.) Data represent averages ± SEM; * by genotype, δ by treatment, *P* ≤ 0.05 by Student's *t* test.

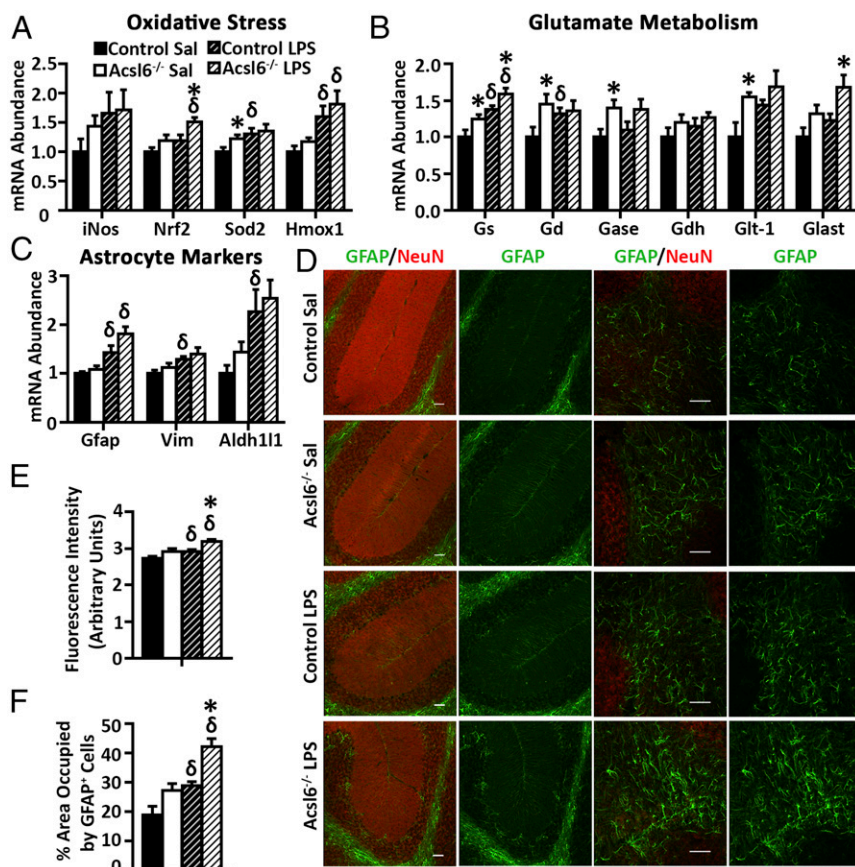


Fig. 7. Increased astrogliosis in *Acs16*^{-/-} mice. mRNA abundance of oxidative stress (A), glutamate metabolism (B), and astrocyte markers (C) in hippocampus of control and *Acs16*^{-/-} saline (Sal) or LPS treated 6-mo-old male mice, $n = 7-8$. Representative (D) and quantification (E and F) of GFAP (green) and NeuN (red) stained in the cerebella of control and *Acs16*^{-/-} mice injected with saline or LPS, $n = 5$. (Scale bars: 50 μ m.) Data represent mean \pm SEM; * by genotype, δ by treatment, $P \leq 0.05$ by Student's *t* test.

Discussion

While DHA is the most abundant polyunsaturated fatty acid in the brain, models to study DHA in the brain are limited. The most predominant model is to modify dietary omega-3 fatty acid intake for multiple generations, a model confounded by whole-body and transgenerational effects. A model of DHA deficiency was reported in mice lacking major facilitator superfamily domain-containing 2A (*Mfsd2a*). These mice have a ~50% reduction of DHA in brain due to impaired uptake of DHA-containing lysophospholipids through the blood-brain barrier (36). While this work provides evidence for a mechanism of DHA uptake into the brain, the contribution of lysophospholipids to brain DHA pool is minimal (37). Here, we report the loss of *Acs16*, resulting in brain DHA deficiency. The requirement of *Acs16* to ligate DHA to the glycerol backbone argues a mechanism for *Acs16*-mediated DHA enrichment that is independent of *Mfsd2a*. To date, the metabolic handling of blood-derived lipids once inside brain parenchyma has remained unclear. Here, we provide critical insight into *Acs16* as a major mediator of brain parenchyma DHA metabolism.

The existence of *Acs16* splice variants in the brain and their reported alternative substrate preferences, as well as *Acs16* cell type-specific expression, have complicated the implications of *Acs16* in lipid biology. Here, we were surprised to find nearly equivalent reductions in ACS activity for saturated, monounsaturated, omega-3 and omega-6 fatty acids in the *Acs16*^{-/-} brains relative to controls. We used the monounsaturated fatty acid oleate to optimize the enzyme assay conditions, thus optimization of the assay conditions using each substrate individually may be warranted to more accurately depict substrate-dependent enzyme activity. However, our lipidomic profiling reveal consistent and significant reductions in DHA-containing lipids, strongly suggesting that, *in vivo*, *Acs16* is critical for DHA incorporation into brain lipids. *Acs16* deficiency induced reduction in brain DHA is likely due to compounding

mechanisms that control substrate (i.e., DHA) accessibility via shuttling-, transport-, or phospholipid remodeling-related processes in a cell type-dependent manner, an area of research that requires further investigation.

DHA has received recent attention for its antiinflammatory properties (9–11, 38–40). However, not all reports are consistent with reduced neuroinflammation by DHA (27–31, 41–43). Because dietary DHA manipulation involves whole-body metabolism of DHA, the neuroprotective effects could be elicited by responses outside the central nervous system. Recently, the i.c.v. injection of LPS to mice with increased DHA content, due to dietary fish oil supplementation or fat-1 transgene expression, revealed little to no protective role for DHA in the neuroinflammatory response to LPS (30). In agreement with these results, our data show that the neuroinflammatory response to LPS was not augmented in male *Acs16*-mediated DHA deficiency. However, at baseline, the loss of *Acs16* did increase microglia activation and astrogliosis. These data suggest that brain neuroinflammatory responses are increased by *Acs16* deficiency, potentially due to the loss of DHA and increase in AA; however, LPS-mediated inflammation is not dependent on *Acs16*-mediated lipid metabolism.

Several human genome mapping studies have linked the *ACSL6* loci to schizophrenia (44–47). Here, we demonstrate motor symptoms, alterations to glutamate and dopaminergic homeostasis, all of which are consistent with characteristics of schizophrenia observed in patient and animal models (6, 48, 49). Several of these characteristics are also indicative of parkinsonism, such as alterations in the motor function, dopaminergic, glutamate, and microglia homeostasis consistent with symptoms and pathology of Parkinson's disease patients and animal models (31, 50, 51). Thus, future investigation into the effects of *Acs16* on age-related neurodegenerative and psychiatric diseases are warranted.

In summary, we show that the loss of *Acs6* reduces DHA content in tissues in which it is highly expressed. The loss of *Acs6* disrupted brain metabolism, impaired motor function, and induced microglia activity and astrogliosis, indicative of neurological stress.

Experimental Procedures

Acs6 knockout mice were created using a vector designed by the NIH-sponsored knockout mouse program to target *Acs6* exon 2 and injected into C57BL/6 embryonic stem cells to generate *Acs6* conditional mice (*Acs6^{flox/flox}*) by Ingenious Targeting, Inc. *Acs6^{flox/flox}* mice were bred to CMV-Cre (Jackson Laboratories stock no. 006054) or GFAP-Cre (Jackson

Laboratories stock no. 024098) transgenic mice to produce germ-line global (*Acs6^{-/-}*) or GFAP-driven astrocyte-specific (*Acs6^{G/-}*) knockout mice. Mice were maintained on chow diet with soy oil as lipid source (Teklad Global 18% Protein Rodent Diet; Envigo) and 12-h light-dark cycles. All experiments were approved by Purdue Animal Care and Use Committee. For the LPS challenge, 6-mo-old male mice were injected intraperitoneally with sterile saline or *Escherichia coli* lipopolysaccharide (0.33 mg/kg; 396,000 EU/kg; serotype 0127:B8; Sigma) and tissues harvested 8 h after injection (52, 53).

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