

iPLA₂β Knockout Mouse, a Genetic Model for Progressive Human Motor Disorders, Develops Age-Related Neuropathology

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Received: 18 November 2013/Revised: 23 April 2014/Accepted: 22 May 2014/Published online: 12 June 2014
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Abstract Calcium-independent phospholipase A₂ group VIa (iPLA₂β) preferentially releases docosahexaenoic acid (DHA) from the *sn*-2 position of phospholipids. Mutations of its gene, PLA2G6, are found in patients with several progressive motor disorders, including Parkinson disease. At 4 months, PLA2G6 knockout mice (iPLA₂β^{-/-}) show minimal neuropathology but altered brain DHA metabolism. By 1 year, they develop motor disturbances, cerebellar neuronal loss, and striatal α-synuclein accumulation. We hypothesized that older iPLA₂β^{-/-} mice also would exhibit inflammatory and other neuropathological changes. Real-time polymerase chain reaction and Western blotting were performed on whole brain homogenate from 15 to 20-month old male iPLA₂β^{-/-} or wild-type (WT) mice. These older iPLA₂β^{-/-} mice compared with WT showed molecular evidence of microglial (CD-11b, iNOS) and astrocytic (glial fibrillary acidic protein) activation, disturbed expression of enzymes involved in arachidonic acid metabolism, loss of neuroprotective brain derived neurotrophic factor, and accumulation of cytokine TNF-α

messenger ribonucleic acid, consistent with neuroinflammatory pathology. There was no evidence of synaptic loss, of reduced expression of dopamine active reuptake transporter, or of accumulation of the Parkinson disease markers Parkin or Pink1. iPLA₂γ expression was unchanged. iPLA₂β deficient mice show evidence of neuroinflammation and associated neuropathology with motor dysfunction in later life. These pathological biomarkers could be used to assess efficacy of dietary intervention, antioxidants or other therapies on disease progression in this mouse model of progressive human motor diseases associated with a PLA2G6 mutation.

Keywords Calcium-independent phospholipase A₂ (iPLA₂β) knockout · Brain · Parkinson disease · Arachidonic and docosahexaenoic acid · Motor disturbances · Neuropathology

Introduction

In vertebrates, the polyunsaturated fatty acid (PUFA) docosahexaenoic acid (DHA, 22:6n-3) is thought to play antioxidant, neuroprotective, and neurotransmission roles in brain [1–4]. DHA must be obtained directly from the diet or by liver synthesis from its dietary essential precursor, α-linolenic acid (α-LNA, 18:3 n-3) [5]. It is found in high concentrations in the *sn*-2 position of brain membrane phospholipids, from where it can be released preferentially by a calcium-independent phospholipase A₂, iPLA₂β or iPLA₂γ [6, 7].

iPLA₂β accounts for 70 % of cytosolic PLA₂ activity in rat brain [6, 8]. Mutations in its gene, PLA2G6, occur in infantile neuroaxonal dystrophy (INAD) [9, 10], neurodegeneration with brain iron accumulation (NBIA) [10, 11],

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early-onset dystonia-parkinsonism [12–14], and Parkinson disease [15]. iPLA₂β knockout mice have been developed to understand the consequences of these mutations [16, 17].

iPLA₂β plays a role in motor behavior, since injection of the iPLA₂β inhibitor bromoenol lactone (BEL) into the rat striatum, thalamus, or motor cortex produces chewing movements [18]. Furthermore, iPLA₂β^{-/-} mice exhibit age-dependent motor dysfunction associated with axonal degeneration and spheroids in the central nervous system by 1 year of age [16, 19]. Similar axonal swelling with spheroids occurs in the central and peripheral nervous systems of INAD and NBIA patients. Thirteen month-old iPLA₂β^{-/-} mice also show cerebellar atrophy with Purkinje cell loss, increased levels of inflammatory cytokines, glial cell activation, and striatal accumulation of α-synuclein [16, 20].

To characterize progressive age-related neuropathology in iPLA₂β^{-/-} mice, we first studied brain PUFA metabolism in 4-month old mice with normal motor function and minimal brain spheroid accumulation [4, 21]. Compared to wild-type (WT) controls, these mice exhibited disturbances in brain DHA metabolism that included reduced esterified brain DHA concentration in ethanolamine and serine glycerophospholipids, reduced DHA incorporation rate from plasma into brain phospholipids at rest or during cholinergic activation, and disturbed fatty acid concentrations in lysophospholipids. In addition, their brains showed increased expression of enzymes involved in arachidonic acid (AA, 20:4n-6) metabolism, including cytosolic cPLA₂-IVα (cPLA₂α), secretory sPLA₂-V and cyclooxygenase (COX)-2 [8, 22].

In the present follow-up study, we measured expression of a number of brain parameters in 15 to 20-month old iPLA₂β^{-/-} mice and in WT mice. These included: (1) enzymes involved in AA metabolism [cPLA₂α, sPLA₂-V, COX-2, COX-1, and microsomal prostaglandin synthase (mPGES) [22]]; (2) enzymes involved in DHA metabolism [acyl-CoA synthetase (Acsl)-6, membrane-bound *O*-acyltransferase (MBOAT)-7, acyl-CoA:lysophosphatidylethanolamine acyltransferase (LPEAT)-2, and 15-lipoxygenase (15-LOX)]; (3) inflammatory cytokines [tumor necrosis factor (TNF)-α and interleukin (IL)-1β]; (4) markers of microglial and astrocytic activation [CD11b, glial fibrillary acidic protein (GFAP), and inducible nitrite oxide synthase (iNOS)]; (5) presynaptic synaptophysin, postsynaptic drebrin and postsynaptic density protein (PSD-95); (6) brain derived neurotrophic factor (BDNF); and (7) Parkinson disease markers [dopamine active reuptake transporter (DAT), α-synuclein, PTEN induced kinase 1 (Pink1) and Parkin].

An abstract of part of this work has been published (Society for Neuroscience Meeting, New Orleans, LA, 2012).

Materials and Methods

Animals

Experiments were conducted in accord with the National Institutes of Health guidelines for the Animal Care and Use Committee (Publication no. 86-23) and followed a protocol approved by the Animal Care and Use Committee of the Eunice Kennedy Shriver National Institute of Child Health and Human Development. Male iPLA₂β^{-/-} mice and their WT littermates [23] were housed in an animal facility having regulated temperature, humidity and light cycle until they reached 15–20 months of age. They had free access to water and to a diet (PicoLab[®] Rodent Diet 20, 5053, LabDiet, Richmond, IN) containing (as % total fatty acid): 20.0 % saturated, 22.2 % monounsaturated, 47.7 % linoleic acid, 5.1 % linolenic acid, 0.1 % AA, 0.2 % eicosapentaenoic acid and 0.9 % DHA. Mice (n = 8 per group) were asphyxiated by CO₂ inhalation and decapitated, and their brains were rapidly excised and frozen in 2-methylbutane at -50 °C and stored at -80 °C for subsequent analyses.

Gene Expression

Half brains were homogenized with an Ultraturax homogenizer (IKA Works, Wilmington, DE) in QIAzol lysis reagent (Qiagen, Valencia, CA) and mRNA was isolated with a phenol–chloroform extraction method using the RNeasy Lipid tissue kit (Qiagen). Total mRNA was reverse-transcribed to cDNA according to the manufacturer's instructions with a high capacity cDNA Archive kit (Applied Biosystems, Carlsbad, CA). Gene expression was determined by real time-polymerase chain reaction (RT-PCR) using the Taqman[®] Universal PCR Mastermix and specific Taqman[®] primers and probe (Applied Biosystems). The PCR reaction was performed in duplicate, using ABI Prism 7000 sequence detection system (Applied Biosystems) as follows: 2 min at 50 °C, 5 min at 95 °C, 40 cycles of 10 s at 95 °C, and 1 min at 60 °C. Relative gene expression was determined using the ΔΔCt method, using the *18S* gene expression for normalization.

Protein Extraction

Half-brains were homogenized in a buffer containing 10 mM HEPES, pH 7.5, 1 mM EDTA, 0.34 M sucrose and protease inhibitors (Complete EDTA-free, Roche Applied Science, Indianapolis, IN), using a Dounce glass homogenizer (Thomas Scientific, Swedesboro, NJ). After ultracentrifugation (100,000g, 1 h, 4 °C), the supernatant was used as the cytosolic fraction. The pellet was resuspended in Tris 20 mM, pH 7.4 containing 0.2 % Triton X-100 for

1 h at 4 °C under agitation. The sample was centrifuged (100,000g, 1 h, 4 °C) and the resulting supernatant contained the membrane fraction. Protein concentrations in the cytosolic and membrane fractions were determined with a Bradford assay [24] and samples were stored at –80 °C until analyzed.

Protein Analysis

Cytosolic or membrane proteins (20 µg) were separated by SDS-PAGE in 4–20 % Tris–HCl polyacrylamide gels (Bio-Rad, Hercules, CA) and transferred on a nitrocellulose membrane (Bio-Rad) for immunoblotting. Membranes were blocked for 90 min at room temperature with a casein-based blocking buffer (Sigma Aldrich, St Louis, MO) before incubation overnight at 4 °C with primary antibodies. Cytosolic proteins were probed with specific antibodies for cPLA₂α (1:500), sPLA₂-V (1:500), iNOS (1:200), COX-1 (1:200), IL-1β (1:200), 15-LOX (1:200), drebrin (1:500) and Pink1 (1:200) (Santa Cruz Biotechnology, Santa Cruz, CA), for COX-2 (1:200), GFAP (1:50,000), PSD-95 (1:1,000), BDNF (1:1,000) (AbCam, Cambridge, MA), for Acs1-6 (Novus Biochemical, Littleton, MO) or for α-synuclein (1:5,000) (Cell signaling, Danvers, MA). Membrane fractions were blotted with antibodies targeting phosphorylated-cPLA₂α (P- cPLA₂α) (1:500, Santa Cruz), mPGES (1:500, Cayman Chemical, Ann Arbor, MI), CD11b (1:500), synaptophysin (1:15,000) (AbCam), MBOAT7 (Aviva Systems Biology, San Diego, CA), LPEAT2 (1:1,500) (ProteinTech, Chicago, IL) and DAT (1:1,000) (Millipore, Billerica, MA). All samples were probed with a β-actin antibody (Sigma Aldrich). Parkin expression was determined in the cytosol and membrane fractions (1:2,000, AbCam). Membranes then were incubated for 90 min at room temperature with the appropriate horseradish peroxidase-conjugated secondary antibodies (Bio-Rad), and peroxidase activity was determined by chemiluminescence using the SuperSignal West Pico reagents (Thermo Fisher Scientific, Rockford, IL). Relative protein expression was determined after normalization with the β-actin expression using ImageJ software [25]. TNF-α protein was quantified from 100 µg of brain cytosolic extract using an enzyme-linked immunosorbent assay (ELISA) method according to the manufacturer's instruction (Thermo Fisher Scientific).

Statistical Analyses

Data are expressed as mean ± SEM (n = 7–8 per group). A two-tailed, unpaired *t* test using GraphPad Prism 5 software (GraphPad Software, Inc., La Jolla, CA) was used to determine statistical significance, when *P* < 0.05. Cohen's *d* effect size was used to interpret differences between the means when the *P* value was between 0.05 and 0.2, since this

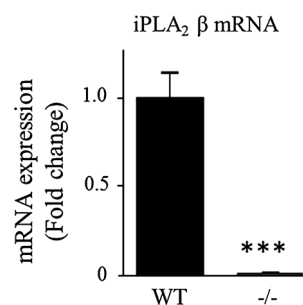


Fig. 1 mRNA expression of iPLA₂β in WT and iPLA₂β^{-/-} mice. mRNA was quantified in duplicate with Taqman[®] RT-PCR using the ΔΔCt method and normalization to 18S expression. Results are expressed as mean ± SEM (n = 8). ****P* < 0.001 (*t* test)

suggested increased risk of type II error associated with the small number of animals available for the study. An effect size is considered small if 0.3 < *d* < 0.5, medium if 0.5 < *d* < 0.8 and high if *d* > 0.8 [26]. We considered effect sizes greater than 0.5 likely to be significant. Outliers were identified using Grubb's test and removed from the statistical analysis.

Results

Brain AA and DHA Metabolism

iPLA₂β protein expression was not measured in this study but iPLA₂β deficiency was confirmed in the iPLA₂β^{-/-} mice by the virtual absence of brain iPLA₂β mRNA compared to WT mice (*P* < 0.001; Fig. 1), whereas the iPLA₂γ mRNA level did not differ between genotypes (Fig. 2c). cPLA₂α mRNA and protein levels were similar between groups, but the protein level of the activated phosphorylated form of cPLA₂α in the membrane fraction was significantly higher for iPLA₂β^{-/-} compared to WT mice (51 %, *P* = 0.04) (Fig. 2a). Although sPLA₂-V mRNA also was higher (64 %, *P* = 0.02), sPLA₂-V protein did not differ significantly between genotypes (Fig. 2b). COX-1 mRNA and protein and COX-2 mRNA also did not differ between genotypes (Fig. 3a), while COX-2 protein was reduced in iPLA₂β^{-/-} mice (12 %, *P* = 0.03) (Fig. 3b). Brain mPGES mRNA was significantly higher in iPLA₂β^{-/-} mice, but mPGES protein did not differ between genotypes (Fig. 3c). Protein levels of Acs1-6, MBOAT7, LPEAT2 and 15-LOX also did not differ between iPLA₂β^{-/-} and WT mice (Fig. 4).

Neuroinflammation and Synaptic Loss

TNF-α mRNA was increased 2.1-fold (*P* < 0.001) in iPLA₂β^{-/-} mice compared to WT, but TNF-α protein levels were similar in both groups (Fig. 5a), as were levels of IL-1β mRNA and protein (Fig. 5b). iNOS mRNA and

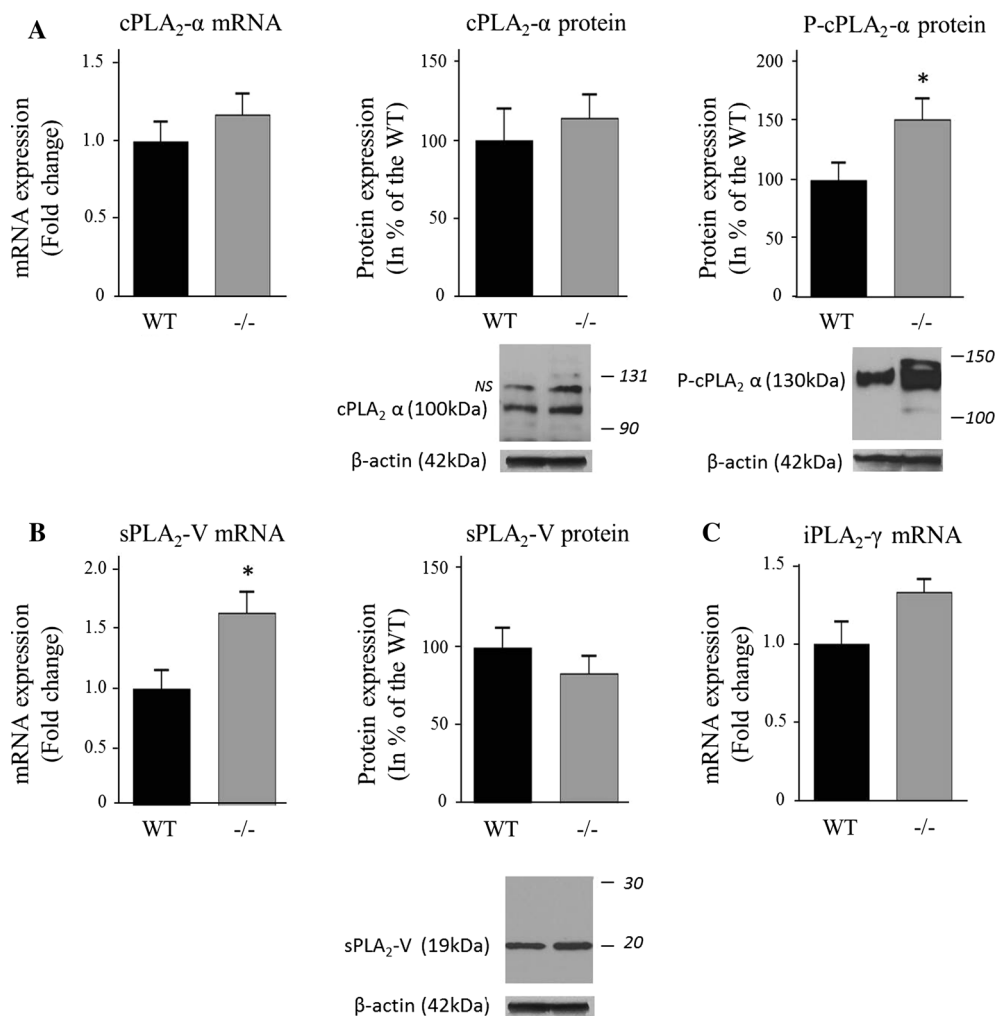


Fig. 2 Expression of cPLA₂α (a), sPLA₂-V (b) and iPLA₂γ in WT and iPLA₂β^{-/-} mice. mRNA was quantified in duplicate with Taqman[®] RT-PCR using the $\Delta\Delta C_t$ method and normalization to *18S* expression. Results are expressed as mean \pm SEM (n = 8). cPLA₂α and sPLA₂-V protein was measured in brain cytosol and P-cPLA₂α was quantified in the membrane fraction by Western blot. Results are

normalized to β -actin expression (representative immunoblot is displayed) and expressed as % of the WT mice as mean \pm SEM (n = 8, except n = 7 for P-cPLA₂ in iPLA₂β^{-/-} because an outlier value of 7.4 was removed). *Numbers in italics* indicate molecular weight markers (in kDa), *NS* : non-specific band. **P* < 0.05 (*t*-test)

protein did not differ significantly on *t* tests (*P* = 0.07 and 0.14 respectively), but their effect sizes measured as Cohen's *d* were large, 0.99 and 0.98 respectively (Fig. 5c).

CD11b mRNA and protein levels were significantly higher in iPLA₂β^{-/-} mice compared to WT (60 and 30 %, *P* < 0.05, respectively) (Fig. 6a), suggesting microglial activation [27]. GFAP mRNA was elevated 2.2-fold (*P* < 0.01) in iPLA₂β^{-/-} mice, but its protein level did not differ significantly between genotypes on *t*-tests (*P* = 0.19); nevertheless, Cohen's *d* test suggested a modest increase (*d* = 0.68) in iPLA₂β^{-/-} mice (Fig. 6b). Protein levels of pre-synaptic synaptophysin and post-synaptic drebrin and PSD95 did not differ between genotypes (Fig. 6c), while BDNF protein was reduced in iPLA₂β^{-/-} mice (22 %, *P* = 0.01) (Fig. 6d).

Parkinson Disease Markers

Protein levels of both reduced DAT (50 kDa) and non-reduced DAT (75 kDa) did not differ between iPLA₂β^{-/-} mice and WT mice (Fig. 7). Alpha-synuclein mRNA was significantly higher (53 %, *P* = 0.01), but α -synuclein protein (Fig. 8a), Pink1 (Fig. 8b) and Parkin (Fig. 8c) mRNA and protein did not differ between groups.

Discussion

These results indicate that long-term disruption of brain DHA metabolism in aged mice due to the absence of PLA2G6 results in microglial and astrocytic activation,

Fig. 3 Expression of COX-2 (a), COX-1 (b) and mPGES (c) in WT and iPLA₂ $\beta^{-/-}$ mice. mRNA was quantified in duplicate with Taqman[®] RT-PCR using the $\Delta\Delta C_t$ method and normalization to *18S* expression. Results are expressed as mean \pm SEM (n = 8). COX-2, COX-1 were measured in brain cytosol and mPGES in the membrane fraction by western blot and normalized to β -actin expression (representative immunoblot is displayed). Results are expressed as % of the WT mice as mean \pm SEM (n = 8, except n = 7 for COX-1 protein in WT due to an outlier value of 198^{-/-}). Numbers in italics indicate molecular weight markers (in kDa). **P* < 0.05, ***P* < 0.01 (*t* test)

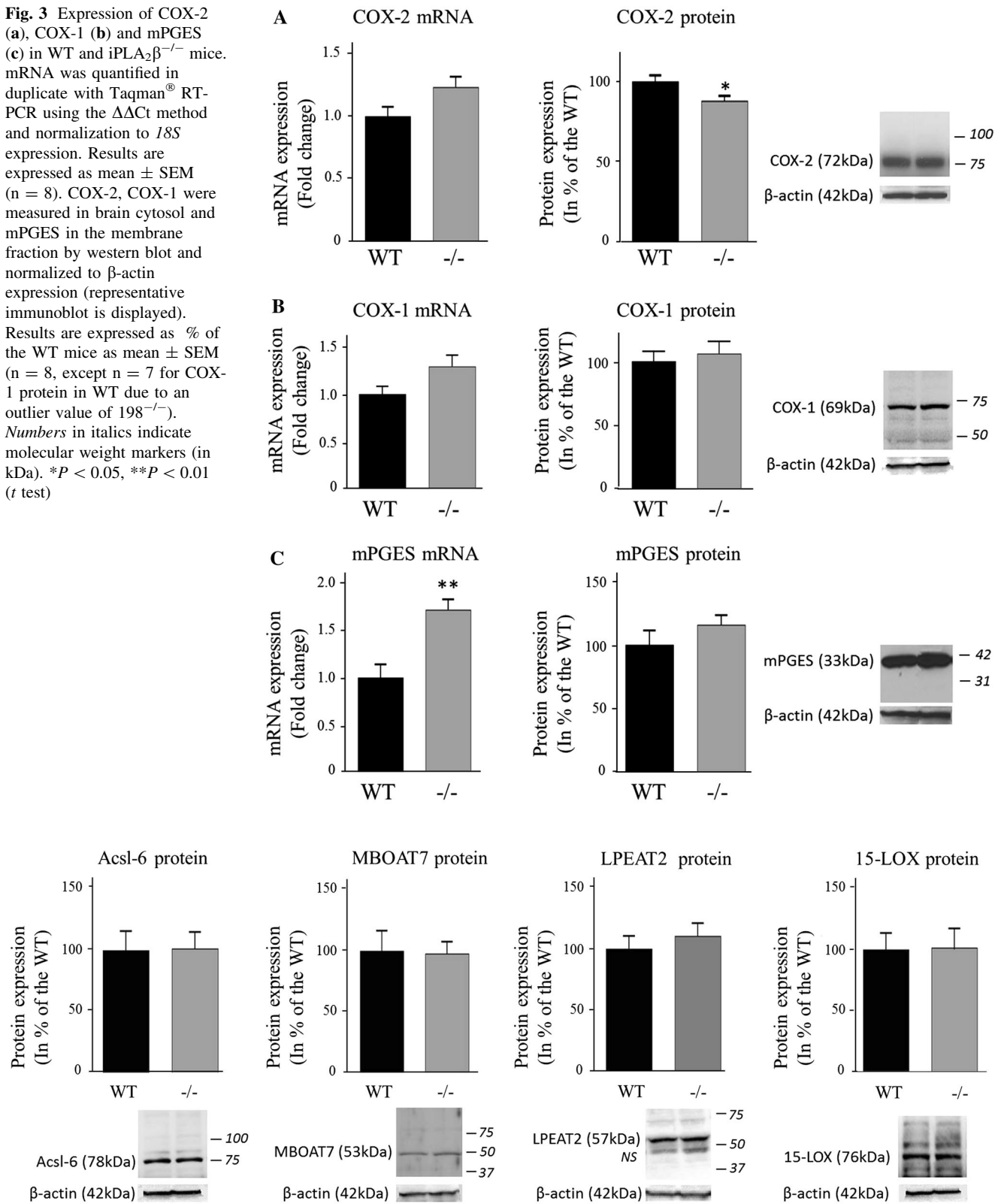


Fig. 4 Expression of brain DHA-metabolizing enzymes in WT and iPLA₂ $\beta^{-/-}$ mice. Acs1-6 and 15-LOX protein was measured in brain cytosol, MBOAT7 and LPEAT2 in the membrane fraction by Western blot and normalized to β -actin expression (representative

immunoblot is displayed). Results are expressed as % of the WT mice as mean \pm SEM (n = 8). Numbers in italics indicate molecular weight markers (in kDa), NS non-specific band

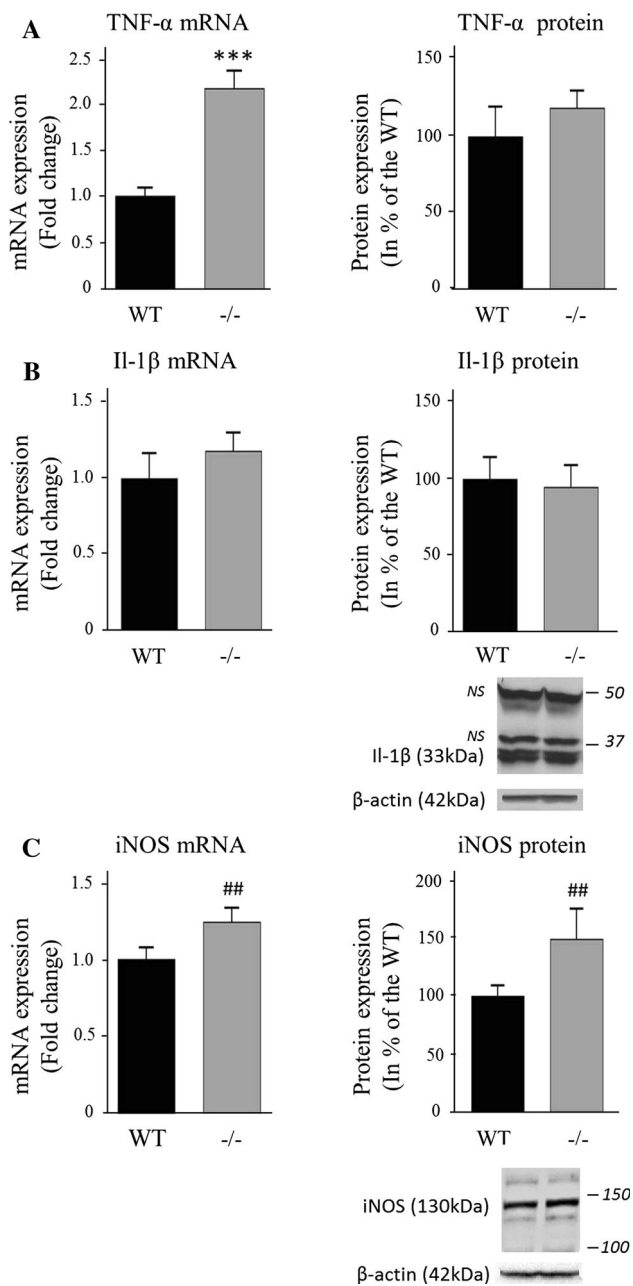


Fig. 5 Expression of the pro-inflammatory cytokines TNF- α (a) and Il-1 β (b) and the iNOS (c) in WT and iPLA $_2\beta^{-/-}$ mice. mRNA was quantified in duplicate with Taqman[®] RT-PCR using the $\Delta\Delta C_t$ method and normalization to 18S expression. Results are expressed as mean \pm SEM (n = 8). An ELISA assay was used to quantify cytosolic TNF- α . Il-1 β and iNOS protein was measured in brain cytosol by Western blot and normalized to β -actin expression (representative immunoblot is displayed). Results are expressed as % of the WT mice as mean \pm SEM (n = 8, iNOS n = 6 for WT and n = 7 for iPLA $_2^{-/-}$ due to unquantifiable signal). Numbers in italics indicate molecular weight markers (in kDa), NS non-specific band. ***P < 0.001 (t test) and ##d > 0.8 (Cohen’s d test)

increased TNF- α and α -synuclein, disturbed expression of enzymes involved in AA metabolism, and a reduced BDNF level. The results also show that iPLA $_2\beta$ and iPLA $_2\gamma$ play

independent roles in brain, because brain iPLA $_2\gamma$ expression was unchanged iPLA $_2\beta^{-/-}$ mice. The large effect sizes of increments in iNOS mRNA and protein and in TNF- α mRNA (and protein by Cohen’s d), and increased CD11b mRNA and protein, suggest microglial activation by age 15–20 months [27]. Motor function was not assessed in the present study, but these neuropathological markers might be associated with appearance of age-dependent motor abnormalities in iPLA $_2\beta^{-/-}$ mice reported by others [16, 19]. The lack of change in IL-1 β levels suggests that full-blown global inflammation is not reached at this age and may require more time to evolve. On the other hand, Purkinje cell loss, glial cell activation and elevated TNF- α and IL-1 β expression have been reported in the cerebellum of iPLA $_2\beta^{-/-}$ mice at age 13 months [20].

The many late-appearing neuropathological changes in the iPLA $_2\beta^{-/-}$ mice suggest that early defective DHA metabolism can contribute to human diseases that result from PLA2G6 mutations, such as INAD, neurodegeneration with brain iron accumulation, and early onset-dystonia parkinsonism (see ‘Introduction’). Thus, this mouse model might be used to develop therapy for these diseases. Since iPLA $_2\beta$ has an anti-oxidant function that protects mitochondria from peroxidation damage [17], one therapeutic approach with the model would be to administer antioxidants, as recommended for Parkinson disease [17, 28, 29]. Feeding DHA has been considered in this regard [2], but the mice already were on a high DHA diet. On the other hand, an AA-free diet low in linoleic acid (18:2n-6) might help to dampen the upregulated AA-metabolizing enzymes in the iPLA $_2\beta^{-/-}$ mouse brain [30–32].

Unesterified DHA is preferentially acylated by Acs1-6 to DHA-CoA [33], which can be reacylated into a lysophospholipid by an acyl-CoA lysophospholipid acyltransferase [34]. Within this latter enzyme family, we analyzed expression of MBOAT7, which recognizes AA-CoA as a substrate [35], although its activity toward DHA-CoA remains to be tested. We also measured LPEAT2, which preferentially acylates ethanolamine glycerophospholipid enriched with DHA [36, 37]. The incorporation rate of unesterified DHA into brain ethanolamine glycerophospholipids and their DHA content are reduced in 4-month old iPLA $_2\beta^{-/-}$ mice [4, 21], but we found no significant difference between genotypes in brain expression of these acyltransferases or of 15-LOX, which is also involved in DHA metabolism [38].

Reduced DHA incorporation from plasma into brain in iPLA $_2\beta^{-/-}$ mice would be expected to reduce production of DHA-derived resolvin D1 and neuroprotectin D1, which have potent anti-inflammatory properties [39, 40]. DHA also may reduce pro-inflammatory AA metabolite production by inhibiting COX-2 [1, 41], consistent with the suggested role of iPLA $_2\beta$ in regulating prostaglandin E $_2$ formation [7]. It would be worthwhile to test whether

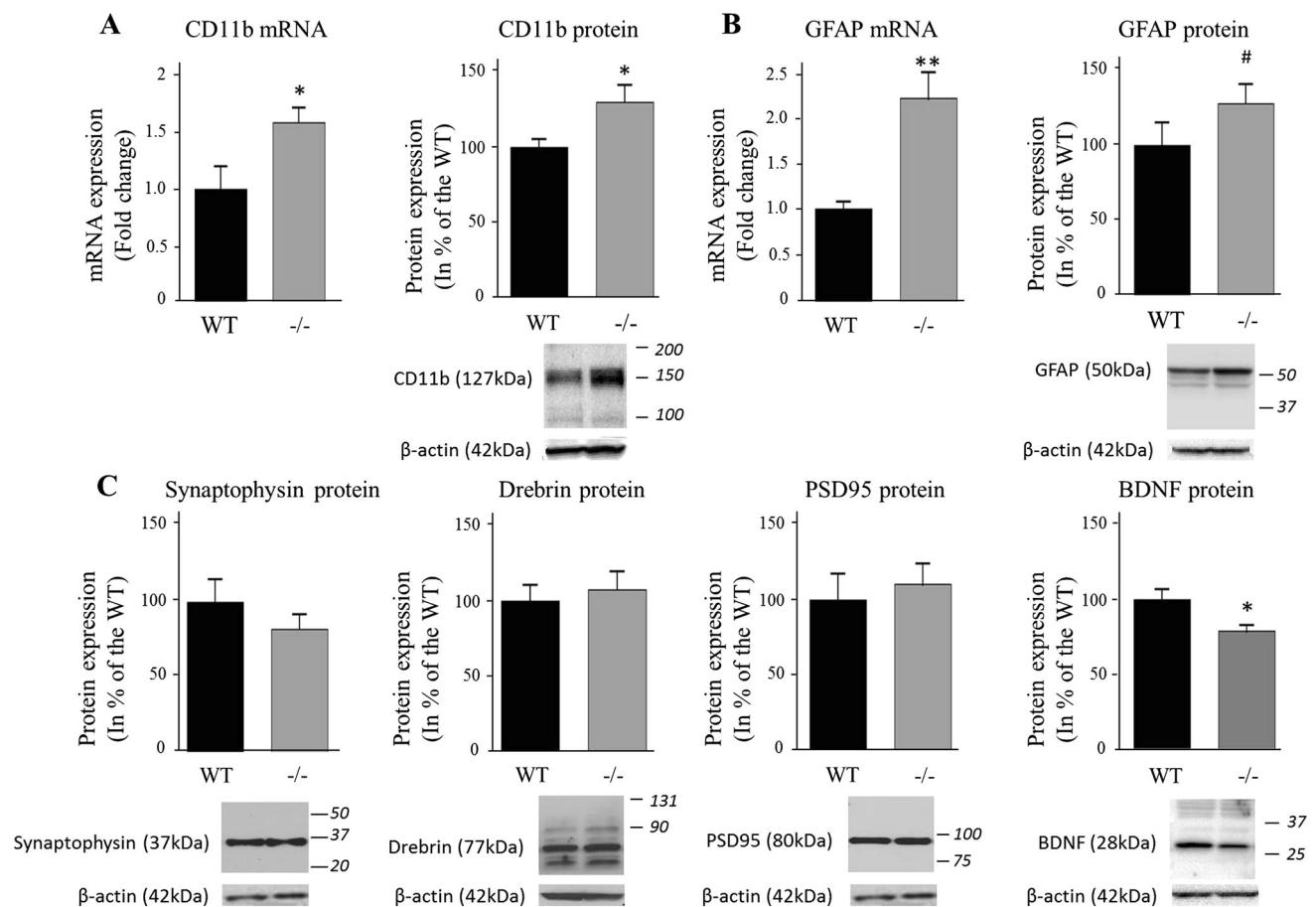


Fig. 6 Expression of microglial, astrocytic, synaptic markers and BDNF in WT and $iPLA_2\beta^{-/-}$ mice. mRNA was quantified in duplicate with Taqman[®] RT-PCR using the $\Delta\Delta Ct$ method and normalization to $I\delta S$ expression. Results are expressed as mean \pm SEM ($n = 8$). CD11b, synaptophysin and PSD-95 expression was measured in brain membrane fractions by Western blot and GFAP, drebrin and BDNF were quantified in the cytosol. Results are

normalized to β -actin expression (representative immunoblot is displayed) and expressed as % of the WT mice as mean \pm SEM ($n = 8$ except $n = 7$ for BDNF in WT and $iPLA_2\beta^{-/-}$, respectively due to the removal of an outlier value of 222 and sample loss). Numbers in italics indicate molecular weight markers (in kDa). * $P < 0.05$, ** $P < 0.01$ (t test) and # $0.5 < d > 0.8$ (Cohen's d test)

$iPLA_2\beta^{-/-}$ mice have reduced DHA-derived metabolites and increased AA-derived products in future studies.

The elevated brain levels in $iPLA_2\beta^{-/-}$ mice of $sPLA_2-V$ mRNA and P- $cPLA_2\alpha$ protein, which represents the catalytically active form of $cPLA_2\alpha$, suggests compensatory upregulation of brain AA metabolism [42]. Upregulation also occurs when DHA metabolism is reduced by dietary n-3 fatty acid deprivation [43]. Increased P- $cPLA_2\alpha$ protein suggests accelerated post-translational phosphorylation of $cPLA_2\alpha$ serine residues [44]. COX-2 expression was reduced, although it was reported to be elevated at 4 months [21]. Expression of COX-1, which can be coupled to $iPLA_2\beta$ [45], was unchanged.

Similar protein levels of drebrin, PSD95, synaptophysin and DAT in the 15-20 month old $iPLA_2\beta^{-/-}$ and WT mice suggest absence of synaptic loss. On the other hand, presynaptic DAT protein is reduced in Parkinson

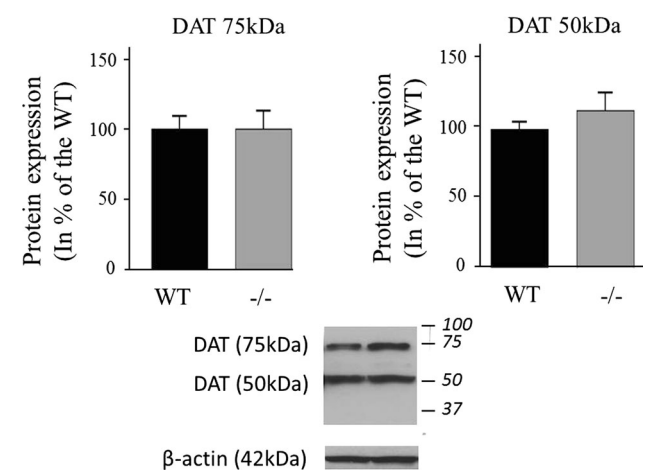
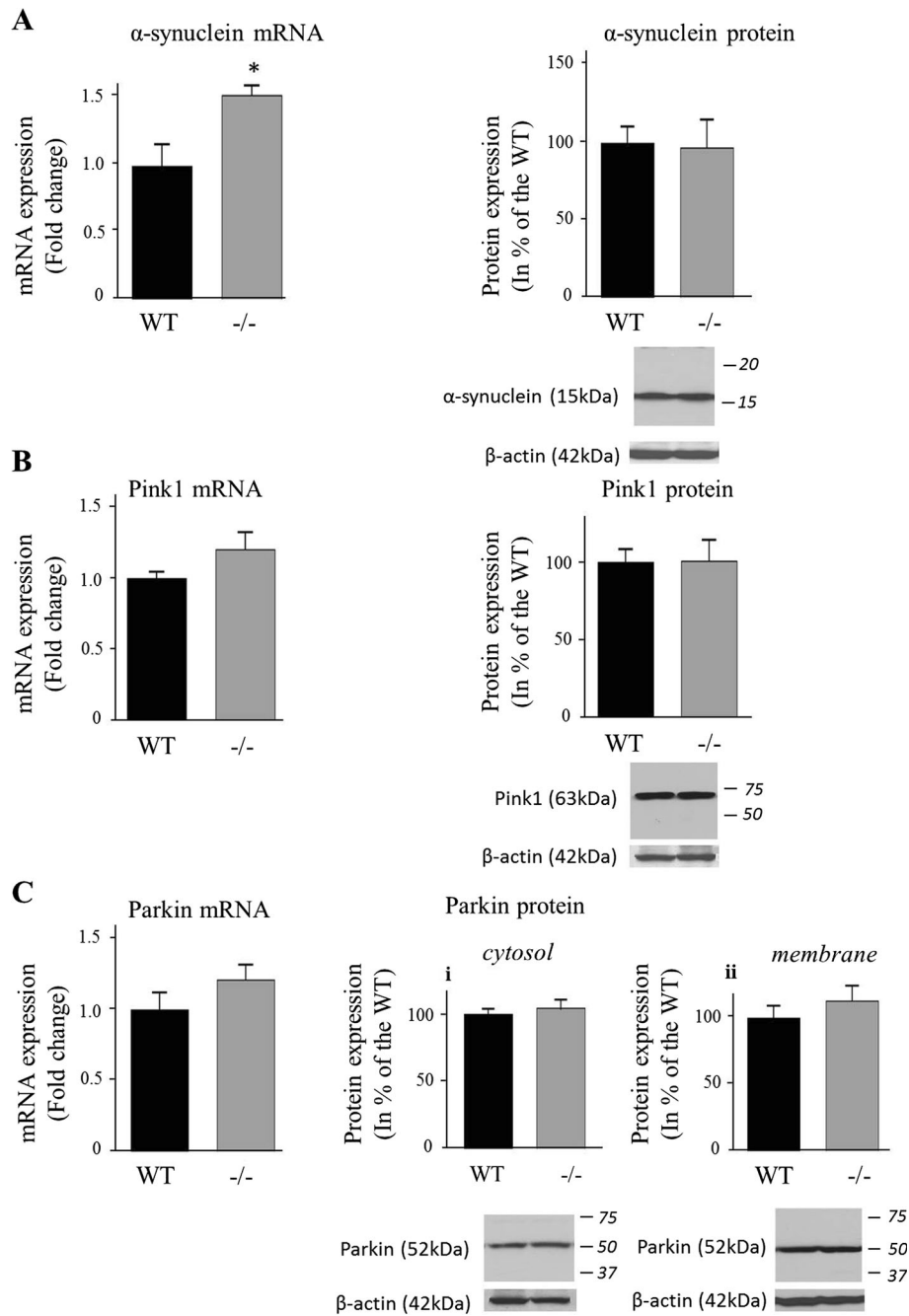


Fig. 7 Expression of DAT in WT and $iPLA_2\beta^{-/-}$ mice. DAT protein was measured in brain membrane fractions by Western blot. Results are normalized to β -actin expression (representative immunoblot is displayed) and expressed as % of WT mice as mean \pm SEM ($n = 8$). Numbers in italics indicate molecular weight markers (in kDa)

Fig. 8 Expression of α -synuclein (a), PINK1 (b) and Parkin (c) in WT and $iPLA_2\beta^{-/-}$ mice. mRNA was quantified in duplicate with Taqman[®] RT-PCR using the $\Delta\Delta Ct$ method and normalization to *18S* expression. Results are expressed as mean \pm SEM (n = 8). α -synuclein (a) and PINK1 (b) were quantified in the cytosolic fraction. Both cytosolic (c-i) and membrane (c-ii) parkin protein levels were determined. After normalization to β -actin expression (representative immunoblot is displayed), results are expressed as % of the WT mice as mean \pm SEM (n = 8, n = 7 for α -synuclein WT (outlier value of 241 was removed) and for n = 7 for Pink1 due to an unquantifiable signal). Numbers in italics indicate molecular weight markers (in kDa). **P* < 0.05 (*t* test)



disease [46], and following ablation of the substantia nigra in rodent models of Parkinson disease [47]. Thus, at 15–20 months, the model does not have all the classical features of Parkinson disease. This also applies to the absence of differences in expression of Parkin (*Park2*) [48] and of Pink1 (*Park6*) [49], which regulate mitochondrial integrity [50]. Regional changes potentially identifiable by immunocytochemistry cannot yet be excluded, especially in the substantia nigra, which is specifically impacted by dopaminergic neuronal loss in Parkinson disease.

Activated microglia produce NO via iNOS, reactive oxygen species, and pro-inflammatory cytokines that might contribute to brain pathology in Parkinson disease [51, 52]. Reduced BDNF expression in the older $iPLA_2\beta^{-/-}$ mice also suggests increased susceptibility to neuronal death [53], which is observed in the substantia nigra of Parkinson disease patients [54].

Brain α -synuclein mRNA was increased in the older $iPLA_2\beta^{-/-}$ mice, consistent with reported α -synuclein-positive spheroids in the striatum of $iPLA_2\beta^{-/-}$ mice [16]. Alpha-synuclein can activate glia [55] and is thought to

promote a self-perpetuating neurotoxic process in Parkinson disease [52]. It impacts PUFA metabolism [56] and may bind long chain fatty acids [57]. On the other hand, dietary DHA supplementation was reported to promote α -synuclein accumulation in a mouse model of Parkinson disease [58].

An iPLA₂ β preference for DHA-containing phospholipid substrates is well established [4, 6, 7, 59], but esterified AA also can be hydrolyzed by iPLA₂ β [60, 61]. Thus, an iPLA₂ β deficiency also might influence AA release and eicosanoid formation.

In summary, life-long distortion of brain DHA content and metabolism in iPLA₂ β ^{-/-} mice is associated with late-appearing motor disturbances accompanied by microglial and astrocytic activation, disturbed expression of enzymes involved in arachidonic acid metabolism, loss of neuroprotective BDNF, and increased neuroinflammatory cytokine expression. Using these biomarkers, efficacy of dietary interventions or suppressors of oxidative stress might be tested on disease progression in this animal model, which mimics many aspects of human progressive motor diseases, including Parkinson disease.

Acknowledgments The authors thank the NIH Fellow Editorial Board and Ms. Mairi Stevens for editorial assistance and Dr. Dede Greenstein for statistical support. Research was supported by the Intramural Research Program of the National Institute on Aging and, for JT, by United States Public Health Service Grants R37-DK34388, P41-RR00954, P60-DK20579, and P30-DK56341.

Conflict of interest Authors declare no competing financial interests.

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