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Alpha-Synuclein Abnormalities in Mouse Models of Peroxisome Biogenesis Disorders

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Abstract

alpha-Synuclein (α S) is a presynaptic protein implicated in Parkinson's disease (PD). Growing evidence implicates mitochondrial dysfunction, oxidative stress and α S-lipids interactions in the gradual accumulation of α S in pathogenic forms and its deposition in Lewy bodies, the pathological hallmark of PD and related synucleinopathies. The peroxisomal biogenesis disorders (PBD), with Zellweger syndrome serving as the prototype of this group, are characterized by malformed and functionally impaired peroxisomes. Here we utilized the PBD mouse models, *Pex2*^{-/-}, *Pex5*^{-/-} and *Pex13*^{-/-}, to study the potential effects of peroxisomal dysfunction on α S-related pathogenesis. We found increased α S oligomerization and phosphorylation and its increased deposition in cytoplasmic inclusions in these PBD mouse models. Further, we show that α S abnormalities correlate with the altered lipid metabolism and specifically, with accumulation of long chain, n-6 polyunsaturated fatty acids, that occurs in the PBD models.

Keywords

Parkinson's disease; lipids; alpha synuclein; peroxisomes

Introduction

α -Synuclein (α S) is a presynaptic protein critically involved in the cytopathology and genetics of Parkinson's disease (PD) (reviewed in (Hardy et al. 2006; Lee and Trojanowski 2006; Moore 2005)). In PD and related human synucleinopathies (Duda et al. 2000), there is a progressive conversion of the normally highly soluble α S protein into insoluble, β -sheet rich filamentous assemblies, resulting in its intraneuronal deposition into Lewy bodies (LB) and Lewy neurites, the cytopathological hallmarks of this group of disorders (Goedert 2001; Spillantini et al.

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1997). However, a biochemical event that occurs prior to these pathological lesions is the cellular accumulation of various α S post translational modifications, including phosphorylation (Fujiwara et al. 2002) (Smith et al. 2005), ubiquitination (Iwatsubo et al. 1996), nitration (Giasson et al. 2000) and oligomerization (Sharon et al. 2003a). The cellular triggers that enhance the accumulation of modified α S proteins and how these pathogenic post-translational modifications enhance α S deposition into the Lewy bodies and Lewy neurites are unknown.

Peroxisomes are involved in cellular metabolic activities including a) β -oxidation of very long chain fatty acids (VLCFA) as well as long chain polyunsaturated fatty acids (PUFAs) (Poulos et al. 1989; Poulos et al. 1988; Sharp et al. 1987) and branched chain fatty acids, b) the conversion of cholesterol to bile acids, and c) the synthesis of ether phospholipids including plasmalogens (Poulos et al. 1988; Robinson et al. 1990; Sharp et al. 1987; Su et al. 2001). Peroxisome biogenesis disorders (PBD) are a group of human genetic disorders, with Zellweger syndrome being the most severe form, that are characterized by the absence of functional peroxisomes due to a disturbance in the peroxisomal protein import machinery (reviewed in (Wanders and Waterham 2005) (Gould et al. 2001)). PBD are caused by mutations in peroxin (Pex) genes encoding proteins involved in the biogenesis and assembly of peroxisomes. Three different Pex genes have been inactivated in the mouse, i.e., Pex2, Pex5 and Pex13 (Baes et al. 1997; Faust and Hatten 1997; Maxwell et al. 2003), in order to generate mouse models for PBD. Importantly, most of the major metabolic and neuronal abnormalities observed in ZS are recapitulated to varying degrees in these three PBD mouse models.

Three major biochemical insults attributable to peroxisomal dysfunction have been described in ZS and the related PBD mouse models: altered lipid metabolism, increased vulnerability to oxidative stress, and mitochondrial dysfunction ((Dirkx et al. 2005; Keane et al. 2007; Maxwell et al. 2003) reviewed in ((Baes and Van Veldhoven 2006; Wanders and Waterham 2005)). Interestingly, these types of insults have also been shown to be involved in PD pathogenesis (reviewed in (Abou-Sleiman et al. 2006; Halliwell 2001; Moore 2005; Scherzer and Feany 2004)). However, the role of peroxisome function in PD has not been tested before.

Here, we used PBD mouse models to study the potential cellular mechanisms underlying α S modification and toxicity in PD. We specifically focused on the shared insults between PD and PBD -- oxidative stress, mitochondrial dysfunction and lipid metabolism -- for their effect on α S oligomerization, phosphorylation and accumulation in Lewy-like inclusions. We show that α S toxicity correlates with altered lipid metabolism and specifically with an elevation of n-6 PUFA concentrations rather than with oxidative stress or mitochondrial dysfunction.

Materials and Methods

Mouse brains

Brains of newborn mice of Pex^{-/-} and control Pex^{+/+} littermates were immediately frozen and shipped to the Hebrew University of Jerusalem. All protocols for animal use and experiments were reviewed and approved by the Institutional Animal Care and Use Committee of Columbia University (Faust and Hatten 1997); University of Leuven (Baes et al. 1997) and Griffith University (Maxwell et al. 2003). Brains were fractionated (Sharon et al. 2001) and samples were processed for oligomers detection. Overall we tested 5-7 brains for each Pex^{-/-} and control groups.

α S over expression

Pex5^{-/-} and control fibroblasts were stably transfected with wt human α S cDNA in the pCDNA 3.1 vector or vector only using Lipofectamine 2000 (Invitrogen CA, USA). The clones were

tested for α S expression every week and maintained their stable α S expression for 3-4 months post transfection (Sharon et al. 2001).

Viral infection of α S expressing virus, the α S cDNA was amplified and sub-cloned into a pADlox vector and used for adenovirus production (Hardy et al. 1997). Recombinant adenovirus encoding α S was produced as described previously (Altschuler et al. 1998; Altschuler et al. 1999). Cells were transduced with α S- expressing adenovirus and GFP control virus (to compare gene transfer efficiency, at ~100 PFU/cells) for 2 hours and the unbound virus was removed by 3 washes in saline. Cells were then maintained in standard serum-supplemented medium for additional 16-18 hours, collected and fractionated as previously described (Sharon et al. 2001).

Western blot

Whole mouse brains were homogenized (20 up-and-down strokes with a Teflon homogenizer, followed by seven passages through a 27-gauge needle) in 1:10 (w/vol) homogenization buffer [20 mM Hepes, pH 7.4, 1 mM MgCl₂, 0.32 M sucrose, 43 mM β -mercaptoethanol, protease inhibitor mix (Sigma), 25 mM β -glycerol phosphate, 20 mM Na-fluoride (Sigma)]. For the detection of α S oligomers and aggregates, protein samples of high speed supernatant (post 280,000 g) were incubated at 65°C for 16-18 hours (Sharon et al. 2003a) prior to loading on an 8-16% NuPAGE Bis-Tris (Invitrogen) or 14% SDS-PAGE. Immunoblots were reacted with H3C anti α S antibody (gift from Julia George, University of Illinois) (George et al. 1995) or Syn-1 (BD Transduction Labs, San Jose, CA), or anti phospho Ser129 α S antibody (Wako-Chem, Osaka, Japan).

Immunocytochemistry

For immunostaining, cells were pre- permeabilized with 0.002% Triton X-100 in PBS for 1 minute. Cells were then fixed with 4% paraformaldehyde for 10 minutes on ice and permeabilized with 0.2% Triton X-100 in PBS and 1% goat serum for 5 minutes at room temperature. The slides were next treated with 10% formic acid (pH 2.0) for 10 minutes at room temperature followed by extensive washes and blocking with 1.5% goat serum in PBS. Slides were then reacted with primary antibodies: anti α S monoclonal antibody (LB509 1:100 Zymed CA, USA); anti ubiquitin polyclonal antibody (1:100 Dako Glostrup, Denmark) and secondary ab at 1:200, anti mouse-Alexa flour 488 (Molecular probes CA, USA) and anti rabbit-Cy5 (Jackson ME, USA). Slides were sealed with mounting medium (cat# M1289 Sigma Rehovot, Israel) and analyzed by confocal microscopy with laser Argon 488 (filter BA 510 IF dichroic mirror filter) and laser helium neon 633 (filter BA 660 IF) (Laser Scanning microscope Zeiss 410, Germany). Total signal per cell was counted and using Image Pro/Image J softwares (Media Cybernetics Inc., Silver Spring, MD). The average count of n=10-13 cells is reported.

rtPCR

RNA was isolated from brain tissue using Tri-reagent (Sigma, Rehovot, Israel). Following isolation, RNA was treated with DNase (RQ1 RNase-free DNase, Promega, Beit Ha'emek, Israel). cDNA was generated with GeneAmp RNA PCR kit (Applied Biosystems, CA, USA). Quantitative amplification of α S was performed with ABsolute QPCR SYBR Green ROX mix (ABgene, Epsom, UK) and normalized to 18S levels. The sequence of α S specific primers:

5' GTCTCAAAGCCTGTGGCATCT

3' TCCACACTTTCGACTTCTG

18S specific primers:

5' GAGCGAGTGATCACCATCAT

3' GCCAGAACCTGGCTGTACTT

Mitochondrial purification and respiratory chain complex I measurements

Mitochondria purification—Cells were grown to confluency, collected and washed. Cells were resuspended in buffer A (0.32 M Sucrose; 0.05 M Tris-HCl pH 7.4; 2 mM EDTA) and homogenized by five strokes in a Teflon dounce homogenizer and centrifuged at $1000 \times g$ to remove nuclei. The supernatant was centrifuged at $12,000 \times g$ and the pellet was resuspended in buffer A containing 0.02% digitonin to release mitochondria. Mitochondria were washed to remove digitonin by centrifugation at $12,000g$, resuspended in minimal amount of buffer A and protein content was determined by Bradford (Bradford 1976). Frozen aliquots were stored at $-70^{\circ}C$ until use.

Enzymatic activities of the mitochondrial respiratory chain complex I were determined as rotenone sensitive NADH–cytochrome *c* reductase (I+III) and rotenone-sensitive NADH–coenzyme Q reductase (I). The activity of citrate synthase, a mitochondrial matrix enzyme was determined in parallel. The spectrophotometric assays were performed as previously described (Saada et al. 2004). Respiratory chain activities were normalized to citrate synthase activity in each sample.

Fatty acids analyses

Frozen brain tissue of newborn (P0) Pex2^{-/-} and control mice was thawed briefly, weighed and homogenized in at least 20 volumes of chloroform:methanol 2:1 (Folch et al. 1957) containing 0.05% butyl hydroxytoluene (BHT) (w/vol). After 1 hour at room temperature the samples were centrifuged, and the supernatant was transferred to a weighed tube. 1/5 total volume of water was added and the mixture was centrifuged. The upper phase was removed and the lower phase was dried under N₂ and weighed. The fatty acids were converted to their methyl esters with 1.5 ml 1N methanolic HCL at $75^{\circ}C$ overnight. Following methanolysis, the fatty acid methyl esters were extracted in hexane, dried, solubilized in 50 μ l hexane, transferred to injection vials with glass inserts and 1 μ l was analyzed by capillary gas chromatography on an Agilent 5890 gas chromatograph. Two capillary columns differing in polarity were used to correctly identify and quantitate the fatty acid methyl esters. A 50 meter \times .2u ID \times .11u film OV-1 and a 100 meter \times .2u ID \times .15u film SP-2560 capillary column. The columns are calibrated with the following standards that are injected at the beginning of each set of samples; NIH-F fatty acid methyl ester (fame) mix plus added known concentrations of phytanic, pristanic, C27:0, and C26:0 and the Supelco 37 fame mix. We also mapped out the retention time of the methyl ester of 24:6w3 that was a generous gift from Dr. Howard Sprecher. The samples are first injected on the polar column, the SP-2560; then after the first analysis the sample vials are decapped, hexane added to the original 50 μ l volume, and recapped before analysis on the second, non-polar OV-1 column. The results are collected from the chemstation, the integration and calibration is checked, the calibrated results are then transferred to Excel and the results are compared and merged using Excel macros that were developed for the preparation of combined reports based on the identification and quantitation of the fatty acid methyl esters. Lipids of known fatty acid composition, including brain phosphatidyl ethanolamine for mapping the 16:0, 18:0, 18:1w9 and 18:1w7 plasmalogens, and reagent blanks are analyzed with each set of samples. The lipids were purchased from Matreya (Pleasant Gap, PA. USA). The fatty acid methyl ester mixes and columns were purchased from Supelco Inc, (Bellefonte, PA. USA)

Cell Viability assay

To determine cell viability, cells were plated at a density of 150,000 cells per well in 96 wells in standard medium one day before they were treated with specific media for the time indicated.

The WST-1 (Roche Diagnostics, Germany) assay kit was used to determine the metabolic activity of the cells according to manufacturer recommendations.

Results

Increased α S oligomerization in brains of mice with defective peroxisome biogenesis

To evaluate the involvement of peroxisomes in endogenous α S oligomerization and potential cytotoxicity in vivo, we used three different mouse models of peroxisome biogenesis disorders (PBD), i.e., Pex 2 (Faust and Hatten 1997), Pex 5 (Baes et al. 1997) and Pex 13 (Liu et al. 1999). α S oligomerization was tested in newborn mouse brains (p 0), as Pex mutations are lethal and mice die soon after birth. Whole brains were fractionated (see Methods), and the soluble fraction was probed for the appearance of soluble α S oligomers by western blotting with anti α S antibodies, H3C and Syn-1 with similar results, using heat delipidation for oligomer detection (see Methods). While levels of the α S monomer (~17 kDa) were not altered, enhanced levels of α S oligomers, including dimers (~35 kDa), trimers (~53 kDa) and higher species, were readily detected in the brains of the three Pex $-/-$ mouse models compared to the control Pex $+/+$ littermates (Fig. 1a-d). Therefore, enhanced levels of endogenous α S oligomers occur in mouse brains modeling PBD.

Overall, α S immunoreactivity (including monomer and oligomers) appeared higher in Pex $-/-$ than control Pex $+/+$ brains (Fig. 1 a-c), whereas, tubulin or actin levels on the same blots were not affected (Fig. 1a-c). We quantified the total immuno-reactivity in the different Pex $-/-$ models and found that while monomer levels were only slightly affected, oligomers levels were ~4 fold significantly higher in the different Pex $-/-$ brains compared with the corresponding control Pex $+/+$ littermates (n=4-7 brains, ttest $p<0.01$) (Fig. 1a-c). Increased oligomer levels may result from increased α S expression or increased protein stability and decreased clearance. To exclude the possible effect of peroxisome deficiencies on α S expression levels, we analyzed α S mRNA levels in Pex5 $-/-$ and Pex13 $-/-$ brains compared with their littermate controls (n=5 each). We did not detect a difference in mRNA levels by quantitative RT-PCR (data not shown) and therefore concluded that the effect on α S protein levels observed in brains of PBD mouse models is mediated at the levels of translational/post translational mechanisms.

Increased oligomerization and phosphorylation in Pex 5 $-/-$ fibroblasts expressing human α S

We next over expressed human α S in immortalized fibroblasts from Pex5 $-/-$ and control cells (Amery et al. 1998). Cells were transduced with an α S expressing viral vector and conditioned in parallel in standard serum containing medium for 16 hours. To compare transduction efficiency in the two cell types, we co- transduced a GFP viral vector together with the α S vector and found similar efficacies in the two cell types. Cells were then collected and fractionated, and the soluble fraction was probed for the appearance of soluble oligomers by western blotting with H3C antibody. The result with human α S in Pex 5 $-/-$ -fibroblasts was very similar to the result obtained for endogenous α S in mouse brains with PBDs. A marked accumulation of α S oligomers, including dimers (~35 kDa), trimers (~53 kDa) and higher species, was readily detected in α S over expressing Pex 5 $-/-$ fibroblasts compared to the normal control Pex 5 $+/+$ fibroblasts over expressing α S (Fig. 2). Quantifications of the western blot indicated ~2 fold increase in the ratio of dimer to monomer in the Pex5 $-/-$ cells. To examine α S phosphorylation at serine 129 in Pex 5 $-/-$ and control cells, we probed an identical blot with anti phospho-S129 α S ab. Higher levels of phosphorylated monomer α S and dimers were detected in the α S over expressing Pex5 $-/-$ -compared with the control cells (Fig. 2). Specifically, ~ six fold increase in the densitometric ratio of phospho-dimer to phospho-monomer was detected in the Pex5 $-/-$ cells than in control cells. Therefore, in Pex5 $-/-$ cells, both oligomerization and phosphorylation of α S are induced.

Induced inclusion formation in α S over expressing Pex5^{-/-} fibroblasts

We wished to assess the cytopathological effects of peroxisomal dysfunction on accumulation of α S pathogenic forms, but endogenous mouse α S does not accumulate into Lewy-like inclusions (Kahle et al. 2001). We therefore performed the following experiments in Pex5^{-/-} and control cells stably expressing human α S. The cells were conditioned in standard serum-supplemented medium in parallel and processed for icc using anti- α S and anti-ubiquitin antibodies, two major constituents of the Lewy bodies, as previously done (Assayag et al. 2007). Overall, we detected higher α S signal in the form of discrete granules in the cytoplasm of Pex5^{-/-} than in control cells. This signal was not washed out by pre-permeabilizing the cells (Assayag et al. 2007). Cytoplasmic inclusions that were immunoreactive to both α S and ubiquitin were consistently observed in α S over expressing Pex5^{-/-} cells and only occasionally occurred in the α S over-expressing control cells conditioned in parallel (Fig. 3). Quantification of total α S or ubiquitin signal per cell revealed that the average signal per cell rose ~4-10-fold in the pex^{-/-} clones.

α S alterations in PBD do not correlate with mitochondrial dysfunction

To test the potential role of mitochondrial dysfunction in the accumulation of α S in pathogenic forms in the PBD models, we used the Pex5^{-/-} and control cells with and without stable α S over expression. Previously, it was shown that complex I is inhibited in livers but not in fibroblasts of Pex5^{-/-} mice (Baumgart et al. 2001). In line with these results, we did not detect differences in activities of complex I, measured by NADH- coenzyme Q reductase and normalized to citrate synthase activity (Figure 4a) or complexes I + III measured by reduction of NADH-cytochrome c (reductions by isolated mitochondria) and normalized to citrate synthase (not shown) in naïve Pex5^{-/-} and control fibroblasts. Moreover, complex I (Figure 4a) and I + III (not shown) activities were not affected upon α S over expression. Therefore, the results suggest that mitochondrial dysfunction can not explain α S accumulation in modified forms in the Pex5 PBD model.

α S abnormalities in PBD are not due to induced oxidative stress

Peroxisomes harbor several enzymes that have dual functions, i.e., generation and detoxification of reactive oxygen species (ROS); these include catalase, xanthine oxidase, superoxide dismutase and glutathione peroxidase (Lopez-Huertas et al. 2000; Schrader et al. 1999; Singh 1996). To determine whether oxidative stress is involved in the accumulation of modified forms of α S in the PBD models, we again examined the untransfected and α S-over-expressing Pex5^{-/-} vs. control cells. Cells were maintained in standard serum-supplemented medium in parallel and treated with H₂O₂ at the low concentration of 10 μ M for 16 hours. To evaluate the effect of α S expression on cell viability we used the WST1 (Roche Diagnostics, Germany) cytotoxicity assay, relying on the cleavage of tetrazolium salts to produce soluble formazan salts. The assay, therefore, determines the metabolic activity of the cells by quantifying the specific enzymatic activity tested. Surprisingly, expressing α S in both control and Pex5^{-/-} cells rescued the H₂O₂ effects, with cell viability values statistically significant from the corresponding control without H₂O₂. Thus, a consistent increase of 15-20% in cell viability values was observed with α S over-expression (Figure 4b). Therefore, oxidative stress occurring in the PBD fibroblasts does not correlate with α S accumulation in pathogenic forms.

Abnormal FA content in Pex2^{-/-} brains suggests the involvement of altered n-6 PUFA in α S abnormalities

Previous reports have documented altered lipid metabolism in the different PBD mouse models, including accumulation of very long chain fatty acids (VLCFA) and an increased ratio of C26/C22, accumulation of branched chain fatty acids and marked deficiency of plasmalogens (Faust and Hatten 1997; Faust et al. 2001) (Baes et al. 1997; Maxwell et al.

2003). Further, in line with the proposed role of peroxisomes for generation of docosahexaenoic acid (DHA, 22:6 n-3), reduced levels of DHA were previously documented in newborn and early postnatal Pex2^{-/-} and Pex5^{-/-} brains (Faust et al. 2001) (Janssen et al. 2000). Additional analyses of PUFAs in newborn Pex2^{-/-} brains demonstrated a similar level of the DHA precursor α -linolenic acid (18:3 n-3) in control and Pex2^{-/-} brains (0.359 ± 0.019 versus 0.334 ± 0.038 , respectively; % of total fatty acids), but a reduced level of most n-3 PUFAs that are intermediates in DHA synthesis in Pex2^{-/-} brains (Table 1). Only 24:6 n-3 was increased in Pex2^{-/-} brain, which is consistent with the need for peroxisomal β -oxidation to retroconvert this penultimate intermediate for DHA production (Su et al. 2001). In contrast to reduced levels of several n-3 PUFA, Pex2^{-/-} brains had elevated levels of linoleic (18:2 n-6) and arachidonic (20:4 n-6) acid, as previously described in human Zellweger brains (Martinez 1995), along with increases in several other n-6 PUFA that are intermediates in arachidonate synthesis (Table 1). These changes in PUFA levels resulted in a higher n-6:n-3 ration in the pex2^{-/-} brains (1.1 and 1.6 for wt and Pex2^{-/-}, respectively). However, the concomitant increases in several n-6 PUFA along with decreases in n-3 PUFA in Pex2 mutant brain led to a similar level of total PUFA species in control versus Pex2^{-/-} brains (32.22 ± 0.67 versus 32.08 ± 0.82 , respectively; % of total fatty acids). Pex2^{-/-} brains also had significant elevations in both long chain (16:0 – 20:0) and very long chain (23:0 – 26:0) saturated fatty acids, with a characteristic elevation in the ratio of C26:0/C22:0, and a significant increase in the level of total saturated FA species (Table 1).

While most n-6 PUFA and saturated FAs are elevated in Pex2^{-/-} brains, the levels for several mono unsaturated fatty acids (MUFA) were reduced, including the most abundant species oleic acid (18:1 n-9) and vaccenic acid (18:1 n-7) (Table 1). Only 26:1 n-9 was elevated in Pex2^{-/-} brain, representing a minor very long chain MUFA species that is not detectable in control brains. The level of total MUFA species was significantly decreased in Pex2^{-/-} versus control brains (Table 1).

Discussion

In this study we examined the effects of peroxisomal deficiency on α S-related abnormalities, including α S oligomerization and aggregation; α S phosphorylation; inclusion formation and its effects on cell viability. We documented enhanced α S accumulation in phosphorylated oligomers in mouse brains harboring non-functioning peroxisomes due to specific null mutations in either Pex2, Pex5 or Pex13 genes. We also detected enhanced deposition of human α S in cytoplasmic ubiquitinated inclusions in α S over expressing Pex5^{-/-} but not in control fibroblasts maintained in parallel under standard serum-supplemented conditioning medium. We show a correlation between accumulation of several long chain n-6 PUFAs and reduced levels of MUFAs with the accumulation of α S pathogenic forms in the Pex2^{-/-} brains. However, the accumulation of α S in pathogenic forms was not accompanied with oxidative stress neither with mitochondrial respiratory chain complex I or I+III dysfunction in Pex5^{-/-} PBD model. Our results suggest a role for peroxisomes in α S oligomerization and toxicity.

Recent results suggested that upon interaction with membrane phospholipids, α S tends to acquire an α -helix-rich structure (Davidson et al. 1998) and enrichment of phospholipids with PUFA induced α S oligomerization in vitro (Perrin et al. 2001). In a series of recent studies we have documented different aspects of the interaction of neuronal α S with FA -- in particular with PUFAs -- under normal and pathological conditions (Assayag et al. 2007; Sharon et al. 2003a; Sharon et al. 2003b; Sharon et al. 2001). We found that the accumulation of α S in soluble oligomers and insoluble aggregates, is associated with alterations in PUFA. We specifically identified longer chained and unsaturated FAs as factors that induce α S oligomerization, aggregation (Sharon et al. 2003a; Sharon et al. 2003b), phosphorylation and Lewy-like inclusion formation (Assayag et al. 2007). Further, we documented accumulations

in certain PUFAs upon α S over expression in dopaminergic cell (Sharon et al. 2003b). These previous studies were performed on PD models with altered α S expression, i.e., over expression in dopaminergic cells, null α S mouse brains and human brains with PD and the related synucleinopathies, Dementia with Lewy Bodies (DLB). In contrast to our previous studies, we have now used the reciprocal approach, i.e., we show α S abnormalities in vivo, in brains of mice with a lipid metabolic disorder. These PBD models do not involve any manipulation of their endogenous α S expression. These models have enabled us to determine an involvement of lipid metabolism in the process of α S accumulations in pathogenic forms.

Our previous analyses of FA profiles in human brains with PD and DLB indicated accumulations of certain PUFAs in the cytosols (Sharon et al. 2003b). Specifically, significantly higher levels of 22:4 n-6 and 22:6 n-3 were measured in the PD and DLB than in control brains. Similar FA analyses in naïve and α S over expressing dopaminergic cells indicated accumulations of both n-3 and n-6 PUFAs in cytosols and membrane fractions upon α S over expression. Analyses of FA profiles of size exclusion chromatography fractions containing α S of wt and the corresponding fractions of α S $-/-$ mouse brains revealed the related reductions in PUFAs in the α S $-/-$ fractions, and specifically, reduced levels of 18:3 and 22:6 n-3 PUFAs. These previous analyses did not indicate a specific role for n-6 rather than n-3 PUFAs in α S pathogenesis. Here, we show that the accumulation of α S phosphorylated oligomers and its deposition in cytoplasmic, ubiquitinated inclusions is correlated mainly with the accumulation of n-6 rather than n-3 PUFA in Pex2 $-/-$ brains. It is important to stress that n-3 PUFAs metabolism is specifically affected in the PBD models due to the role of peroxisomes in the biosynthesis of DHA (22:6 n-3). Indeed the level of DHA is reduced while the level of 24:6 n-3, the penultimate precursor in 22:6 biosynthesis, is elevated in the Pex2 $-/-$ brains. Therefore, it is possible that the finding herein, suggesting a role for n-6 but not n-3 PUFA in α S pathogenesis is strongly influenced by this specific effect of peroxisomes on n-3 PUFA metabolism. While further studies are needed to determine the precise role of n-6 vs n-3 in α S pathogenesis, the results herein support our previous observations that alterations in PUFA levels are correlated with α S expression and PD.

While the role of peroxisomes in neonatal neurodegeneration has been widely studied (reviewed in (Crumrine 2001)), only limited information concerning the potential role of peroxisomes in age-related neurodegeneration can be found in the literature. For example, in relation to Alzheimer's disease, peroxisomal proliferation attenuated A β -dependent toxicity and protected hippocampal neurons from A β -induced degenerative changes (Santos et al. 2005). Nevertheless, growing evidence correlates α S abnormalities, PD and lipid metabolism. Abnormal accumulations of α S were recently reported in neurons and glia of adrenoleukodystrophy (ALD) patients (Suzuki et al. 2007). ALD is a peroxisomal disorder due to loss of the ABCD1 gene, a peroxisomal membrane transporter (Moser et al. 2007). Abnormal α S accumulations were also observed in brains of patients with lysosomal storage diseases such as Sandhoff disease, Tay-Sachs disease, metachromatic leukodystrophy and β -galactosialidosis (Suzuki et al. 2007). Importantly, homozygous mutations in the glucocerebrosidase gene causing the glycosphingolipid-storage disorder, Gaucher's disease, were recently shown to be linked to familial forms of PD in diverse populations (Aharon-Peretz et al. 2004). These reports collectively suggest that brain lipid metabolism may have a role in specific forms of PD. Considering the profound effects of peroxisomal deficiency on lipid metabolism in general and on brain lipid metabolism in particular, it is now suggested that the involvement of peroxisome dysfunction in PD is resulting from its effects on brain lipid metabolism.

Mitochondrial complex-I inhibitors such as rotenone, maneb and paraquat clearly lead to aggregation and accumulation of α S in vitro and in animal models (Betarbet et al. 2000) (Manning-Bog et al. 2002) (Norris et al. 2007). The absence of a correlation between enhanced

α S oligomerization and mitochondrial dysfunction reported herein may indicate that α S toxic effects on mitochondrial activities are more complex than previously estimated. For example, it was recently shown that α S contains a cryptic mitochondrial targeting sequence at its N terminus (Devi et al. 2008) and that mitochondrial accumulation of α S has a role in mitochondrial dysfunction and PD pathogenesis. In this regard, it will be interesting to find out whether α S oligomers are also present in the mitochondria.

Zellweger syndrome is a fatal disease, with life expectancy of about 6 month. The peroxisomal dysfunction in ZS and the related PBD involves severe neurological abnormalities related to neural development and neuronal migration (reviewed in (Faust et al. 2001; Wanders and Waterham 2005)). Here we used this severe metabolic disorder to model an age-related neurodegenerative disorder. The rationale being that in sporadic, age-related neurodegenerative diseases, gradual accumulation of cellular insults may progressively affect cellular metabolic activities in the brain to the point where neurodegeneration may occur.

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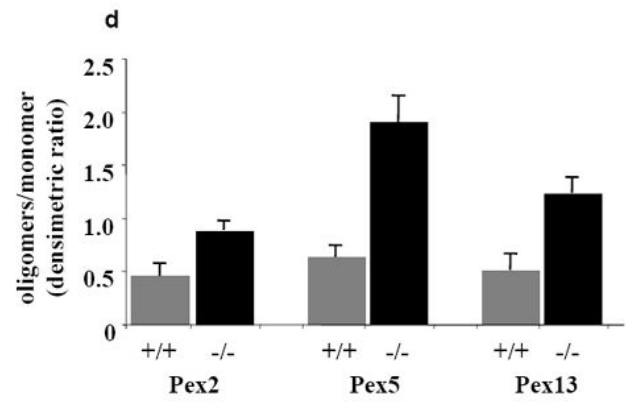
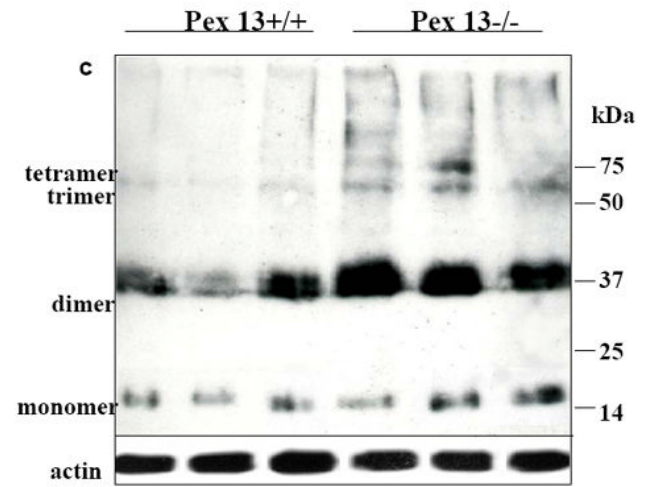
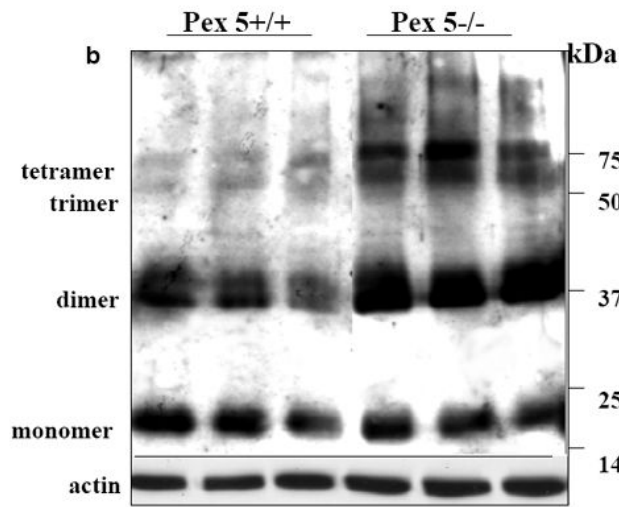
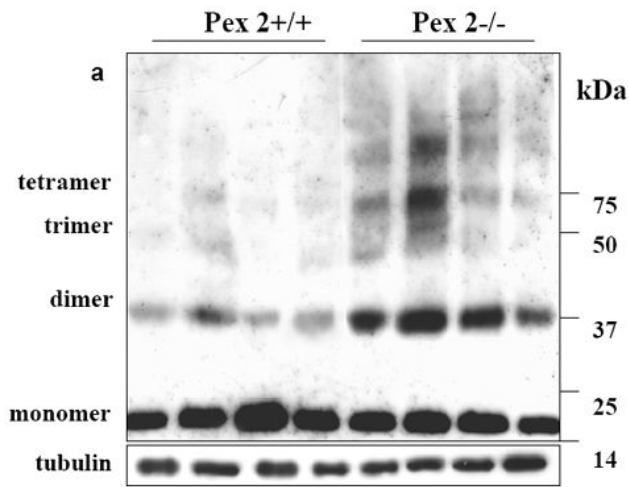
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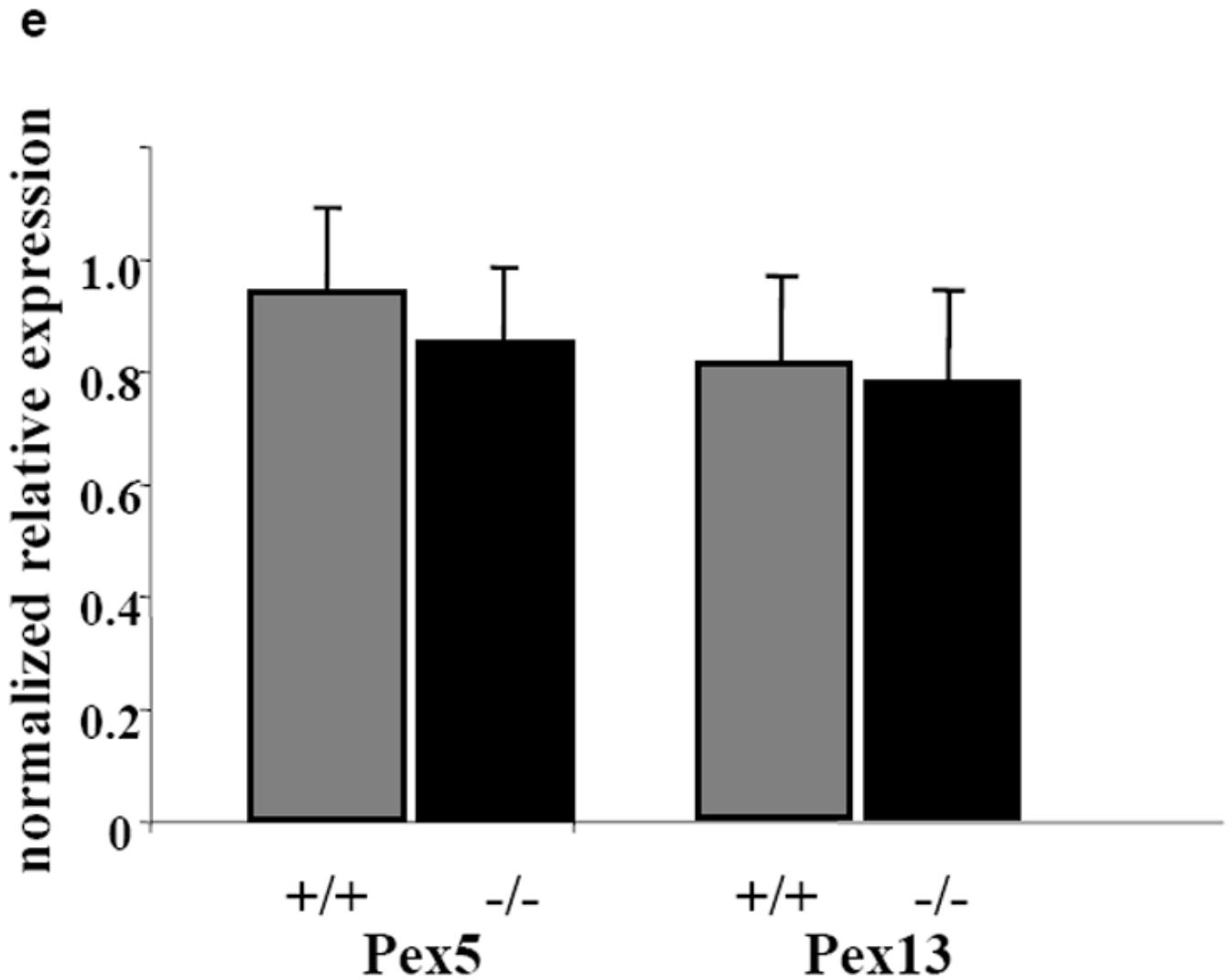


Figure 1. Induced accumulation of α S oligomers in vivo in peroxisome Biogenesis Disease mouse models

Samples of high-speed cytosol, post 100,000g (15 μ g protein) extracted from whole newborn mouse brain. Samples were treated at 65°C overnight prior to gel loading and blotting with anti α S antibody.

Each lane represents a different brain processed in parallel. Representative immunoblots for a) Pex2^{-/-} and control newborns; b) Pex5^{-/-} and control newborns and c) Pex13^{-/-} and control newborns. For each mouse model we tested four-seven individual brains with highly similar results. d) densitometric ratio of oligomers to monomer for each mouse model (mean \pm SE, n=4-7 mice).

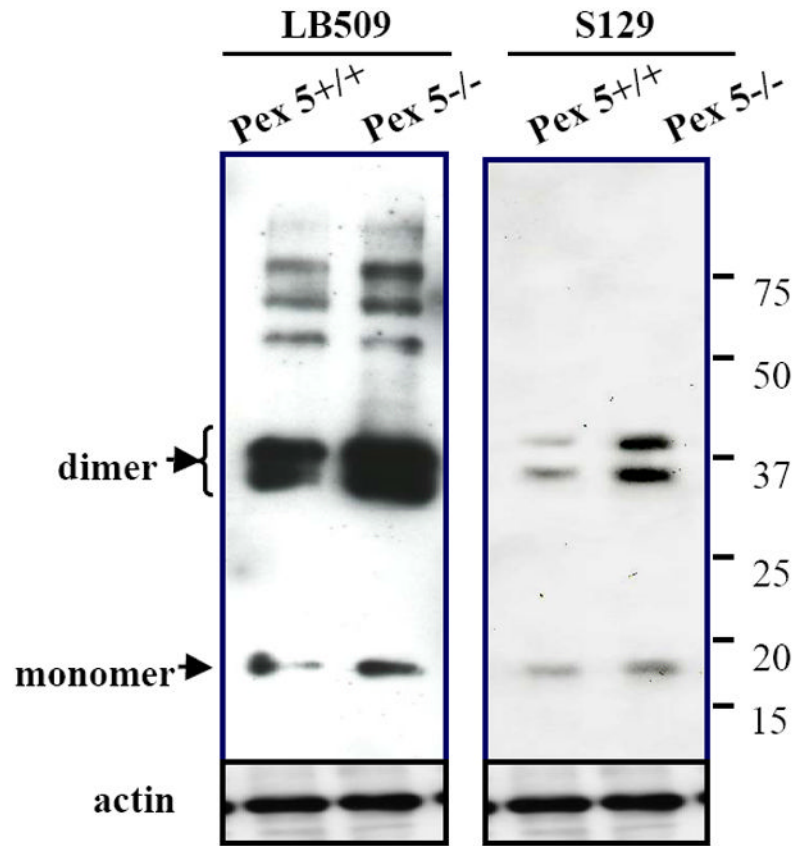


Figure 2. Induced oligomerization and phosphorylation of human- α S in Pex5^{-/-} cells
 High-speed cytosols (15 μ g protein) of human wt α S-transduced Pex5^{-/-} and control cells conditioned in standard serum-supplemented medium for 48 hours post transduction. Samples were treated at 65°C overnight prior to gel loading and blotting with anti α S antibody LB509 or anti-phospho Ser129 α S antibody. Blot reacted with anti actin for loading control.

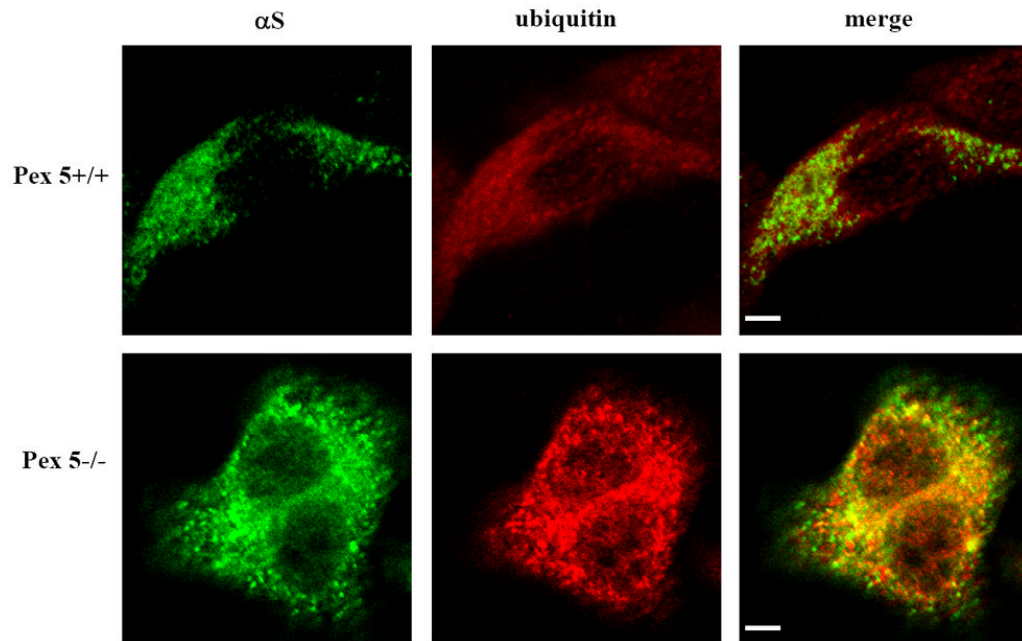


Figure 3. Induced Lewy-like inclusion formation in α S over expressing Pex5^{-/-} fibroblasts
 α S stably-transfected Pex5^{-/-} and control cells were maintained in culture under standard serum conditions. Cells were pre-permeabilized with 0.002% Triton X-100 and then processed for icc using antibodies against α S (LB509) and ubiquitin (Dako), followed by Alexa 488 and Cy5, respectively. Bars represents 10 μ m.

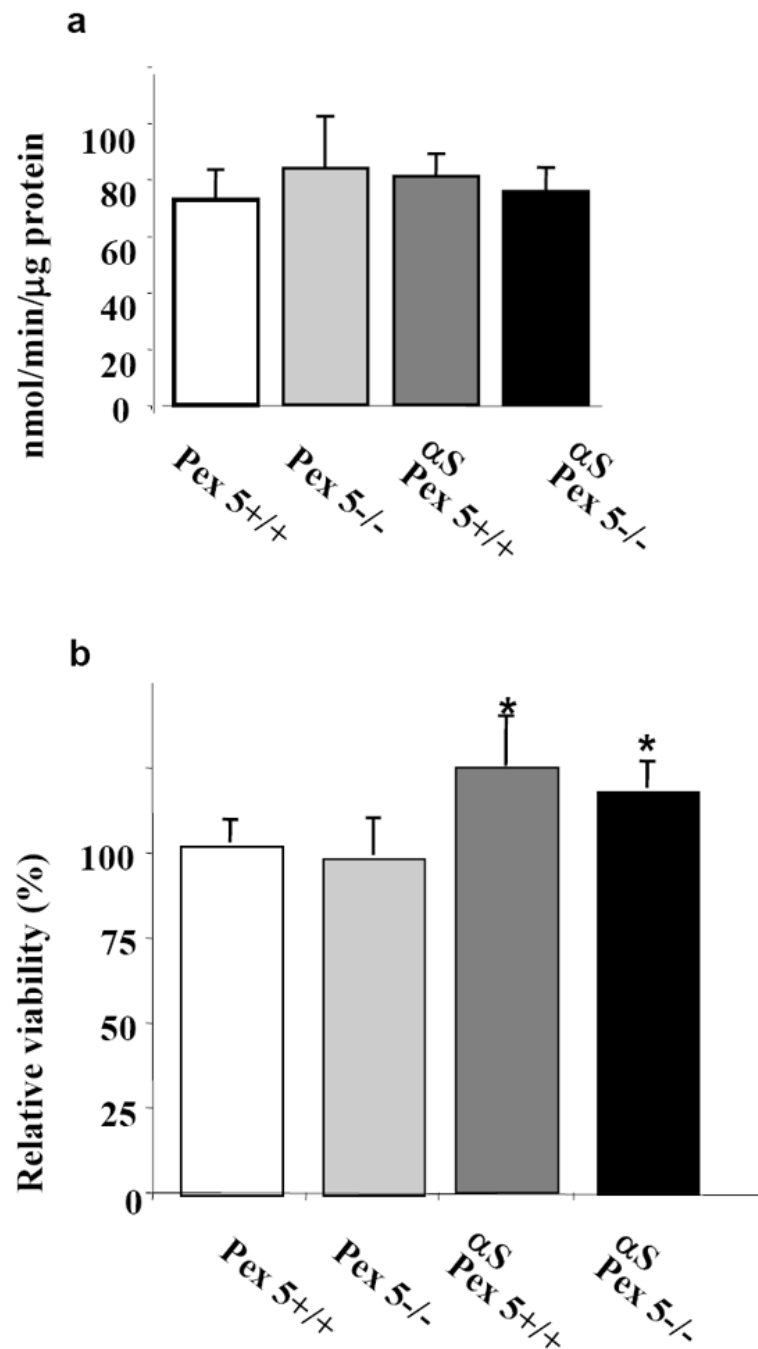


Figure 4. α S stable over expression did not inhibit mitochondrial complex I activity or induce oxidative stress in Pex5^{-/-} fibroblasts

a) Mitochondrial complex I enzymatic activity was measured in isolated mitochondria of Pex5^{-/-} and control cells, with and without stable overexpression of α S, and normalized to the activity of citrate synthase, a mitochondrial matrix enzyme, in the same sample. Mean \pm SE of 2-3 mitochondrial preparations of each clone (2-3 different α S stable clones). b) Cell viability was measured in Pex5^{-/-} and control cells without and with α S stable-overexpression in response to the addition of H₂O₂ (10 μ M for 16 hours) to the conditioning medium. Results are presented as percent of viability of Pex5^{+/+} control cells (normalized to 100%). Mean \pm SE 2-3 different α S stable clones.

Table 1
The relative amounts of SFAs, MUFAs and PUFAs in Control and Pex2-/- newborn mouse brains.

	Elevated levels		Reduced levels		
	Control	Pex2-/-	FA	Control	Pex2-/-
16:0	24.87 ± 0.25	28.77 ± 1.07**	C14:0	0.993 ± 0.063	0.775 ± 0.058**
17:0	0.090 ± 0.12	0.104 ± 0.009*			
18:0	16.34 ± 0.12	18.81 ± 0.23**			
20:0	0.079 ± 0.05	0.131 ± 0.010**			
23:0	0.296 ± 0.20	0.849 ± 0.086**			
24:0	0.253 ± 0.15	0.302 ± 0.039**			
25:0	0.016 ± 0.09	0.031 ± 0.011*			
26:0	0.002 ± 0.00	0.031 ± 0.009**			
C26/C22	0.025 ± 0.03	0.363 ± 0.122**			
Total Sat.	43.10 ± 0.33	49.96 ± 1.12**			
26:1n-9	0.000 ± 0.000	0.018 ± 0.009**	16:1n-9	1.19 ± 0.08	0.97 ± 0.14
			18:1n-9	13.07 ± 0.37	11.17 ± 0.91**
			18:1n-7	3.41 ± 0.08	2.63 ± 0.25**
Total MUFA	20.61 ± 0.49	17.84 ± 1.50**			
18:2 n-6	1.070 ± 0.250	1.845 ± 0.173**	20:3W9	0.51±0.04	0.16±0.04**
18:3 n-6	0.088 ± 0.025	0.114 ± 0.017*	22:4 n-6	2.70 ± 0.25	1.88 ± 0.31**
20:2 n-6	0.232 ± 0.086	0.446 ± 0.029**	22:5 n-6	0.780 ± 0.052	0.016 ± 0.046**
20:3 n-6	0.403 ± 0.055	0.715 ± 0.083**	18:4 n-3	0.136 ± 0.009	0.039 ± 0.007**
24:2 n-6	0.045 ± 0.005	0.064 ± 0.010**	20:5 n-3	0.111 ± 0.023	0.053 ± 0.023**
20:4 n-6	11.49 ± 0.21	14.06 ± 0.48**	22:5 n-3	0.402 ± 0.070	0.197 ± 0.045**
24:6 n-3	0.269 ± 0.025	0.811 ± 0.097**	22:6 n-3	13.56 ± 0.44	11.15 ± 0.29**
Total PUFA	32.18±1.57	32.05±1.76			

Mean \pm SD of n=6 and 7 for controls and Pex2^{-/-} respectively

* $P < 0.05$,

** $P < 0.001$, Student's t-Test