Drosophila Carrying Pex3 or Pex16 Mutations Are Models of Zellweger Syndrome That Reflect Its Symptoms Associated with the Absence of Peroxisomes

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Abstract
The peroxisome biogenesis disorders (PBDs) are currently difficult-to-treat multiple-organ dysfunction disorders that result from the defective biogenesis of peroxisomes. Genes encoding Peroxins, which are required for peroxisome biogenesis or functions, are known causative genes of PBDs. The human peroxin genes PEX3 or PEX16 are required for peroxisomal membrane protein targeting, and their mutations cause Zellweger syndrome, a class of PBDs. Lack of understanding about the pathogenesis of Zellweger syndrome has hindered the development of effective treatments. Here, we developed potential Drosophila models for Zellweger syndrome, in which the Drosophila pex3 or pex16 gene was disrupted. As found in Zellweger syndrome patients, peroxisomes were not observed in the homozygous Drosophila pex3 mutant, which was larval lethal. However, the pex16 homozygote lacking its maternal contribution was viable and still maintained a small number of peroxisome-like granules, even though PEX16 is essential for the biosynthesis of peroxisomes in humans. These results suggest that the requirements for pex3 and pex16 in peroxisome biosynthesis in Drosophila are different, and the role of PEX16 orthologs may have diverged between mammals and Drosophila. The phenotypes of our Zellweger syndrome model flies, such as larval lethality in pex3, and reduced size, shortened longevity, locomotion defects, and abnormal lipid metabolisms in pex16, were reminiscent of symptoms of this disorder, although the Drosophila pex16 mutant does not recapitulate the infant death of Zellweger syndrome. Furthermore, pex16 mutants showed male-specific sterility that resulted from the arrest of spermatocyte maturation. pex16 expressed in somatic cyst cells but not germ line cells had an essential role in the maturation of male germ line cells, suggesting that peroxisome-dependent signals in somatic cyst cells could contribute to the progression of male germ cell maturation. These potential Drosophila models for Zellweger syndrome should contribute to our understanding of its pathology.

Introduction
The peroxisome biogenesis disorders (PBDs) are human recessive hereditary diseases that arise from mutations in PEX genes, which encode the Peroxins, essential proteins for the biogenesis of peroxisomes [1]. Currently, 13 PEX genes have been identified as causative genes for PBDs [1,2]. The hallmark of PBDs is the malformation or complete absence of peroxisomes in patients’ cells [2]. PBD patients exhibit multiple organ dysfunctions, including developmental and progressive neurological defects, and those with the most severe manifestation, Zellweger syndrome, usually die before they are 1 year old [3]. However, although the disruption of peroxisome functions is thought to be the direct or indirect cause of these disorders, a better understanding of the pathogenesis of PBDs is needed to develop effective treatments.

Mouse models for PBDs, in which Pex2 [4], Pex5 [5], Pex7 [6], or Pex13 [7] is disrupted, have been developed. Mice homozygous for any of these mutants show various defects that are similar to the symptoms of Zellweger syndrome [8]. However, although important insights into the pathogenesis of PBDs have been obtained from studies of these mouse models, the cellular and molecular bases of the PBD-associated defects are still elusive.

Peroxisomes participate in diverse metabolic processes, including the β-oxidation of VLCFAs (very long chain fatty acids), oxidation of phytic acid, biosynthesis of ether-phospholipids, and H2O2 metabolism [9,10]. Therefore, PBD patients show increased levels of VLCFAs and reduced levels of a polyunsaturated fatty acid, docosahexaenoic acid (DHA), and of plasmalogens (ether-phospholipids). These altered lipid levels are among the diagnostic markers for PBDs [2]. However, the links between the change in lipid content, abnormal cellular functions, and the development of PBDs are unclear.

Classically, peroxisomes were thought to arise through the growth and division of preexisting peroxisomes [11]. However,
accumulating evidence supports an ER-dependent mode of peroxisome biogenesis (de novo biogenesis), especially in yeast [12, 13, 14] and plants [15, 16]. In addition, a recent report showed that peroxisomes also arise de novo from the ER in mammalian cells [17]. Therefore, the existence of two pathways for peroxisome proliferation, the growth and fission pathway and the de novo pathway, are now largely accepted [18].

The functions of three genes, pex3, pex16, and pex10, are reported to be essential for the de novo biogenesis of peroxisomes [17, 19], in which their products contribute to peroxisomal membrane protein targeting [20, 21]. On the other hand, pex1, pex2, pex5, pex6, pex7, pex10, pex12, pex13, and pex14 are required for peroxisomal matrix protein import [22, 23]. Recently, pex2 and pex10 Drosophila mutants were reported [24]. The analysis of these mutants revealed that the import of some peroxisomal matrix proteins is required for spermatogenesis and the metabolism of VLCFAs [24]. However, these mutants do not show other phenotypes reminiscent of PBD symptoms, such as defects in neuronal development and function [24]. These results suggested that some level of peroxisome activity is still maintained in the pex2 and pex10 mutants. In contrast, the mutation of genes involved in the peroxisomal membrane protein targeting, including pex3, pex16, and pex19, has not been reported in Drosophila. Pex3 and Pex16 encode integral membrane proteins: PEX16 is a receptor for PEX3, which acts as a docking receptor for incoming peroxisomal membrane proteins [21]. PEX19 binds nascent peroxisomal membrane proteins (PMPs) in the cytoplasm and targets them to PEX3 on the peroxisomal membrane [25].

Here we describe the Drosophila lines bearing mutations in the pex3 and pex16 genes. In contrast to the pex2 and pex10 mutants, which show developmental defects only in spermatogenesis [24], the pex3 mutant was larval lethal, and the pex16 mutant showed a reduced lifespan and various defects in development and neural function. We conclude that these mutants reflect broad symptoms of PBDs, and can be viewed as Drosophila models of these diseases, especially of Zellweger syndrome, although the Drosophila pex16 mutant does not recapitulate the infant death seen in Zellweger syndrome patients.

**Results**

**pex3 and pex16 are the Drosophila lines bearing mutant pex genes**

To understand the roles of Drosophila Pex genes required for peroxisomal membrane protein targeting, we developed loss-of-function mutants of the pex3 (CG6839) and pex16 (CG3947) genes [24]. Using the P-element imprecise excision approach, we isolated deletion mutants of pex3 and pex16 (Figure 1A). pex3 is a deletion mutant lacking the 3′-region of the pex3 locus, which is therefore missing two-thirds of its coding region (Figure 1A). To confirm that the mRNA corresponding to the deleted genomic region was not synthesized in the pex3 null homozygote, we performed reverse transcription polymerase chain reaction (RT-PCR). No RT-PCR product originating from the deleted genomic regions was detected in the pex3 null homozygote, whereas a product from an intact region was detected (Figure S1). In pex16 and pex16, most of the coding region was deleted (Figure 1A). We also confirmed that no mRNA corresponding to the deleted genomic region in pex16 was synthesized in the pex16 null homozygote (Figure S1). Based on the molecular lesions of these mutants, it is likely that they were all null alleles. pex3 null homozygotes and trans-heterozygotes of pex3 and a deletion mutant of the entire pex3 locus, Df(3L)ri-XT1, and pex16 null homozygotes lacking the maternal contribution were viable (data not shown).

**pex3 and pex16 homozygotes lack normal peroxisomes**

The absence of peroxisomes in skin biopsy samples is one of the crucial diagnostic markers of PBDs [1, 2]. Therefore, to evaluate whether our pex3 and pex16 mutants could be considered as Drosophila models of PBDs, we first confirmed that they lacked peroxisomes. To visualize peroxisomes in vivo, we overexpressed proteins with peroxisome-targeting signals. One, EGFP-SKL is an EGFP derivative tagged with the SKL peptide, also designated as PTS1 (peroxisomal targeting signal-1) [26]. The other, PMP70-ECFP, is a chimeric protein of ECFP and PMP70, whose mammalian orthologue localizes to the peroxisomal membrane via its mPTS (peroxisomal membrane-targeting signal) [27]. We co-expressed EGFP-SKL with PMP70-ECFP in Drosophila S2 cells and found that the two proteins were colocalized at small cytoplasmic granules (Figure S2), even though each protein carried a different peroxisome-targeting signal. Therefore, we concluded that these intracellular particles were Drosophila peroxisomes.

To determine whether peroxisomes were absent from pex3 or pex16 homozygotes, we ubiquitously expressed UAS-EGFP-SKL or UAS-PMP70-ECFP in the mutant homozygotes or wild-type flies using the GALA/UAS system (driven by Act-GAL4) [27]. In wild-type flies, in the cells of the larval malpighian tubule, EGFP-SKL and PMP70-ECFP specifically localized to peroxisomes (Figure 1B and 1E). However, the EGFP-SKL-positive or the PMP70-ECFP-positive peroxisomes were absent in the same cells in the pex3 homozygote (Figure 1C and 1F), although a small number of granules (less than one in 10 cells) labeled by PMP70-ECFP, the nature of which was unknown, were detected in these cells (data not shown). These results suggested that pex3 is essential for the presence of peroxisomes.

In contrast to the pex3 mutant, the malpighian tubule cells of the pex16 homozygotes still contained peroxisome-like granules detected by EGFP-SKL and PMP70-ECFP, although their number was greatly reduced compared with wild-type (Figure 1D and 1G). To determine the nature of these peroxisome-like granules in pex16, we stained the tissues of wild-type and pex16 homozygotes with 3′-diaminobenzidine (DAB) and observed them by transmission electron microscopy. In the wild-type malpighian tubules, peroxisomes were detectable by DAB staining (Figure 1H) [28]. In contrast, the pex16 homozygotes did not contain cells with DAB-positive organelles (Figure 1I). Therefore, although some peroxisomes apparently remained in the pex16 mutants, they were present at only a very low frequency or they had lost their normal enzymatic activity, which made them undetectable by the DAB reaction.

pex3 was a recessive lethal mutant as mentioned above, whereas pex16 homozygotes lacking the maternal contribution could develop to adulthood, and a small number of peroxisome-like granules were still found in them (data not shown). These results suggested that a small number of peroxisomes are still maintained in the absence of PEX16 in Drosophila. The pex16 mutant of the yeast Yarrowia lipolytica contains peroxisome-like structures [29]. Therefore, similar to our finding using Drosophila pex16, pex16 is not essential for the presence of peroxisomes in Yarrowia lipolytica [29]. In contrast, both PEX3 and PEX16 are known to be essential for the presence of peroxisomes in mammals [30, 31]. Thus, the requirement of Pex16 orthologs in peroxisome biosynthesis may be different among species.

In Yarrowia lipolytica, an overexpression of its pex16 ortholog results in fewer but enlarged peroxisomes [29]. Therefore, if the function of pex16 orthologs is conserved between yeast and
Drosophila, we thought that the overexpression of Drosophila pex16 would give similar defects in peroxisomes in Drosophila. To address this, we overexpressed UAS-pex16 and UAS-EGFP-SKL in wild-type flies, and found that the peroxisomes labeled by EGFP-SKL became fewer and larger in the malpighian tubule cells or spermatocytes overexpressing pex16, compared with wild-type (Figure S3 A–D’). Quantitative analysis revealed that these findings were statistically significant (Figure S3 E and F). These results suggested that the function of pex16 genes may be evolutionarily conserved between these two species, and an excess amount of PEX16 affects the formation or homeostasis of peroxisomes.

Figure 1. pex31 and pex161 lack normal peroxisomes. (A) Genomic lesions induced in pex3 and pex16. Untranslated regions and coding regions are shown as open and filled boxes, respectively. The P-element insertion sites in GS9829 and GS14106 are indicated by triangles. Genomic regions deleted in the mutants are indicated by dashed lines. Scale bar represents 0.5 Kb. (B–G) Peroxisomes detected from the larvae of wild-type (B, E), pex31 homozygotes (C, F), and pex161 homozygotes (D, G), ubiquitously expressing UAS-EGFP-SKL (B–D) or UAS-PMP70-ECFP (E–G) driven by Act-GAL4 are shown. Insets at upper right are higher-magnification images of the area enclosed by broken-line squares. Scale bars in B and E represent 10 μm. (H and I) Electron micrographs of adult malpighian tubule sections stained with DAB in wild-type (H) and pex161 homozygous flies (I). Arrowheads in H indicate DAB-stained peroxisomes. Scale bar in H represents 1 μm.

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pex16 homozygous adult flies showed a reduced body size and rosy eyes

Severe clinical types of PBDs, including Zellweger syndrome, result in infant death [2]. However, patients with PBDs also develop postnatal disorders; thus, it is important to understand the mechanisms that cause these defects to arise after birth. Therefore, in this study, we focused on the analysis of pex16 mutants, which survived to the imaginal stage. Trans-heterozygotes of pex16 and Df(3L)ri-XT1, uncovering pex16 locus, developed into adult at normal ratio. However, eclosed pex16 mutants appeared smaller than wild-type (Figure 2A and 2B). Mean body weight of pex16 mutants was reduced by 70% in females and 85% in males compared with those of control flies at the same days (two days) after eclosion (Figure 2C). We could not find impaired feeding activity (data not shown), suggesting that reduced body size in pex16 mutant is probably not due to their starvation. Adult flies homozygous for pex16 also showed an eye color phenotype similar to that of rosy (Figure 2D-F). The Drosophila rosy gene encodes xanthine dehydrogenase, which is involved in the production of drosopterin, a component of eye pigments, and the gene product of rosy functions in peroxisomes [28,32]. This result is consistent with our idea that the functions of peroxisomes were largely abolished in the pex16 homozygote.

VLCFAs accumulated in the pex16 homozygotes

The accumulation of VLCFAs in blood plasma is a diagnostic marker of PBDs [1,2]. In patients with Zellweger syndrome, the plasma level of VLCFAs is 2-10-fold greater than normal [33]. Therefore, we measured the fatty acid content in an extract of whole flies by gas chromatography. Compared with the levels of fatty acids in wild-type flies, which we defined as 100%, the level of VLCFAs with a chain length greater than C18 was two-fold higher in the pex16 homozygotes (Figure 2G). However, fatty acids with chain lengths shorter than C16 were not affected in these flies (Figure 2G). Thus, the fatty-acid metabolism was altered in the Drosophila pex16 mutants, much as it is in PBD patients. It was also reported that VLCFAs are increased in a mutant of pex10, required for the peroxisomal matrix protein import, in Drosophila [24]. Taken together with our finding that the number of peroxisomes is severely reduced in the pex16 homozygotes, these results suggest that the pex16 mutant can serve as a potential Drosophila model of Zellweger syndrome, although it does not recapitulate the infant death associated with this syndrome.

pex16 homozygotes show locomotion defects

Patients with PBDs exhibit a range of neurological abnormalities [1,2], including motor dysfunctions. The Drosophila pex gene mutants previously reported show defects in spermatogenesis and fatty acid metabolism, but they do not show other phenotypes reminiscent of the symptoms found in PBDs, such as locomotion defects and a shortened lifespan [24]. Hence, we first studied two different locomotion behaviors in adult pex16 homozygotes: climbing [34,35] and flight [36,37]. Wild-type adults have a strong negative geotactic response. Flies tapped to the bottom of a vial quickly climb the wall and tend to stay near the top [34,35]. We found that pex16 homozygotes climbed less actively, even immediately after eclosion (Figure 3A). Furthermore, their performance declined more rapidly with age than that of wild-type flies (Figure 3A).

To test the flying ability of pex16 homozygotes, we used the sticky-cylinder assay [36,37]; when flies are dropped into a cylinder whose inside is sticky, those with greater flying ability tend to stick higher up on the cylinder wall. In this assay, most of the flies heterozygous for pex16 stuck to the wall between levels 4 and 5 (Figure 3C). In contrast, pex16 homozygotes tended to stick at the lowest level (Figure 3C). Both locomotion defects were rescued by the simultaneous tissue-specific expression of pex16 in the fat body (driven by Lsp2-GAL4) and differentiated neurons (driven by clav-GAL4), but not by its expression in either tissue alone (Figure 3B and 3D). In contrast, the overexpression of pex16 in other tissues, including the gut, malphigian tubules, and salivary glands, did not rescue these defects (Figure 3B and 3D). Therefore, these locomotion defects are attributable to multiple causes associated with the absence of peroxisomes.

In addition to the defects in neural functions, the lifespan of pex16 homozygotes was severely reduced. The mean longevity of the females was reduced to one-third and that of the males to one-fourth of the wild-type lifespan (Figure 3E and data not shown). The shortened lifespan of the pex16 homozygotes was also rescued by the simultaneous overexpression of pex16 in the fat body and differentiated neurons (Figure 3F). Since the locomotion defects and reduced lifespan of the pex16 homozygotes were both rescued by the overexpression of pex16 in the same tissues, we speculate that the short lifespan of the pex16 homozygotes was caused by their locomotion defects.

pex16 homozygotes show defects in nervous system development

Among the neurological abnormalities of PBD, these patients show structural defects of the nervous system [1]. We therefore examined whether the Drosophila pex16 mutants also showed structural abnormalities in the adult brain. We found a structural abnormality of the dendritic trees in the lobula plate of the optic lobe (Figure 3G and 3H). In the wild-type brain, the dendritic trees were densely distributed (Figure 3G). In contrast, in the pex16 homozygotes one day after eclosion, areas of low-density dendrites were observed (Figure 3H), whereas other parts of the brain appeared normal (data not shown). The glial cells and presynaptic structures in the optic lobe also appeared to be unaffected (Figure S4). The reduction of dendrites in the pex16 homozygotes was already detectable at the pupal stage, and the defect had not worsened at 10 days after eclosion (data not shown), suggesting that this abnormality was associated with developmental defects instead of neuronal degeneration. In addition, we did not find that this defect worsened with age (data not shown).

We also found that the abnormality of the lobula plate was rescued by the tissue-specific expression of pex16 either in the fat body (driven by Lsp2-GAL4) or differentiated neurons (driven by clav-GAL4) (Figure 3I and 3J). These results indicate that the developmental defects in neurons that were caused by the absence of peroxisomes could be rescued by the functions of peroxisomes in different organs. Considering that the locomotion defects of the pex16 homozygote were rescued by the simultaneous tissue-specific expression of pex16 in the fat body and differentiated neurons, but not by its expression in either tissue alone (Figure 3B and 3D), we speculated that the observed defect in the lobula plate is not a cause of the locomotion abnormalities in the pex16 homozygote. This idea is also consistent with our finding that the locomotion defects progressed with age in adult flies, whereas the structural defect of the lobula plate did not.

Maturation of male germ cells is arrested in the testes of pex16 homozygotes

In addition to the above-described phenotypes, which showed obvious similarities to the well-characterized symptoms of patients with PBDs, pex16 homozygotes exhibited male sterility. Because
patients with Zellweger syndrome die well before reaching sexual maturity, this possible role of peroxisomes has not been studied in humans. In the *Drosophila* testis, cells in each stage of spermatogenesis can be observed at once (Figure 4A). In wild-type testes, the gonialblast is formed by the asymmetric division of a germline stem cell. Each gonialblast undergoes four rounds of mitotic division to produce 16 early spermatocytes. After this period of mitotic proliferation, each spermatocyte enters a growth phase, which is accompanied by sequential morphological changes as the cells differentiate from the early spermatocyte to the late spermatocyte stage (Figure 5A).

The *pex16* homozygote testis was smaller than the wild-type testis (Figure 4B) and did not contain mature sperm cells (Figure 4D). However, early spermatocyte cysts, which are composed of 16 spermatocytes and two cyst cells, were found in these testes (data not shown), which suggests that the mitotic division of the gonialblast occurred normally in the *pex16* mutant testes. However, we found neither normal postmeiotic spermatids nor elongated spermatids in the mutant testes (Figure 4D and 4E), although these cells were abundant in the wild-type testes (Figure 4B and 4C). These results suggested that the maturation of spermatocytes is arrested during the growth phase in the *pex16* mutants.

Next, we examined the maturation of the *pex16* mutant spermatocytes in detail (Figure 5A) [38]. Early spermatocytes develop into polar spermatocytes, whose mitochondria form a
Peroxisomes in somatic cyst cells are required for germ-cell maturation

The spermatocyte cyst of *Drosophila* is composed of spermatocyte and cyst cells (Figure 4A), and peroxisomes were present in both cell types in the wild-type testes (Figure S5A and S5E). On the other hand, in the testes of *pex16* homozygotes, peroxisomes were absent from the spermatocytes and cyst cells, although the cyst cells were morphologically normal (Figure S5B, S5D, and S5F). Therefore, we determined whether peroxisomes were required in the spermatocytes or the cyst cells for spermatocyte maturation. We overexpressed the *pex16* gene specifically in cyst cells (driven by ptc-GAL4) or germ line cells (driven by nos-GAL4) in the *pex16* homozygote background. Peroxisomes were detectable in the cells overexpressing *pex16* (Figure 6B, D and Figure S5). When *pex16* was overexpressed in cyst cells, but not germ line cells, the fertility of the *pex16* males was rescued (data not shown). Morphologically normal spermatids and moving mature sperm were found in these flies, even though the germ cells lacked peroxisomes (Figure 6A and 6B). In contrast, *pex16* expression in germ cells did not rescue the sterility or defective spermatogenesis of the *pex16* homozygotes (Figure 6C and 6D). These results indicated that peroxisomal functions in somatic cyst cells were essential for spermatogenesis, whereas those in germ cells were dispensable. Interestingly, this finding was not comparable with the previously reported results that *Drosophila pex2* in germ cells, but not in cyst cells, is required for germ-cell maturation [24]. This discrepancy may suggest that *pex2* and *pex16* have distinct roles in germ-cell maturation.

Discussion

In this study, we developed *Drosophila* models of PBDs, in which *Drosophila pex3* or *pex16* genes were disrupted. Based on the molecular lesions of these mutant loci, the *pex3* and *pex16* mutations were null alleles. We found that *pex3* homozygosity caused larval lethality, and peroxisomes were not detected in the cells of the larvae. On the other hand, *pex16* homozygotes were viable, and a very small number of peroxisome-like particles were still observed in their cells. These differences could be attributed to distinct requirements for PEX3 and PEX16 in the formation of the peroxisome membrane in *Drosophila*.

Studies using human cells from PBD patients show that PEX3 and PEX16 are indispensable for the PMP sorting pathway, which is essential for the formation of the peroxisome membrane [20,21]. However, the necessity of PEX16’s contribution to PMP sorting seems to vary among species, although the role of PEX3 is probably conserved evolutionarily. Most yeast species do not have a Pex16 orthologue, with the exception of *Yarrowia lipolytica*, whose Pex16 orthologue is Pex16p [42]. In *Yarrowia lipolytica*, Pex16p is involved in the import of peroxisome matrix proteins and peroxisome proliferation, but not in peroxisome membrane biogenesis [29]. Here we showed that *Drosophila* PEX16 is closely related to yeast Pex16p. Considering that PMP sorting is thought to be essential for the synthesis of peroxisomes, and a small number of peroxisomes are maintained in the absence of PEX16 in yeast and *Drosophila*, some other protein may substitute for PEX16 in the PMP sorting pathway in these species. However, the mechanisms of this substitution remain to be understood.

Peroxisomes participate in many aspects of lipid metabolism [9,10]. Therefore, it is difficult to identify physiological links between peroxisomal dysfunctions and the pathology of PBDs. In adrenoleukodystrophy (ALD) patients, VLCFA levels in the white matter of the brain correlate with phenotypic severity, so the abnormal accumulation of VLCFAs is thought to be the cause of the neuronal damage associated with ALD [43]. In *Drosophila*, homozygotes for *pex2* or *pex10* also show the accumulation of VLCFAs [24], and the high level of VLCFAs was suggested to be responsible for the defective spermatogenesis in these mutants [24]. However, these flies do not show other phenotypes reminiscent of PBDs, including neuronal function disorders [24]. These results suggest that the accumulation of VLCFAs may not...
be the cause of the neuronal function disorders in Drosophila. On the other hand, we found that pex16 homozygotes demonstrate phenotypes that have some homology to the disorders found in Zellweger syndrome patients, including a reduced lifespan, locomotion defects, and abnormal neuronal development, with some exceptions such as infant death. Given that none of these phenotypes is found in the homozygotes for pex2 or pex10 [24], abnormalities in other lipids metabolized in peroxisomes besides VLCFAs could contribute to these disorders. Animal models of PBDs, including our Drosophila models, may aid in identifying the causes of these diseases.

Our results showed that peroxisomes were essential for the maturation of male germline cells in Drosophila, although their presence was required in the somatic cyst cells, rather than in the spermatocytes. These results are not consistent with the previous report that pex2 in germline cells but not in cyst cells is required for

Figure 4. The maturation of germline cells is arrested in the testis of pex16 homozygotes. (A) Schematic representation of early spermatogenesis. Germline stem cells (s) and somatic cyst progenitor cells, anchored to somatic hub cells, produce a new stem cell and a gonialblast (g), which are enclosed by two somatic cyst cells (Cyst). A single gonialblast cell undergoes four rounds of mitotic divisions to produce 16 early spermatocytes that then enter the growth phase. After the growth phase, the late spermatocytes undergo two meiotic divisions, producing 64 haploid spermatids. (B–E) Phase-contrast micrographs of the wild-type (B and C) and pex16¹ homozygote (D and E) testes. The bundles of elongated spermatids (arrow in B) and postmeiotic spermatids (inset in C) were missing in the pex16¹ homozygote testis. Inset in C is a higher magnification of the area enclosed by broken lines. Scale bars represent 100 µm.

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spermatogenesis in *Drosophila* [24]. Three RING proteins, Pex2, Pex10, and Pex12 in yeast are involved in the ubiquitination of PTS1 receptor Pex5 and contribute to PTS1-dependent peroxisomal matrix protein import [44]. However, the *pex10* in germ cells is not required for spermatogenesis, although mutations of *pex2* and *pex10* result in similar spermatogenesis defects in

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**Figure 5. Maturation of spermatocytes is arrested in the spermatocyte growth phase.** (A) Schematic representation of spermatocyte growth phase. Nu, nucleus; MT, mitochondria. (B–G) Maturation of spermatocytes in the testes of wild-type (B–E) and *pex16<sup>1</sup>* homozygote (F–G) flies. Y-chromosome loops and chromatin were stained with the S5 antibody (center panels) and Hoechst 33258 (right panels), respectively. Polar spermatocytes (B and F) and young apolar spermatocytes (C and G) were observed in both wild-type and *pex16<sup>1</sup>* mutant testes, whereas mature spermatocytes (D) and spermatocytes with meiotic chromosome condensation (E) were observed only in wild-type testes. Degenerated spermatocytes (arrows in H) were observed in the *pex16<sup>1</sup>* homozygote testes in squash preparations of live cells. Scale bar represents 20 μm. doi:10.1371/journal.pone.0022984.g005

**Figure 6. Peroxisomes in somatic cyst cells are essential for male germ cell maturation.** (A–D) Phase-contrast micrographs of a *pex16<sup>1</sup>* homozygote testis expressing UAS-pxe16 and UAS-EGFP-SKL driven by *ptc*-GAL4, expressed in cyst cells (A and B) or *nos*-GAL4, expressed in germline cells (C and D). Elongated spermatids (arrow in A) and morphologically normal spermatids (arrow in B) are indicated. (B’ and D’) Peroxisomes detected by EGFP-SKL. The fluorescent images in B’ and D’ correspond to the phase-contrast micrographs of B and D, respectively. Insets showing single spermatocytes are higher magnifications of the areas enclosed by broken lines. Scale bars represent 100 μm. doi:10.1371/journal.pone.0022984.g006
**Materials and Methods**

**Fly stocks**

Fly stocks were maintained at 25°C on a standard cornmeal media. Canton-S and white1118 were used as wild-type controls. The G9892 and GS14106 lines were used, respectively, to generate the pex3 and pex16 mutants [47]. Df(3L)ED218 and Df(3L)ri-XT1 are deletions uncovering the pex3 and pex16 loci, respectively. The following GAL4 driver strains were used: nos-GAL4 expresses GAL4 in germline cells [48]; ptc-GAL4 [49] express GAL4 in cyst cells; Lsp2-GAL4 expresses it in the fat body [50]; elav-GAL4 expresses it in all differentiatated neurons; and NP5021 drives GAL4 expression ubiquitously in the gut [51].

**Construction of UAS-pex16**

To generate UAS-pex16, the sole intron in the pex16 locus was removed by a PCR-based method, and the resulting fragment, containing the entire coding region of pex16, was cloned into the Nol and XhoI sites of pUAST [27]. Transgenic fly lines expressing UAS-pex16 were generated using a standard procedure.

**Construction of UAS-EGFP-SKL and UAS-PMP70-ECFP**

To generate UAS-EGFP-SKL, EGFP was amplified by PCR using the following primers: forward, CCGAATTCCAGCATGTTGAGCAAAGGGCCAGG; reverse, GCCTCGAGTACAGCTTGCTCCT-TTGTAGCTGGCATGACATCGTGGCTCATGCC. The reverse primer encodes a PTS1 (C-terminal SKL sequence). The resulting fragments were digested by EcoRI and XhoI, and cloned into the EcoRI and XhoI sites of pUAST [27]. Transgenic fly lines expressing UAS-EGFP-SKL and UAS-PMP70-ECFP were generated using standard procedures.

**RT-PCR**

Total mRNA was extracted from whole flies using the SV Total RNA Isolation System (Promega). cDNA was synthesized with random hexamer primers using the PrimeScript 1st strand cDNA Synthesis Kit (Takara). The following oligonucleotides were used as PCR primers: F1, 5’-CACGTTATGCACACCGCCG-3’; R1, 5’-CAGGTCCGTCCGTGCGTCG-3’; F2, 5’-CCAGCGCAAACGACAGAACAAGACGGCCG-3’; R2, 5’-GGCGAATGTGTACGAGGCGCC-3’; F3, 5’-CCACAGCCAAATGATGATATCAGG-3’; R3, 5’-TCTCCTGGCAATGGGTGCGTCG-3’; F4, 5’-GCCAATGTTGCGGCGCC-3’; R4, 5’-CCTTAAAGCCGCGCGATGC-3’. The RT-PCR products were analyzed by 1% agarose gel electrophoresis.

**Detection of peroxisomes in S2 cells and in vivo**

Drosophila S2 cells were cultured and transfected as described previously [53]. The slide was treated with 0.5 mg/ml concanavalin A (Sigma) and allowed to air-dry before the cells were transferred to it. The cells were observed using an LSM5 confocal microscope (Zeiss).

**Histological analysis of the brain**

The brain of adult or pupal flies was dissected in PBS (137 mM NaCl, 2.68 mM KCl, 10.14 mM Na 2HPO4, 1.76 mM KH 2PO4), fixed with 4% paraformaldehyde in PBS at 4°C for 2 hr, and stained with an antibody to microtubule-associated protein 1B (22C10, 1:5 dilution, DSHB), anti-Bruchpilot (ncl02, 1:20 dilution, DSHB), anti-Repo (8D12, 1:20 dilution, DSHB), or anti-Homer [52] (1:200 dilution), and an Alexa Fluor 488 Goat Anti-mouse IgG secondary antibody (1:100 dilution, Invitrogen). The samples were observed using an LSM5 confocal microscope (Zeiss).

**Quantitative analysis of peroxisome number**

In each confocal image of Malpighian tubule cells and spermatocytes, the number of peroxisomes, detected by EGFP-SKL, per 1,000 μm² cytoplasmic region was counted. In addition, the size of the peroxisomes was estimated from the number of pixels comprising each peroxisome in confocal images using the Photoshop histogram function. A peroxisome with over twice the pixel number compared with the average pixel number of wild-type peroxisomes was defined as an enlarged peroxisome.
Histological analysis of the testes

To observe the maturation of spermatocytes, the testes of newly eclosed male flies were examined by phase-contrast light microscopy (Zeiss). To observe the Y-chromosome loops in the spermatocytes, the testes were squashed on a slide glass, and the spermatocytes were frozen in liquid nitrogen and fixed with methanol-acetone as described [54]. The fixed spermatocytes were stained with an anti-S3 antibody (1:20 dilution) [41] and a Cy3-conjugated Donkey Anti-mouse IgG secondary antibody (1:100 dilution, Jackson IR).

Electron microscopy

The malpighian tubules were fixed with 2% glutaraldehyde in 0.1 M sodium cacodylate (pH 7.4) for 1 hr on ice. Then peroxidase cytochemistry was performed as described [26][55]. After the peroxidase reaction, the specimens were postfixed with 1% OsO4 for 1 hr, dehydrated, and embedded in Epon as described elsewhere [56].

Measurement of fatty acids

Lipids of whole male or female flies were extracted according to a method described previously [57]. The extracted lipids were treated with a dehydrated methanol:acetyl chloride mixture (10:1) to extract the fatty acid methyl esters. The fatty acid methyl ester derivatives were analyzed on a GC 353B gas chromatograph equipped with a flame ionization detector (GL Sciences, Tokyo, Japan) and a TC-FFAP capillary column (60 m × 0.25 mm internal diameter, 0.25 μm; GL Sciences). The oven temperature was programmed to increase from 170°C to 230°C at 5°C/min followed by a hold of 15 min. The injector and detector temperatures were both set at 250°C. Helium was used as the carrier gas, at 1 ml/min. Individual fatty acids were identified by comparing the retention times with those of known fatty acid standards.

Supporting Information

Figure S1 Full-length mRNAs are not synthesized from pex3Δ and pex16Δ mutant loci. RT-PCR was performed using wild-type (wt), pex3Δ homozygote, and pex16Δ homozygote template DNA. RT-PCR products were obtained using the indicated primers (F1, R1, F2, R2, F3, R3, F4, and R4), whose location in the pex3Δ and pex16Δ loci are shown by arrows. Rpl32 was used as a positive control. The sizes of the PCR products were 152 base pairs (bp) (RpL32), 179 bp (F1+R1), 180 bp (F2+R2), 200 bp (F3+R3), and 284 bp (F4+R4). Scale bar represents 0.5 Kb. (TIF)

Figure S2 EGFP-SKL is co-localized with PMP70-ECFP in S2 cells. Peroxisomes were detected in S2 cells by EGFP-SKL (green in left panel) and PMP70-ECFP (magenta in middle panel). The merged image is shown at right. (TIF)

Figure S3 Overexpression of pex16 results in fewer but enlarged peroxisomes. UAS-EGFP-SKL was driven by NP5021 (for expression in whole gut, A) or nos-GAL4 (for expression in germ cells, C). Both UAS-pex16 and UAS-EGFP-SKL were driven by NP5021 (B) or nos-GAL4 (D). Malpighian tubules (A and B) and spermatocytes (C and D) are shown. The fluorescent images in the A’ to D’ correspond to the phase-contrast micrographs in A to D, respectively. Arrowhead in D’ indicates an enlarged peroxisome. Scale bars represent 20 μm (A’ and 10 μm (C’). (E and F) Average number of peroxisomes per 1,000 μm² of cytoplasm in the confocal images of malpighian tubule cells (E) and spermatocytes (F). Magenta in F indicates the number of enlarged peroxisomes, which were defined as being over twice the average size of wild-type peroxisomes. (TIF)

Figure S4 Presynaptic structures and glial cells appear unaffected in pex16Δ flies. (A and B) Brains from adult flies were stained with an ncl2 antibody to observe presynapses. Confocal images of the optic lobe are shown: wild-type (A) and pex16Δ (B). (C and D) Brains from adult flies were stained with anti-Repo (Green) and anti-Homer (Magenta) antibodies to show glial cells and neuropile, respectively. Projection images of the optic lobe are shown: wild-type (C) and pex16Δ (B). Scale bars represent 20 μm. (TIF)

Figure S5 Cyst cells form normally in the testis of Pex16 homozygotes. (A and B) Peroxisomes were detected in the spermatocytes or cyst cells of the wild-type testes (A), but not in the pex16Δ homozygote (B) testes expressing UAS-EGFP-SKL driven by Act-GAL4. Scale bar in A represents 100 μm. (C and D) The cyst cells were morphologically normal in the testes of pex16Δ homozygotes. UAS-EGFP was driven by ptc-GAL4, expressing GAL4 in cyst cells, in the testes of wild-type (C) and pex16Δ homozygotes (D). Cyst cells were detected by anti-GFP antibody staining and are indicated by white arrowheads in C and D. (E and F) Peroxisomes are absent in the spermatocytes of pex16Δ homozygotes. Phase-contrast micrographs of spermatocytes in wild-type (E) and pex16Δ homozygote (F) testes expressing UAS-EGFP-SKL driven by nos-GAL4 are shown. The fluorescent images shown in E’ and F’ correspond to the phase-contrast micrographs of E and F, respectively. Scale bar in E represents 20 μm. (TIF)

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Author Contributions

Conceived and designed the experiments: MN KM. Performed the experiments: MN HS TO NF NK. Analyzed the data: MN KM. Contributed reagents/materials/analysis tools: HA ES. Wrote the paper: MN HA MU HOI KM.

References