Sphingolipid desaturase DEGS1 is essential for mitochondria-associated membrane integrity

Laura Planas-Serra, … , Estela Area-Gómez, Aurora Pujol


Sphingolipids function as membrane constituents and signaling molecules, with crucial roles in human diseases, from neurodevelopmental disorders to cancer, best exemplified in the inborn errors of sphingolipid metabolism in lysosomes. The dihydroceramide desaturase Δ4-dihydroceramide desaturase 1 (DEGS1) acts in the last step of a sector of the sphingolipid pathway, de novo ceramide biosynthesis. Defects in DEGS1 cause the recently described hypomyelinating leukodystrophy-18 (HLD18) (OMIM #618404). Here, we reveal that DEGS1 is a mitochondria-associated endoplasmic reticulum membrane–resident (MAM-resident) enzyme, refining previous reports locating DEGS1 at the endoplasmic reticulum only. Using patient fibroblasts, multiomics, and enzymatic assays, we show that DEGS1 deficiency disrupts the main core functions of the MAM: (a) mitochondrial dynamics, with a hyperfused mitochondrial network associated with decreased activation of dynamin-related protein 1; (b) cholesterol metabolism, with impaired sterol O-acyltransferase activity and decreased cholesteryl esters; (c) phospholipid metabolism, with increased phosphatidic acid and phosphatidylserine and decreased phosphatidylethanolamine; and (d) biogenesis of lipid droplets, with increased size and numbers. Moreover, we detected increased mitochondrial superoxide species production in fibroblasts and mitochondrial respiration impairment in patient muscle biopsy tissues. Our findings shed light on the pathophysiology of HLD18 and broaden our understanding of the role of sphingolipid metabolism in MAM function.

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Sphingolipid desaturase DEGS1 is essential for mitochondria-associated membrane integrity

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Sphingolipids function as membrane constituents and signaling molecules, with crucial roles in human diseases, from neurodevelopmental disorders to cancer, best exemplified in the inborn errors of sphingolipid metabolism in lysosomes. The dihydroceramide desaturase A4-dihydroceramide desaturase 1 (DEGS1) acts in the last step of a sector of the sphingolipid pathway, de novo ceramide biosynthesis. Defects in DEGS1 cause the recently described hypomyelinating leukodystrophy-18 (HLD18) (OMIM #618404). Here, we reveal that DEGS1 is a mitochondria-associated endoplasmic reticulum membrane–resident (MAM-resident) enzyme, refining previous reports locating DEGS1 at the endoplasmic reticulum only. Using patient fibroblasts, multiomics, and enzymatic assays, we show that DEGS1 deficiency disrupts the main core functions of the MAM: (a) mitochondrial dynamics, with a hyperfused mitochondrial network associated with decreased activation of dynamin-related protein 1; (b) cholesterol metabolism, with impaired sterol O-acyltransferase activity and decreased cholesteryl esters; (c) phospholipid metabolism, with increased phosphatidic acid and phosphatidylserine and decreased phosphatidylethanolamine; and (d) biogenesis of lipid droplets, with increased size and numbers. Moreover, we detected increased mitochondrial superoxide species production in fibroblasts and mitochondrial respiration impairment in patient muscle biopsy tissues. Our findings shed light on the pathophysiology of HLD18 and broaden our understanding of the role of sphingolipid metabolism in MAM function.

Introduction

Sphingolipids (SLs) are fundamental components of cellular membranes and bioactive signaling molecules that are constituted by a sphingoid base backbone coupled to a fatty acyl chain. Ceramide (Cer) serves as the central building block for more complex SL species. Generation of Cer mainly occurs via 3 pathways: (a) the de novo pathway, which uses palmitoyl-CoA and serine as its precursors, (b) the sphingomyelinase pathway, which converts sphingomyelin (SM) into Cer bidirectionally, and (c) the salvage pathway, which converts complex SLs into Cer (1, 2) (see Supplemental Figure 1; supplemental material available online with this article; https://doi.org/10.1172/JCI162957DS1).

The regulation of SL metabolism is critical in human physiology, as underscored by the numerous neurological and multisystemic inborn errors of SL metabolism that are caused by faulty enzymes of lysosomal SL degradation, such as Gaucher disease, Niemann-Pick disease, Krabbe disease, and metachromatic leukodystrophy (2, 3, 4). Recently, the advent of clinical genomics technologies and whole-exome and genome sequencing has uncovered the genetic causes of novel disease entities in the de novo synthesis pathway of SLs (see Supplemental Figure 1). Mutations in the coding gene of its first and rate-limiting enzyme, serine palmitoyltransferase long chain base subunit 1 (SPTLC1), cause a childhood-onset form of amytrophic lateral sclerosis (S) and also a peripheral neuropathy (6, 7). Likewise, malfunction

Conflict of Interest: The authors have declared that no conflict of interest exists.

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of Δ4-dihydroceramide desaturase 1 (DEGS1), which converts dihydroceramide (DhCer) into Cer (8) at the last step of this de novo pathway, causes severe hypomyelinating leukodystrophy-18 (HLD18) (OMIM #618404) (9, 10, 11). Beyond this rare disease, intriguing emerging evidence associates DEGS1 expression and aberrant levels of Cer and/or DhCer with the appearance of comorbidities in the context of obesity, including type 2 diabetes, insulin resistance, and cardiovascular diseases (12, 13, 14, 15, 16). However, the molecular mechanisms by which alterations in SL metabolism trigger human pathology are still under debate.

Although several enzymes of SL metabolism are located in lysosomes (17), numerous reports indicate that sphingomyelinase and Cer synthase activity, which are responsible for Cer biosynthesis, are significantly increased in specific domains of the ER found in close apposition to mitochondrial membranes, called mitochondria-associated ER membranes (MAMs) (18, 19, 20, 21). These ER structures are transient and dynamic lipid raft-like membranes that are pivotal for mitochondrial and cellular physiology. MAMs recruit multiple enzymes to orchestrate essential metabolic cascades, including phospholipid (PL) synthesis and transport, lipid droplet (LD) biogenesis, cholesterol esterification, cell metabolism of fatty acid esters, calcium homeostasis, and mitochondrial dynamics (22, 23, 24, 25), among other functions.

Here, we show that DEGS1 is not homogenously distributed in the ER as reported previously (10, 26, 27), but is enriched in MAM domains, expanding the known role of MAMs in Cer synthesis to the de novo branch of the pathway. Furthermore, we report that DEGS1 deficiency induces substantial alterations in lipid metabolism, the disruption of mitochondrial dynamics, and bioenergetic failure, broadening our understanding of this enzyme in rare and complex metabolic diseases.

Results

Aberrant mitochondrial homeostasis in DEGS1 patient muscle biopsies. The clinical presentations of several DEGS1 patients evaluated here (Supplemental Table 1) were compatible with those with a primary mitochondrial disorder, which prompted some centers (patients 9 [Pat. 9] and Pat. 20) to include muscle biopsies during the diagnostic workup prior to the establishment of a molecular diagnosis by whole-exome sequencing. For instance, histological and histochemical analysis of the quadriceps muscle biopsy from Pat. 20 revealed moderate variability in fiber size, with a population of hypotrophic fibers by H&E staining. Furthermore, there was an increase in myofibrillar lipid content, with larger LDs in both type I and II fibers, as revealed by Sudan black and Oil Red O staining (Figure 1A). No increase in the endomysial connective tissue, ragged red fibers, and subsarcolemmal accumulations of mitochondria were detected by modified Gomori trichrome stain, although granular structures inside the fibers were observed (Figure 1A). Moreover, our immunofluorescence data from Pat. 20 showed that these granular and larger structures were mitochondria, as they contained with complex I and the mitochondrial voltage-dependent anion channel 1 (VDAC1) (Figure 1B).

Moreover, muscle tissues from both Pat. 9 and Pat. 20 presented with a population of fibers in mosaic with pale cytochrome c oxidase (COX) staining, showing an immature pattern in the absence of mitochondrial proliferation (Figure 1C). These findings suggest a loss of enzymatic activity for complex IV. In the same fibers, we observed a mosaic pattern with pale succinate dehydrogenase (SDH) staining (Figure 1C) indicating loss of complex II enzymatic activity. In line with the complex I and VDAC1 data for Pat. 20, SDH and COX stains revealed a coarse granular appearance compared with that for controls (Figure 1C).

The quadriceps muscle biopsy of Pat. 9 was further studied by transmission electron microscopy (TEM) and displayed increased numbers of LDs in close apposition to mitochondria (Figure 1D). Furthermore, in most muscle fibers, mitochondria showed alterations in size, length, and shape, with higher transverse diameter (500 to 800 nanometers) in comparison with controls (400 nanometers) and length up to 3 microns (Figure 1D and Supplemental Figure 2A). Additionally, some mitochondria presented irregular shapes, such as triangular, angular, branched, and alternation of strangulation and dilation areas (Figure 1D). Moreover, some mitochondrial cristae were abnormally profuse and densely packed (Figure 1D). These findings may suggest an impairment in the regulation of mitochondrial dynamics.

To further characterize these mitochondrial abnormalities, we measured the oxygen consumption rate (OCR) in isolated mitochondria from the muscle tissue from Pat. 9 and in total fibroblasts from Pat. 9 and Pat. 20, confirming a defect in the oxidative phosphorylation system (OXPHOS) complexes (Table 1 and Supplemental Table 2). In isolated mitochondria from muscle tissue, in the presence of either pyruvate or succinate as carbon sources, the OCR was significantly decreased compared with that of controls, as was the activity of all OXPHOS complexes. In addition, citrate synthase activity was decreased, and lactate dehydrogenase activity was increased in muscle from Pat. 9 (Table 1). The respiratory chain data indicated a very low mitochondrial activity with decreased mitochondrial mass in DEGS1 patient muscle and fibroblasts, which is a similar finding to that of genetic disorders of complex subunits encoded by mitochondrial DNA (mtDNA). Together, these data indicate that dysfunction of DEGS1 affects mitochondrial morphology and respiration in quadriceps muscle and fibroblasts, inducing important bioenergetic defects.

Mitochondrial aberrant morphology in DEGS1 patient fibroblasts. We explored mitochondrial morphology in fibroblasts using TEM. The mitochondrial area was increased in DEGS1 patient fibroblasts in comparison with those of controls (Figure 2, A and B). Moreover, we observed that the mitochondrial crests presented abnormal morphologies in DEGS1 patient cells (Figure 2, C and D). Since OXPHOS complexes are found at the mitochondrial crests (28), the abnormal morphology of the crests may help explain the decreased activity observed in DEGS1 patient muscle and fibroblasts.

DEGS1 deficiency induces mitochondrial dynamics defects and increased mitochondrial ROS production. We next performed live-cell imaging studies in fibroblasts to obtain a 3D view of the mitochondrial morphology. Using MitoTracker as a fluorescence marker, we confirmed that mitochondria appeared hyperfused and exhibited increased mitochondrial area and sphericity in DEGS1 patient fibroblasts compared with controls (Figure 3, A–C). To investigate whether fusion and fission imbalances could underlie this hyperfused phenotype, we compared the numbers of disconnected mitochondria at the end of the live-cell imaging experiment (4 hours) to the ones at the beginning of it, using Imaris...
Figure 1. Mitochondrial damage in vivo. (A) Muscle histopathology. Sudan black and Oil Red O staining for neutral lipids, H&E staining for fiber size, and modified Gomori trichrome staining for the endomysial connective tissue of the quadriceps muscle biopsy from Pat. 20 and a child who served as a control (CTL). (B) Immunofluorescence for complex I and VDAC1 markers in the quadriceps muscle biopsy from Pat. 20 and a child who served as a control. (C) Skeletal muscle histochemistry. COX and SDH staining of quadriceps muscle biopsies from Pat. 9 and Pat. 20 and a child who served as a control. (D) TEM of the quadriceps muscle biopsy in the longitudinal plane from Pat. 9 and a child who served as a control. Mitochondria and LDs are highlighted in orange and pink, respectively.
software. We observed that the numbers of disconnected mitochondria in DEGS1 patient fibroblasts decreased, suggesting lesser fission events than in controls (Figure 3D and Supplemental Videos 1–4).

We then measured the levels of the main essential proteins involved in these fusion and fission processes: dynamin-related protein 1 (DRP1) and its phosphorylated form (pDRP1566), mitofusin 2 (MFN2), and optic atrophy protein 1 (OPA1). DRP1 is a GTPase responsible for mitochondrial fission and mitochondrial membrane scission, and it requires phosphorylation at serine 616 to become active. Once phosphorylated, pDRP1566 translocates to mitochondria, where it oligomerizes and binds to its adaptors at constriction sites, leading to mitochondrial fission (29). MFN2 and OPA1 are GTPases that mediate inner and outer mitochondrial membrane fusion, respectively (30, 31). However, a shift toward shorter OPA1 isoforms has been associated with increased mitochondrial fission (31). Consistent with the hyperfused phenotype, the ratio pDRP1566/DRP1 was significantly decreased in DEGS1 patient fibroblasts. Conversely, while we found a decrease in OPA1 levels, MFN2 levels were not significantly altered (Figure 3, E and F). We evaluated the mitochondrial protein levels using VDAC1 as a mitochondrial marker and observed no differences between DEGS1 patient fibroblasts and controls (Supplemental Figure 2, B and C).

DEGS1-dependent morphological alterations are reflected in function defects. Mitochondrial membrane potential (ΔΨm) is a key indicator of mitochondrial activity and depends on the permeability of the membranes (32). The ΔΨm of fibroblasts treated with the uncoupler carbonyl cyanide 4-(trifluoromethoxy) phenylhydrazone (FCCP) was significantly decreased in DEGS1 patients (Figure 3G).

We have recently reported that total intracellular ROS production was increased in DEGS1 patient fibroblasts (9). Cellular sources of ROS production are varied, including the ER, mitochondria, peroxisome, xanthine oxidase, cyclo-oxygenases, cytochrome p450 enzymes, lipooxygenases, flavin-dependent demethylase, oxidases for polyamines and amino acids, and nitric oxide synthases that produce oxidants (33). Given the abnormal mitochondrial morphology, we compared the total superoxide species production in the cell (using dihydroethidium [DHE]) to the superoxide generated only at mitochondria (using MitoSOX), as previously described (34). Our results revealed that the mitochondrial compartment is a superoxide overproduction site in DEGS1 patient fibroblasts (Figure 3H), although we cannot rule out other sources.

**DEGS1 is localized at the MAMs.** In light of these data indicating the malfunction of mitochondrial respiration and dynamics, we set out to revisit the reported localization of DEGS1 at the ER (26, 27). We first explored the subcellular localization of DEGS1 in control fibroblasts. We performed immunofluorescence costaining with markers for specific cell compartments: ER (calnexin), mitochondria (MitoTracker), MAM (ERLIN2, ACSL4, DRP1 and MFN2), and Golgi apparatus (GM130). We found that DEGS1 was enriched in the ER areas next to mitochondria, colocalizing with MAM-resident proteins. In contrast, we detected less colocalization with markers for specific cell compartments: ER (calnexin), mitochondria (MitoTracker), MAM (ERLIN2, ACSL4, DRP1 and MFN2), and Golgi apparatus (GM130). We found that DEGS1 was enriched in the ER areas next to mitochondria, colocalizing with MAM-resident proteins. In contrast, we detected less colocalization with MitoTracker or calnexin and essentially no colocalization with GM130 (Figure 4 and Supplemental Figure 3).

To confirm these results in a tissue with high myelin content, we isolated subcellular fractions from human brain subcortical white matter of healthy individuals and analyzed them by Western blot using specific markers for each compartment. In agreement with our immunofluorescence colocalization data, DEGS1 was present in several cell compartments, although it was significantly enriched in the MAM fraction (Figure 5 and Supplemental Figure 4). Likewise, quantitative proteomics analysis of enriched MAM fractions from the spinal cord of WT mice revealed high levels of DEGS1 and known MAM-resident proteins such as ERLIN2 among others (Table 2), further supporting the contribution of SL homeostasis to the integrity of this dynamic domain.

As a lipid raft–enriched fraction, the MAM is a transient functional membrane domain formed by local increases in cholesterol (35). Therefore, we used an additional technique to more directly

### Table 1. Spectrophotometric assay of respiratory chain enzyme activities in muscle biopsy

<table>
<thead>
<tr>
<th>Enzyme activity (nmols/min/mg protein)</th>
<th>Pat.9</th>
<th>Control range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pyruvate (+malate)</td>
<td>13</td>
<td>20–83</td>
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<tr>
<td>Succinate</td>
<td>26</td>
<td>33–141</td>
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</table>

**Activity ratio**

<table>
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<th>Activity ratio</th>
<th>Pat.9</th>
<th>Control range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Succinate OX/pyruvate OX</td>
<td>2</td>
<td>1.2–2.0</td>
</tr>
<tr>
<td>Complex II+III/succinate OX</td>
<td>1.7</td>
<td>2.9–6.1</td>
</tr>
</tbody>
</table>

**OXPHOS activity (nmols/min/mg protein)**

<table>
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<tr>
<th>Complex</th>
<th>Pat.9</th>
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</thead>
<tbody>
<tr>
<td>Complex I</td>
<td>26</td>
<td>60–123</td>
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<tr>
<td>Complex I+III</td>
<td>38</td>
<td>210–469</td>
</tr>
<tr>
<td>Complex II</td>
<td>31</td>
<td>105–270</td>
</tr>
<tr>
<td>Complex II+III</td>
<td>45</td>
<td>202–525</td>
</tr>
<tr>
<td>Complex III</td>
<td>200</td>
<td>1007–2465</td>
</tr>
<tr>
<td>Complex IV</td>
<td>161</td>
<td>1100–2800</td>
</tr>
</tbody>
</table>

**Enzyme activity (nmols/min/mg protein)**

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<tr>
<th>Enzyme activity</th>
<th>Pat.9</th>
<th>Control range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cytochrome oxidase</td>
<td>52</td>
<td>175–385</td>
</tr>
<tr>
<td>Lactate dehydrogenase</td>
<td>3,044</td>
<td>1,200–2,450</td>
</tr>
<tr>
<td>Citrate synthase</td>
<td>57</td>
<td>70–150</td>
</tr>
<tr>
<td>OX, oxidase.</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Complex IV/succinate OX**

| Complex I+III/succinate OX | 1.5  | 2.7–4.3      |
| Complex II/succinate OX    | 1.2  | 1.5–2.3      |
| Complex II+III/succinate OX| 1.5  | 1.8–2.6      |
| Complex III/succinate OX   | 6.5  | 7.9–11.9     |
| Complex IV+II+III/succinate OX | 3.6 | 4.1–5.7     |
| Complex IV/succinate OX    | 5.2  | 8.7–12.7     |
| Complex IV+II+III/succinate OX | 1.2 | 3.9–5.5     |
| Complex IV+II+III/succinate OX | 0.8 | 0.8–1.6     |

**Complex IV/citrate synthase**

| Complex IV/citrate synthase | 0.9  | 2.3–3.9      |
| Lactate dehydrogenase/citrate synthase | 58.5 | 2.6–7.4    |
verify whether DEGS1 was located at the MAM. We incubated WT mouse embryonic fibroblasts (MEFs) with PhotoClick cholesterol, a cholesterol analog conjugated to a photoreactive alkyne that mimics native cholesterol. Using these cells, we next isolated MAM domains by subcellular fractionation and pulled down click cholesterol by conjugation to an azide-biotin tag followed by binding streptavidin beads, as described (36), and performed a proteomics analysis. Our results showed that several well-known MAM markers, such as ERLIN2 and ACLS4, were detected bound to cholesterol at MAM domains. Moreover, we were also able to detect DEGS1 bound to cholesterol in the MAM fractions, confirming our previous localization studies (Table 3).

**DEGS1 is required for MAM integrity and function.** We next tested the potential functional impact of DEGS1 deficiency on MAM activities, focusing first on the synthesis of phosphatidylethanolamine (PE). This process involves the following steps: (a) phosphatidylserine (PS) synthesis by PS synthases 1 and 2 (PTDSS1/2) at the MAM, (b) its transport, and (c) its decarboxylation into PE by PS decarboxylase (PISD) in the mitochondria (37) (Figure 6A). For that, DEGS1 patient and control fibroblasts were incubated in a medium
Figure 3. Mitochondrial dynamics and bioenergetics impairment in DEGS1 patient fibroblasts. (A) Analysis of the mitochondrial morphology by MitoTracker (MitoT) staining in 4-hour live-cell imaging; disconnected mitochondria are each shown in different colors. Mitochondrial (B) area and (C) sphericity quantifications. (D) Quantification of numbers of disconnected mitochondria over time. DEGS1 patient (n = 6) and control (n = 5) fibroblasts. (E) Western blot analysis of fusion and fission proteins and (F) their quantification. DEGS1 patient (n = 5) and control (n = 5) fibroblasts. (G) Quantification of ΔΨm by measuring TMRE intensity. FCCP was used as a mitochondrial oxidative phosphorylation uncoupler. DEGS1 patient (n = 6) and control (n = 5) fibroblasts. (H) Quantification of intracellular (DHE) and mitochondrial (MitoSOX) superoxide species production levels. The complex III inhibitor antimycin A (200 μM) was used for treatment for 1 hour as a positive control for ROS production. DEGS1 patient (n = 5) and control (n = 4) fibroblasts. All experiments were done in triplicate. Data are represented as box-and-whisker plots (median, interquartile interval, minimum, maximum). *P < 0.05; **P < 0.01; ***P < 0.001, Wilcoxon’s test.
containing 3H-serine, and after 12 hours, we measured the incorporation of the label into newly synthesized 3H-PS and 3H-PE. Notably, compared with control fibroblasts, all patient fibroblasts showed a decrease in the conversion of 3H-PS into 3H-PE (Figure 6B). This finding suggests a defect in MAM function and indicates impaired ER-mitochondria crosstalk in DEGS1 patients. In agreement, the activity of sterol O-acyltransferase 1 (SOAT1, also known as ACAT1), a MAM-resident enzyme that catalyzes the conversion of free cholesterol (FC) to cholesteryl ester (CE) (20, 38) (Figure 6A), was significantly decreased in DEGS1 patient fibroblasts (Figure 6C).

We and others previously reported that dysfunction of DEGS1 increases the DhCer/Cer ratio, and it also affects the ratios of other dihydro sphingolipids (dihydrosLs) in patient fibroblasts (9, 10, 11). To expand the molecular characterization of this phenotype, we performed a targeted lipidomics analysis of total fibroblasts and isolated MAMs from fibroblasts of DEGS1 patients and controls. Our results indicated that DEGS1 impairment increased the levels of DhCer and dihydro sphingomyelin (DhSM) in both the total homogenate and the MAM fraction compared with their unsaturated forms, Cer and SM (Figure 6, D and E). Moreover, in DEGS1 patient fibroblasts, the levels of dihydrohexosyl ceramide (DhHexCer) were increased compared with the levels of their unsaturated form hexosyl ceramide (HexCer) in both total homogenate and MAM-isolated membranes (Figure 6, F and G). Galactosyl ceramide (GalCer) is the main lipid constituent of myelin, which in addition to glucosyl ceramide (GluCer) are the two types of HexCer that are found in mammals. Thus, it appears that DEGS1 activity is not only necessary for the conversion of DhCer to Cer, but is also necessary for the conversion of most, if not all, of the dihydroSLS to their saturated forms. This aberrant lipidic composition likely drives the myelinization defects observed in our patients (9).

We next performed TEM in DEGS1 patient and control fibroblasts to assess the distance between the mitochondria and the ER, which usually ranges from 10 to 50 nm in this cell type (39). We observed that the mean distance between the 2 organelles was increased more than 2-fold in DEGS1 patient cells (mean = 80.955 ± 6.293 nm) compared with controls (mean = 30.048 ± 3.923 nm) (Figure 6, H and I). This abnormally larger distance suggests that MAM formation may be physically hampered. Taken together, these data indicate that the impairment of DEGS1 induces remarkable alterations in the functional and structural connection between the ER and mitochondria.

DEGS1 deficiency affects the homeostasis of LDs, neutral lipids, and PLs. Alterations in the SL composition of the MAM result in significant changes in cellular lipid metabolism. In turn, these dysfunctions can disturb the formation of LDs, as it is regulated in MAM microdomains (40). Notably, as mentioned above, histological analysis of muscle tissues from DEGS1 patients showed increases in the number and size of LDs in the cytosol. To confirm that LDs were larger in DEGS1 patients, we stained patient fibroblasts with Oil Red O, a staining specific for neutral lipids and CE. We observed a significant increase in LD compartment size, as quantified by Feret’s diameter, and in the number of droplets per cell in patient fibroblasts (Figure 7, A–C).

LDs are composed of a core of neutral lipids and mainly consist of triacylglycerides (TAGs) and CE. TAGs are synthesized de novo from diacylglycerides (diacylglycerol [DAGs]) by diacylglycerol O-acyltransferase 1/2 (DGAT1/2), among others. When in excess, DAGs can also be stored in LDs (41). Notably, our targeted lipidomics data showed a significant increase in DAG levels in DEGS1 patient fibroblasts. Additionally, the levels of its immediate biosynthetic precursor, phosphatidic acid (PA), were increased (Figure 7D). However, the levels of TAGs in DEGS1 fibroblasts were not significantly increased compared with controls (Figure 7D).

To gain insight into the mechanism behind these alterations, we measured the expression of the genes encoding key enzymes involved in the regulation of DAGs and TAGs. We observed increased mRNA levels of DGAT2 and diacylglycerol kinase alpha (DGKA), which phosphorylates DAGs into PA. There were no differences in the mRNA levels of DGAT1 (Figure 7E). Of note, DGAT2, but not DGAT1, is localized at the MAM (42). These genes are controlled by the expression of master regulators of lipid homeostasis sterol regulatory element binding factors 1a, 1c, and 2 (SREBF1/a/1c/2). The expression levels of these genes were also significantly increased in DEGS1 patient fibroblasts (Figure 7F).

To validate the activation of SREBFs, we assessed the expression of its additional central target genes HMGCSS, HMGCR, MVD, and SQUE. All of these genes, which are involved in cholesterol synthesis, were upregulated in DEGS1 fibroblasts (Figure 7G). SREBF2 expression is generally modulated by cholesterol-mediated negative feedback; in contrast, SREBF1 activation is not primarily controlled by cholesterol levels (43). In agreement with our SOAT1 activity assay results, we observed that the CE/FC ratio was decreased in DEGS1 patient fibroblasts (Figure 7H), suggesting an impairment in the regulation of this enzyme. Therefore, increased FC levels do not inhibit the expression of SREBF2 in this context.

The expression and activation of SREBFs are also involved in the regulation of PL homeostasis. In Drosophila melanogaster, when PE levels were increased, the activation of SREBF1 was inhibited. In contrast, when PE levels were low, the SREBF pathway was stimulated (44). Moreover, in Caenorhabditis elegans and mammalian cells, phosphatidylcholine (PC) inhibited the activation of SREBF1. However, when PC synthesis was attenuated in C. elegans, human hepatoma cells, and mouse livers, the expression levels of SREBF and its target genes increased (45). Consequently, we evaluated the levels of the main mammalian PLs, PS, PE, and PC. In DEGS1 patient fibroblasts, PS levels were increased, while the levels of PE were diminished and PC showed a decreasing trend (Figure 7I). These expected results are consistent with the PL synthesis and trafficking assay reflecting MAM activity shown in Figure 6, B and C.

Taken together, our data indicate that DEGS1 deficiency affects the regulation of TAG metabolism and TAG storage into LDs, as observed in muscle biopsies (Figure 1, A and D), as well as the regulation of PL homeostasis.

Discussion

Biallelic loss-of-function mutations in DEGS1 have been recently reported by our group and others as the genetic cause of HLD18 (9, 10, 11), but little is known about the mechanisms underlying the pathophysiology of this ultra-rare disorder. Our results suggest that the disruption of the structure and function of the MAM is likely a key process underlying the metabolic and bioenergetic failure observed in DEGS1 patient fibroblasts and tissues (Figure 8).
Figure 4. DEGS1 localizes at the MAM. Immunofluorescence analysis in control fibroblasts (n = 5). Colocalization between DEGS1 (in green) and ERLIN2, ACSL4, DRP1, and MFN2 (MAM-resident proteins), MitoTracker (mitochondria marker), calnexin (ER marker), and GM140 (Golgi marker) (all in red). Colocalization area (coloc) is shown in white.
In this work, we show that, in contrast with what was shown in previous reports (10, 26, 27), DEGS1 is not homogeneously distributed in the ER, but is substantially enriched at MAM domains. This distribution is similar to that of other Cer-producing enzymes, such as sphingomyelinase and Cer synthases (Supplemental Figure 1) (18, 19, 21). Given that SLs are principal MAM constituents and essential components in lipid rafts, we posit that their imbalance may alter the MAM composition. In turn, disrupted MAMs may impair the correct synthesis of SLs in a vicious cycle, underscoring and expanding the critical role of MAMs in the regulation of SL metabolism and vice versa (46).

Our results also indicate that DEGS1 is necessary for both MAM integrity and its core functions in lipid metabolism, such as PL and CE biosynthesis (20, 37), which are severely affected in fibroblasts from DEGS1 patients. These results expand the impact of DEGS1 deficiency beyond the SL pathway. Of note, the structure and activities of MAMs are intimately dependent on its lipidic composition. The MAM is a transient domain formed by a local elevation of cholesterol and SM in the ER, with the characteristics of a lipid raft (35, 47). This change in the lipid milieu of the ER induces the partitioning of lipid-binding ER proteins into discrete lipid domains and changes their conformation and functional regulation. Of direct relevance to this, defective DEGS1 causes an increase in the DhsM/SM ratio, as reported in this work and others (10, 11). Elevations in DhsM increase the rigidity of lipid raft microdomains (48). This is probably due to the enhanced affinity of DhsM for cholesterol in membranes, as shown by biophysical studies (49). MAM formation results in the activation of neutral sphingomyelinases, subsequent decreases in SM, and increases in Cer levels in MAMs and mitochondrial membranes (50, 51). Conversely, MAM-deficient cells present with decreased sphingomyelinase activity and lower SL turnover (52). Therefore, the functionality of MAMs and SL balance are intertwined, and DEGS1 is pivotal for their homeostasis.

Following on membrane composition, the myelin sheath is made of approximately 80% lipids and 20% proteins, with the principal constituent being GalCer (53). Of note, excess of GalCer due to the malfunction of galactosylceramidase causes demyelination in Krabbe disease (17). Because the MAM regulates the synthesis of Cer, which is the primary GalCer precursor, DEGS1 intrinsic dysfunction combined with disruption of the MAM may explain the defects in myelin formation and maintenance found in DEGS1 patients.

Furthermore, we show that muscle tissue and fibroblasts from DEGS1 patients exhibit a higher proportion of aberrantly elongated mitochondria, linked to an alteration in the regulation of mitochondrial dynamics, similar to that described in other primary mitochondria diseases, such as Leigh syndrome (54) or Charcot-Marie-Tooth type 2A (55). This, together with the impaired respiration in muscle biopsies and fibroblasts from patients, could be a consequence of altered mitochondrial morphology. Similar alterations occur in some mitochondriopathies in which cristae morphology defects are accompanied by OXPHOS dysfunction (28), as exemplified in optical atrophy 1 disease (OMIM #165500) (56). Defects in the regulation of the MAM in DEGS1 patients could also help explain the mitochondrial hyperfused phenotype and bioenergetic impairment. An imbalance in the levels of Cer in ER-Mitochondria connections has been suggested as inducing mitochondrial membrane damage and bioenergetic defects (57). Indeed, alterations in MAM protein recruitment and/or the lipidome of the mitochondrial outer and inner membranes can alter the control of the fusion and fission processes through DRP1 or MFN2 (30, 58, 59, 60). Mutations in DRP1 cause optical atrophy 5 disease (OPAS) (OMIM #610708) and lethal encephalopathy (EMPFI) (OMIM #614388). Some patients with these DRP1 mutations display decreased activity of complex IV (61) and complexes I, III, and IV (62) and defects in mitochondrial dynamics. In DEGS1 deficiency, however, MAM dyshomeostasis would induce a secondary impact on the mitochondrial shape and function of the OXPHOS complexes.

The MAM is involved in the regulation of PL synthesis and metabolism and in TAG and CE production (19, 42). Specifically, the MAM governs the synthesis of PA that is then transferred to mitochondria to produce cardiolipin (CL), a mitochondrial lipid that is essential for the maintenance of OXPHOS (63). Our data suggest that defects in MAM functionality may underlie the significant increases in the levels of PA that were observed in DEGS1 patient fibroblasts. Notably, the mitochondrial fission protein DRP1 has a specific affinity for PA. This PL blocks DRP1 after its oligomerization onto mitochondria, leading to continuous assemblly. Thus DRP1 is inhibited, which leads to a lower mitochondrial division/fission rate (63). Therefore, elevations in PA and a subsequent decrease in DRP1 activity could be the leading cause of the mitochondrial hyperfused phenotype that was observed in patient fibroblasts. Of note, PA itself can stimulate mitochondrial fusion by creating negative mitochondrial membrane curvatures (63). As a result of this hyperfused morphology, mitochondria may generate superoxides that in turn contribute to mitochondrial damage in a vicious cycle. In addition, PA is the immediate precursor of DAG synthesis in the glycerol-3-phosphate pathway. Therefore,
impairments in the transfer of PA to mitochondria for CL production may promote a shift toward DAG synthesis, which could explain the higher DAG levels that were detected in DEGS1 patient fibroblasts. Puzzlingly, despite these elevations in DAGs and in the expression of DGAT2, DEGS1 patient fibroblasts showed normal levels of TAGs. Notably, DGAT2 is a MAM-resident enzyme whose expression is controlled by SREBFs, which are the master regulators of lipid metabolism (42). SREBFs were also increased in this context. One plausible explanation may be that SREBFs act as lipid biosensors in response to the decreased levels of PE and PC. Thus, SREBFs can cause an aberrant lipogenesis program and increase the formation and accumulation of LDs.

Finally, we showed the accumulation of supersized LDs in DEGS1 patients, which could be a proxy for increased ROS formation, as proposed previously (64). Since MAM regulation has been suggested as a key factor in the formation of LDs (40), it is plausible that defects in MAM functionality could interfere with LD biogenesis in HLD18 pathogenesis. In the last decade, it has been reported that loss of LD homeostasis is disease causing in several monogenetic hereditary spastic paraplegias (65). However, whether LD malfunction is a contributing factor or rather plays a protective role in the context of broadly defined, complex neurodegenerative disorders is a matter of debate. Some authors posit an instrumental role of LDs in mitochondrially induced increased ROS and cellular demise (66), while others advocate for LDs as protective agents against potentially harmful lipids sequestered within, including Cer (67, 68).

This study highlights the importance of evaluating MAM and mitochondrial functionality in lipid disorders beyond primary mitochondrialopathies. Taken together, our findings provide a conceptual basis for the underlying pathogenesis of HLD18 and may have implications for the management of this and other diseases caused by SL imbalance. The present study also exemplifies how rare monogenic diseases may help elucidate fundamental cellular metabolic functions. In this case, the knowledge gained could be applied to tackling more complex disorders, given the emerging role of DEGS1 in type 2 diabetes and cardiovascular disease (12, 13, 14, 15, 16).

### Methods

#### Patients and genetic studies

Muscle biopsies were obtained from the quadriceps muscles of DEGS1 patients and a 5-year-old child who served as a control. Skin-punch biopsies were performed to obtain primary human fibroblasts of DEGS1 patients and controls. The fibroblasts were grown in DMEM (Thermo Fisher Scientific) containing 10% fetal bovine serum, 100 U/ml penicillin, and 100 μg/ml streptomycin and maintained at 37% in a humidified 95% air/5% CO2 incubator. Brain tissue (white matter of frontal lobes) from controls was obtained from the Brain and Tissue Bank for Developmental Disorders at the University of Maryland. More information about controls can be found in Supplemental Table 3.

#### Mouse lines

Twelve-month-old male WT mice on a pure C57BL/6 background were used for all experiments. The mice were housed under a 12-hour light/12-hour dark cycle, with ad libitum access to food and water. The animals were sacrificed. The spinal cord was removed and stored at –80°C.

#### Reagents

The reagents used are described in Supplemental Methods.

#### Antibodies

The antibodies used for Western blots and immunofluorescence experiments are described in Supplemental Table 4. For DEGS1 colocalization with ERLIN2, these antibodies were conjugated with Alexa secondary antibodies. Briefly, anti-DEGS1 and anti-ERLIN2 antibodies were conjugated with Abberior STAR 635P, NHS ester, and Abberior STAR 580, NHS ester dyes, respectively. Briefly, the antibody-labeling reaction was performed by incubating a mixture containing the primary antibody, NaHCO3, and the appropriate pair of activator/reporter dyes diluted in DMSO for 40 minutes at room temperature (RT). Finally, purification of labeled antibodies was performed using NAP5 Columns (GE HealthCare).

### Table 2. Protein levels of DEGS1 and reported MAM-resident proteins in MAM fractions recovered from WT mouse spinal cords

<table>
<thead>
<tr>
<th>Protein</th>
<th>Mean</th>
<th>SEM</th>
</tr>
</thead>
<tbody>
<tr>
<td>DEGS1</td>
<td>25.535</td>
<td>0.087</td>
</tr>
<tr>
<td>ERLIN2</td>
<td>28.966</td>
<td>0.050</td>
</tr>
<tr>
<td>ACAT1</td>
<td>29.677</td>
<td>0.080</td>
</tr>
<tr>
<td>MFN2</td>
<td>26.723</td>
<td>0.055</td>
</tr>
<tr>
<td>DRP1</td>
<td>28.932</td>
<td>0.093</td>
</tr>
<tr>
<td>ERO1L</td>
<td>27.180</td>
<td>0.072</td>
</tr>
<tr>
<td>ATAD3</td>
<td>25.984</td>
<td>0.136</td>
</tr>
<tr>
<td>GRP75</td>
<td>29.535</td>
<td>0.062</td>
</tr>
<tr>
<td>VCP</td>
<td>30.976</td>
<td>0.085</td>
</tr>
<tr>
<td>VDAC1</td>
<td>32.590</td>
<td>0.066</td>
</tr>
<tr>
<td>APP</td>
<td>29.294</td>
<td>0.052</td>
</tr>
</tbody>
</table>

Mean is presented as label-free quantification (LFQ) intensity. n = 5.

### Table 3. Protein levels of DEGS1 and reported MAM-resident proteins in the MAM fractions recovered from WT embryonic fibroblasts

<table>
<thead>
<tr>
<th>Protein</th>
<th>Mean</th>
<th>SEM</th>
</tr>
</thead>
<tbody>
<tr>
<td>DEGS1</td>
<td>23.201</td>
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<tr>
<td>ERLIN2</td>
<td>25.248</td>
<td>0.096</td>
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<tr>
<td>ACSL4</td>
<td>22.852</td>
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<tr>
<td>MFN2</td>
<td>20.170</td>
<td>0.316</td>
</tr>
<tr>
<td>SOAT1</td>
<td>32.896</td>
<td>1.735</td>
</tr>
<tr>
<td>VCP</td>
<td>24.231</td>
<td>0.074</td>
</tr>
<tr>
<td>ITPR3</td>
<td>12.386</td>
<td>1.350</td>
</tr>
<tr>
<td>ERLIN1</td>
<td>6.194</td>
<td>0.476</td>
</tr>
<tr>
<td>VDAC1</td>
<td>9.037</td>
<td>0.373</td>
</tr>
<tr>
<td>APP</td>
<td>12.898</td>
<td>1.151</td>
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<tr>
<td>PDZD8</td>
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<tr>
<td>ATAD3</td>
<td>5.113</td>
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</tr>
<tr>
<td>SPTC1</td>
<td>4.227</td>
<td>0.832</td>
</tr>
<tr>
<td>SPTC2</td>
<td>2.292</td>
<td>0.798</td>
</tr>
</tbody>
</table>

Mean is presented as spectrum counts. n = 5.
Figure 6. DEGS1 impairment leads to MAM disruption. (A) Schematic representation of PL synthesis and trafficking and cholesterol esterification at the MAM. (B) PL synthesis and trafficking assay. \( ^{3}H\)-PS/\( ^{3}H\)-PE lipid ratio reflecting incorporation after 12 hours of \( ^{3}H\)-serine into \( ^{3}H\)-PS and \( ^{3}H\)-PE in human fibroblasts from patients with DEGS1 mutations \((n = 3)\) and control individuals \((n = 3)\). (C) SOAT1 activity assay. \( ^{3}H\)-CE lipid levels reflecting the incorporation of \( ^{3}H\)-cholesterol into \( ^{3}H\)-CE after 6 hours in human fibroblasts from patients with DEGS1 mutations \((n = 4)\) and control individuals \((n = 5)\). (D and E) DhCer/Cer, DhSM/SM, and (F and G) DhHexCer/HexCer lipid levels in the total and MAM fractions from fibroblasts of patients with DEGS1 mutations \((n = 3–5)\) and control individuals \((n = 4–5)\). (H) Distance between the ER and the mitochondria (M) in fibroblasts using TEM and its (I) quantification. DEGS1 patient \((n = 3)\) and control \((n = 3)\) fibroblasts. Data are represented as box-and-whisker plots (median, interquartile interval, minimum, maximum). * \(P < 0.05\); ** \(P < 0.01\), 2-tailed Student’s t test.
TEM

Fresh muscle biopsies and growing fibroblasts were fixed in 2.5% glutaraldehyde (16210, Electron Microscopy Sciences) in 0.1M sodium cacodylate buffer (12310, Electron Microscopy Sciences), pH 7.1-7.4, for 2 hours at 4°C. Samples were washed 3 times in the same buffer.
Measurement of mitochondrial respiration chain function

Mitochondria enrichment. Muscle mitochondria were isolated as previously described (70); see Supplemental Methods.

Polarographic study of substrate oxidation. The oxidation of pyruvate was measured by the polarographic method as previously described (70, 71); see Supplemental Methods.

Spectrophotometric assays of respiratory chain enzyme activities. Respiratory chain enzyme activities were quantified as previously described (70, 71); see Supplemental Methods.

Immunofluorescence

Fibroblasts were seeded on coverslips prior to fixation, and MitoTracker Orange CMTMRos (M7510, Thermo Fisher Scientific) was used to stain mitochondria according to the manufacturer’s instructions. Briefly, 100 nM MitoTracker reagent in DMEM was added to the culture. After 15 minutes of incubation at 37°C, the cells were washed 3 times with PBS. Fibroblasts were fixed for 30 minutes with 2 ml per well of...
10% formalin at RT. To permeabilize and block the cells, coverslips were incubated for 20 minutes at RT in blocking buffer (1% BSA, 0.2% powdered milk, 2% NCS, 0.1M glycine, 0.1% Triton X-100). Fibroblasts were immunostained with the indicated primary antibodies overnight at 4°C. Following incubation with secondary antibodies for 1 hour at RT, the slides were mounted using Mowiol. The slides were analyzed with an SP5 confocal microscope (Leica TCS). Confocal images were acquired using a Leica TCS SL laser scanning confocal spectral microscope (Leica Microsystems), and images were analyzed with ImageJ. Mitochondria morphology (area and sphericity) and Manders’ correlation coefficient were quantified using Imaris software, version x64 9.7.2. The 3D image reconstruction of patient fibroblasts was also performed using Imaris software.

**Live-cell imaging.** Fibroblasts were seeded in μ-Slide 8-Well High (80806, Ibidi) chambers. Growing fibroblasts were stained with MitoTracker as previously described. We optimized the conditions to avoid photobleaching, decreased the concentration of MitoTracker to 50 nM, and decreased laser intensity to the minimum. 3D images of fibroblasts were acquired using a Leica TCS SP8 STED 3X Laser Scanning Confocal Microscope (LSCM) with an HC PL APO CS2 ×100 oil objective (pixel size = 113 nm). Fluorescence excitation was achieved with a pulsed white-light laser source, and fluorescence emission was collected using a Leica HyD SMD detector. Images were obtained every 16 minutes for 4 hours and analyzed with Imaris software by means of the disconnected number of counts for automatic quantification of mitochondria units over time.

**Inner ΔΨm quantification.** Growing fibroblasts were washed with PBS and incubated with 50 nm tetramethylrhodamine, ethyl ester (TMRE) (Molecular Probes) in prewarmed PBS for 30 minutes at 37°C. Cells were trypsinized, centrifuged at 1,000g for 5 minutes, and resuspended in prewarsmed PBS. All samples were captured by a Gallios Analyzer (Beckman Coulter), which recorded 20,000 cells for each genotype tested. FCCP (200 μM for 10 minutes) was used as a positive control. Histograms showing the inner ΔΨm levels were obtained after gating live cells. The data were analyzed with Kaluza Analysis software, version 2.1. (Beckman Coulter).

**Evaluation of ROS production.** Intracellular and mitochondrial superoxide anion levels were estimated using DHE and MitoSOX Red probes (Thermo Fisher, D11347 and M36008), respectively. Briefly, after incubating with 5 μM DHE or MitoSOX for 10 minutes, fibroblasts were washed twice with PBS and scraped into water. The homogenate were transferred into a 96-well plate for fluorescence detection with a spectrofluorimeter. The fluorescence of DHE- and MitoSOX-stained cells was measured with a spectrofluorometer (FLUOstar Omega Microplate Reader, BMG Laubetec). The excitation wavelength was 530 nm, and the emission wavelength was 590 nm for DHE and MitoSOX. Fluorescence values were corrected with protein content, which was measured using an HPLC system (EASY-nanoLC 1000, Thermo Scientific), with the Mascot search engine (version 2.5, Matrix Science) was used for peptide identification and quantification. Samples were analyzed using the Proteome Discoverer software suite (version 2.0, Thermo Fisher Scientific), and the Mascot search engine (version 2.5, Matrix Science) was used for peptide identification and quantification. Samples were searched against a SwissProt database containing entries corresponding to human (version of January 2018), a list of common contaminants, and all the corresponding decoy entries. Trypsin was chosen as an enzyme, and a maximum of 3 miscleavages were allowed. Carbamidomethylation (C) was set as a fixed modification, whereas oxidation (M) and acetylation (N-terminal) were used as variable modifications. Searches were performed using a peptide tolerance of 7 ppm and a product ion tolerance of 0.5 Da. Resulting data files were filtered for FDR of less than 1%.

**PhotoClick cholesterol assay.** To further study the MAM resident proteins, a method developed by Hulce et al. (36) was used. Briefly, MEFs were incubated in serum-free medium for 2 hours to remove all exogenous lipids. After that, 5 μM photoClick cholesterol (Hex-50-ynyl 3b-hydroxy-6-diazirinyl-5a-
cholan-24-oate), previously complexed with an aqueous saturated solution of MβCD (38 mM), was added to the cells and incubated for 4 hours. Upon washing with DPBS, photoClick cholesterol was cross-linked under 365 nm-UV (0.75 J/cm², UVC 500 Ultraviolet Crosslinker; Amersham Biosciences), washed again, collected, and used for subcellular fractionation as described above. Protein (500 μg) (adjusted to a final 150 μl volume with PBS supplemented with protease inhibitors) of the MAM fraction was briefly sonicated and subjected to click chemistry by the addition of 500 μM biotin-azide, 100 μM Tris(1-benzyl-1H-1,2,3-triazol-4-yl)methyl)amine (TBTA), 1 mM CuSO₄ and 1 mM Tris(2-carboxyethyl)phosphine (TCEP). It was incubated for 15 minutes at RT in the dark. Then samples were diluted in 50 mM Tris pH 7.4 with protease inhibitors (removing an aliquot as input) and incubated with streptavidin beads overnight under rotation at 4°C. After several washes with 50 mM Tris pH 7.4, the beads were collected by centrifugation at 2,000g for 1 minute, boiled with NuPAGE® LDS Sample Buffer (1×) at 95°C for 5 minutes, and used for immunodetection.

PL synthesis and trafficking assay
Fibroblasts were incubated for 2 hours with serum-free medium to ensure the removal of exogenous lipids. The medium was then replaced with MEM containing 2.5 μCi/ml ³H-serine for the indicated periods of time. Fibroblasts were washed and collected in DPBS. They were pelleted at 2,500g for 5 minutes at 4°C and resuspended in 0.5 ml water, removing a small aliquot for protein quantification. Lipid extraction was performed by the Bligh and Dyer method. Briefly, 3 volumes of chloroform/methanol 2:1 were added to the samples and vortexed. After centrifugation at 8,000g for 5 minutes, the organic phase was washed twice with 2 volumes of methanol/water 1:1. Then, the organic phase was evaporated under nitrogen to dryness. Dried lipids were resuspended in 60 μl of chloroform/methanol 2:1 (v/v) and applied to a TLC plate. PLs were separated using 2 solvents composed of petroleum ether/diethyl ether/acetic acid 84:15:1 (v/v/v) and chloroform/methanol/acetic acid/water 60:50:1:4 (v/v/v/v). Development was performed by exposing the plate to iodine vapor. The spots corresponding to the relevant PLs were separated using 2 solvents composed of petroleum ether/diethyl ether/acetic acid 190:9:1 (v/v/v) was used as a solvent. Iodine stains corresponding to the relevant PLs were separated using 2 solvents composed of petroleum ether/diethyl ether/acetic acid 190:9:1 (v/v/v). Each sample was run in triplicate, and the mean value was used to calculate mRNA expression using the comparative (2−ΔΔCt) method, according to the manufacturer’s instructions.

SOAT1 activity assay
To measure SOAT1 activity in vivo, whole fibroblasts were incubated in serum-free medium for 2 hours to remove all exogenous lipids. After that, 2 μCi/ml ³H-cholesterol was added to FBS-free DMEM containing 2% FAF-BSA and allowed to equilibrate for at least 30 minutes at 37°C. Then the radiolabeled medium was added to the cells for the indicated periods of time. Fibroblasts were then washed and collected in DPBS, removing a small aliquot for protein quantification. Lipids were extracted as described above, and samples were analyzed by TLC along with an unlabeled CE standard. A mixture of chloroform/methanol/acetic acid 190:9:1 (v/v/v) was used as a solvent. Iodine stains corresponding to CE bands were scraped and counted.

Lipidomics profiling
Lipidomics experiments were performed at the Lipidomics Facility of Columbia University and analyzed by LC-MS. Lipids were separated via chloroform-methanol extraction and analyzed with a 6490 Triple Quadrupole LC-MS system (Agilent Technologies) according to the manufacturer’s instructions. Glycerophospholipids were separated with normal-phase HPLC using an Agilent Zorbax Rx-Sil column (inner diameter, 2.1 × 100 mm).

Oil Red O staining in fibroblasts
A concentrated solution was prepared by dissolving 100 mg Oil Red O (Sigma-Aldrich, O0625) in 12 ml of triethyl phosphate of 99.8% or more (Sigma-Aldrich, 538728) and 8 ml of distilled H₂O. The resulting solution was stirred overnight at RT. After filtering with a 0.2 μm filter, 15 ml of the concentrated solution was diluted with 10 ml of distilled H₂O to obtain the working solution. The medium was removed from the wells with a glass pipette, and the fibroblasts were rinsed once with PBS. Fibroblasts were fixed for 30 minutes with 2 ml per well of 10% formalin at RT. After fixing, the wells were rinsed with PBS 3 times for 30 seconds each. Prior to use, the coverslips were rinsed once with distilled H₂O. Oil Red O working solution was applied (2 ml per well) for 1.5 hours at RT. The staining solution was removed, and the cells were washed twice with distilled H₂O for 1 minute. Hematoxylin (2 ml per well) was added for 10 minutes to counterstain the nuclei. This was followed by one more rinse with distilled H₂O for 1 minute. The coverslips were allowed to dry completely at RT and then mounted with 12 ml Mowiol. The Feret’s diameter function of ImageJ software was used to determine the LD diameters. This parameter measures the longest distance between any 2 points along the selection boundary and is also known as the maximum caliper. ImageJ software was also used to count the number of LĐs per cell. Between 30 and 50 fibroblasts per clone were quantified.

Quantitative real-time PCR
Total RNA was extracted using the RNeasy Mini Kit according to the manufacturer’s instructions. 1 μg of RNA was transcribed into complementary DNA (cDNA) using SuperScript IV reverse transcriptase in a final volume of 25 μl. TaqMan real-time PCR and SYBR Green real-time PCR were performed in the LightCycler 480 Real-Time PCR System (Roche Diagnostics). Primers used are described in Supplemental Table 5. The expression of the genes of interest was normalized to that of the human reference gene RPLPO. Each sample was run in triplicate, and the mean value was used to calculate mRNA expression using the comparative (2−ΔΔCt) method, according to the manufacturer’s instructions.

Statistics
Statistical significance was assessed using Student’s t test or Wilcoxon’s test when 2 groups (CTL versus DEGS1mut) were compared using parametric and nonparametric tests, respectively. P < 0.05 was considered statistically significant. Manders’ correlation coefficient was performed using ImageJ software, and 2-tailed Student’s t test and Wilcoxon’s tests were performed using R software.

Study approval
All procedures involving human and animal samples were approved by the Animal Experiments Committee of IDIBELL (PR076/14). All animal experiments were conducted following protocols approved by the Animal Experiments Committee of Generalitat de Catalunya. Written, informed consent was obtained for all affected children from parents or legal guardians.

Author contributions
LPS designed, performed, and analyzed the results of most of the experiments, assembled the figures, and wrote the manuscript. NL...
assisted in the immunofluorescence assays. MPO and EAG developed the MAM functional assays and lipidomics assays. LG performed the ROS experiments. CDLT performed proteomics assays. In-depth clinical and pathological characterization and recruitment of patients were carried out by CJ, NJP, AGC, AG, BH, AF, IF, MR, CC, and SF. MM and PLA assisted in confocal studies. AP designed and supervised the overall research and wrote the manuscript. All authors critically reviewed the report and approved the final version.

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