A disease-associated Aifm1 variant induces severe myopathy in knockin mice

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ABSTRACT

Objective: Mutations in the AIFM1 gene have been identified in recessive X-linked mitochondrial diseases. Functional and molecular consequences of these pathogenic AIFM1 mutations have been poorly studied in vivo.

Methods/results: Here we provide evidence that the disease-associated apoptosis-inducing factor (AIF) deletion arginine 201 (R200 in rodents) causes pathology in knockin mice. Within a few months, posttranslational loss of the mutant AIF protein induces severe myopathy associated with a lower number of cytochrome c oxidase-positive muscle fibers. At a later stage, Aifm1 (R200 del) knockin mice manifest peripheral neuropathy, but they do not show neurodegenerative processes in the cerebellum, as observed in age-matched hypomorphic Harlequin (Hq) mutant mice. Quantitative proteomic and biochemical data highlight common molecular signatures of mitochondrial diseases, including aberrant folate-driven one-carbon metabolism and sustained Akt/mTOR signaling.

Conclusion: Our findings indicate metabolic defects and distinct tissue-specific vulnerability due to a disease-causing AIFM1 mutation, with many pathological hallmarks that resemble those seen in patients.

Keywords Akt/mTOR signaling; Apoptosis-inducing factor (AIF); 1C metabolism; Mitochondria; Mitochondrial diseases; Oxidative phosphorylation

1. INTRODUCTION

Apoptosis-inducing factor (AIF) was originally described as a pro-death molecule that is released from mitochondria during caspase-dependent and independent cell death [1–3]. Upon proteolysis of the membrane-tethered precursor, AIF translocates into the nucleus, where it participates in chromatin condensation and DNA degradation (reviewed in [4–6]). Apart from its contribution to various cell death pathways, AIF has a fundamental housekeeping role in mitochondrial bioenergetics (reviewed in [5,6]). In an evolutionarily conserved manner, lack of AIF alters the expression of several respiratory complex subunits at the posttranscriptional level, resulting in aberrant oxidative phosphorylation (OXPHOS) [7]. Since AIF is a FAD- and NADH-binding low-turnover oxidoreductase [4,8], it was initially proposed that AIF could act as a broad range antioxidant enzyme in the mitochondrial intermembrane space [9]. However, recent insights provide a clearer molecular mechanism underlying AIF regulation of the OXPHOS system. In patient-derived fibroblasts as well as in various cells from transgenic mice, AIF deficiency causes decreased expression of the coiled-coil-helix-coiled-helix domain containing 4 (CHCHD4) (orthologue of the yeast Mia40). As a result of its binding to CHCHD4, AIF contributes indirectly to mitochondrial import and oxidative folding pathways, thereby regulating the assembly of the respiratory complexes [10–12]. Although these coherent findings seem to provide conclusive molecular mechanisms, the complex pleiotropic effects of AIF deficiency may alter mitochondrial bioenergetics through additional pathways. For instance, among the newly identified interacting partners, AIF and CHCHD4 are both targets of thioredoxin-like proteins, which regulate the redox status of the cell [12]. Moreover, AIF directly binds the tumor suppressor PTEN (phosphatase and tensin homog on chromosome ten) and prevents its oxidative inactivation [13], thereby altering Akt activity and, consequently, overall metabolism. Therefore, we believe that a substantial number of AIF-binding partners may participate in the stepwise-regulated structural assembly and correct maintenance of the OXPHOS system.

Over the past few years, several pathogenic mutations in the AIFM1 locus have been causally implicated in a set of X-linked recessive human disorders (reviewed in [6]). Although clinical manifestations are extremely variable, in most of the reported cases patients exhibited metabolic changes and altered mitochondrial bioenergetics, with many associated features commonly observed in multisystemic diseases generally known as human mitochondrial disorders [14–17]. The spectrum of AIFM1-related disorders includes many syndromes with various clinical symptoms and clear signs of degenerative processes. The first documented cases of AIFM1 mutations were two male infants with severe encephalomyopathy [18]. In the AIFM1 locus, an ablation of an entire nucleotide triple coding for the arginine residue 201 (R201 del) results in a mutant AIF protein. Biochemical and structural studies...
of recombinant wild type and mutant AIF proteins demonstrate aberrant folding and FAD incorporation [18,19], while patient-derived fibroblasts show altered expression of complex III (CIII) and complex IV (CIV) subunits [18]. Since the first reported case, additional pathogenic mutations in the AIFM1 gene have been described in individuals with complex multisystem disorders featuring a wide range of clinical manifestations, including prominent neurological deficits, progressive muscular wasting and ataxia, hearing loss, optic atrophy, retinopathy, neuropathy, hypomyelination, and spondyloimetaphyseal dysplasia [18,20–29]. Notably, additional variants in the AIFM1 gene seem to co-segregate with certain forms of childhood-onset hearing loss, further expanding the spectrum of AIFM1-linked diseases [23]. Most of the annotated pathogenic mutations have structural and functional consequences on AIF properties [18,19]. However, these in vitro findings correlate only partially with the clinical profiles of patients, making the interpretation of their physiological relevance extremely difficult, especially in the context of drug development.

AIF deficiency has been widely studied in a few animal models, such as the hypomorphic Harlequin (Hq) mutant mice [9]. Contrary to the observed embryonic lethality of Aifm1 knockouts [30], Hq mutant mice are viable and show significant temporal variability in terms of phenotypic abnormalities and degenerative lesions [9,31]. At the biochemical level, Hq mutant mice show an 80% reduction of AIF expression that leads to a compromised expression of respiratory complex subunits in the optic nerve, retina, brain and skeletal muscle [7,31]. In an apparent discrepancy, the OXPHOS system is basically unaffected in the heart and liver of Hq mutant mice, whereas it is considerably impaired in organ-specific Aifm1 knockout mice [7,31–33]. Throughout different tissues, a certain degree of correlation exists between the residual complex I (Cl) activity, pathology onset and progression. However, body weight, growth retardation, fur anomalies and neurological symptoms vary considerably among individual mice. In terms of pathology, Hq mutant animals show extensive neurodegeneration in the cerebellum and retina and, consequently, develop progressive ataxia and become blind between 4 and 7 months of age [9,31,34]. Despite these caveats, hypomorphic Hq mutant mice, along with tissue-specific Aifm1 knockout animals, have been widely used to study AIFM1-mediated mitochondrial dysfunction. Nevertheless, since these transgenic mice are models of AIFM1 gene disruption rather than AIF dysfunction, they may not recapitulate the exact molecular pathogenesis of AIFM1 mutations, resulting in animals with pathophysiological profiles and phenotypic traits different from those observed in human patients. Consistent with this view, Hq mutant mice are generally accepted as valuable in vivo models of mitochondrial disorders associated with Cl deficiency [32,35,36].

Given the clinical heterogeneity of AIFM1-linked disorders and the unclear relationship between the genetic etiology and clinical outcomes, the study of AIFM1-related diseases is extremely challenging, with impaired mitochondrial bioenergetics as the only common denominator. As a consequence, there is a lack of reliable tractable models that recapitulate most of the relevant features observed in patients, undermining preclinical drug testing and the development of future therapies. Here, we provide the first unequivocal evidence that a disease-associated mutation in the Aifm1 gene causes pathology in vivo in mice. In a newly developed Aifm1 (R200 del) knockin mouse model, we show that Aifm1 mutant allele has an mRNA expression pattern similar to the wild type one. Across different tissues, the mutant AIF polypeptide is consistently downregulated in a post-translational manner. Importantly, the residual amount of the AIF (R200 del) variant is comparable to the wild type AIF protein in Hq mice. As in patients, Aifm1 (R200 del) mice display OXPHOS deficiency in the skeletal muscle, including accumulation of nemaline rod-like structures, reduced COX activity and consequent muscular weakness. At 3 and 6 months of age, Aifm1 (R200 del) animals do not exhibit cerebellar degeneration, but instead show consistent and evident signs of peripheral neuropathy (i.e., swelling and demyelination of axons in the sciatic nerve) between 6 and 12 months of age. In line with previously published findings [7.9–11,31,32], we show that AIF deficiency causes mitochondrial dysfunction in a tissue-specific fashion. As in other mouse models of mitochondrial diseases, we provide evidence that the AIF (R200 del) variant leads to hyperactive Akt/mTOR signaling, aberrant folate-driven one-carbon (1C) metabolism [37–39] and potential catastrophic adaptations linked to enhanced glycolysis. Together, our findings describe molecular and metabolic signatures associated with a distinct disease-causing mutation in the Aifm1 gene, highlighting further the complex etiology of AIFM1-linked mitochondrial diseases.

2. MATERIALS AND METHODS

2.1. Animals

Hq mutant (JAX stock number: 000501) breeding pairs were obtained from The Jackson Laboratory (Bar Harbor, Maine, USA). All mice were housed in groups of two to four under a 12/12 h light/dark cycle (lights on at 6:00 am) with free access to food (ssniff® V1534-300) and tap water. All experiments were approved and performed in conformity to the guidelines of the State Agency for Nature, Environment and Consumer Protection in North Rhine Westphalia. Taconic Biosciences GmbH (Cologne, Germany) generated the targeting vector and performed transfection of ES cells, homologous recombination, in vitro removal of neomycin and puromycin cassettes, ES cells injection in the blastocysts, selection of chimeric mice, and heterozygous transgenic female founders.

2.2. Antibodies

The following antibodies were used: mouse anti-actin (Abcam ab14128), rabbit anti-AIF (Cell Signaling 5318), rabbit anti-Akt (Cell Signaling 4058), rabbit anti–fil tubulin (Cell Signaling 5666), rabbit anti-calbindin (Swant CD 409-08), rabbit anti-calbindin (Swant CD 68), rabbit anti-Diablo (Abcam ab8115), rabbit anti-GAPDH (Cell Signaling 2118), mouse anti-GFAP (Cell Signaling 3670), rabbit anti-Iba1 (Wako 019–19741), rabbit anti-Grp (Abcam, ab16801), rabbit anti-

Figure 1: Aifm1 (R200 del) mice have reduced AIF protein levels across organs and display homogenous phenotypic traits. (A) Schematic representation of the human AIF protein. MLS indicates the mitochondrial localization sequence; FAD and NADH are the FAD-binding and NADH-binding motifs, respectively. Numbers define distinct domains within the AIF protein. Arrows indicate mutated residues identified in patients (in red, R201 deletion). (B) Schematic representation of the genetic targeting strategy, enabling the generation of conditional Aifm1 (R200 del) knockout (KO) as well as Aifm1 knockout (KO) mice. (C) Overexpression of PhiC31-GFP in Aifm1 (R200 del) MEFs resulted in AIF knockout. Green–positive cells displayed loss of AIF staining (red). Hoechst-33342 (blue) was used to visualize nuclei. Scale bar = 20 µm. (D) Aifm1 (R200 del) knockin (KI) mice were born at almost the expected Mendelian ratio. (E) Immunoblot and (F) RT-PCR analyses for Aifm1 expression levels in wt, Aifm1 (R200 del) KI and Hq mutant mice across different organs (for RT-PCR: mean ± SEM, Student’s t-test, n = 3–5 per genotype, **p < 0.01, ***p < 0.001, *p < 0.05 compared to littermates). (G–H) Aifm1 (R200 del) KI mice developed (G) hind limb clasping and (H) kyphosis around 6 months of age. (I–J) Hq mutant mice showed high variability in phenotypic traits, such as (I) fur loss and (J) body weight changes (n = 15–20 per genotype); (I) compared to littermate controls, Aifm1 (R200 del) KI mice had a consistent decrease in body weight (n = 18–20 per genotype).
MAP2 (Abcam ab 40390), rabbit anti-MBP (Abcam ab40390), rabbit anti-MIA40 (CHDH4, Protein Tech 21090-1 AP), rabbit anti-MTHFD2 (Abcam ab151447), mouse anti-NDUFA9 (Abcam, ab14713), rabbit anti-NDUFb7 (Protein Tech 14912-1 AP), mouse anti-NDUFS3 (Abcam ab14711), mouse anti-Neurofilament (SMI 312, BioLegend 837904) mouse anti-OXPHOS rodent cocktail (Mitosciences MS604), rabbit anti-p70-S6K (Cell Signaling 2902), rabbit anti-phospho-p70-S6K (Cell Signaling 9205), rabbit anti-PCK1 (Cell Signaling 12940), rabbit anti-PCK2 (Cell Signaling 6924), rabbit anti-PKM2 (Cell Signaling 4053), rabbit anti-PRAS40 (Cell Signaling 2691), rabbit anti-phospho-PRAS40 (Cell Signaling 13175), rabbit anti-RPS6 (Cell Signaling 9205), rabbit anti-phospho-RPS6 (Cell Signaling 2217), rabbit anti-phospho-AMPK (Cell Signaling 5832), rabbit anti-PKM1 (Cell Signaling 7067), rabbit anti-RPS6 (Cell Signaling 2217), rabbit anti-phospho-AMPK (Cell Signaling 5832). Cells were kept in culture for 5 days and then either collected and maximum intensity projections of acquired z-stacks was done in ImageJ. Image analyses were performed in a blinded manner using ImageJ.

2.6. Immunohistochemistry

Tissue sections were blocked for 1 h at room temperature in blocking buffer containing 10% normal goat serum and 0.1% Triton X-100. Following incubation with primary antibodies overnight at 4 °C, sections were washed and incubated with appropriate Alexa Fluor conjugated secondary antibodies for 2 h at room temperature. After counterstaining with Hoechst-33342, sections were mounted and covered with fluorescence mounting medium (DAKO).

2.7. Modified Gomori trichrome staining

Fresh-frozen quadriceps were cross-sectioned at 10 μm on a cryostat, stained with hematoxylin and eosin (Sigma—Aldrich) and ultimately incubated for 20 min in Gomori staining solution (0.6% chromotrop 2R, 0.3% Fast Green FCF, 0.6% phosphotungstic acid, 1% acetic acid in distilled water). Following dehydration in ascending ethanol series, sections were cleared with Xylene and coverslipped with DePeX® (VWR). Three non-adjacent sections and at least 60 muscle fibers per animal were analyzed, and the number of fibers showing myopathic features was counted manually.

2.8. Oxygen consumption rate

Oxygen consumption rate (OCR) of cells was measured with an XF24 Extracellualr Fluor oximeter (Seahorse Bioscience). Cells were seeded at 4 × 104 cells/well 24 h before the assay. One hour before the measurement, cells were incubated at 37 °C in a CO2-free incubator. Baseline OCR was measured for 15–20 min, while changes in OCR were assessed following addition of oligomycin, carbonyl cyanide 4-(trifluoromethoxy) phenylhydrazone (FCCP) and rotenone/antimycin A (final concentrations were 1, 0.5 and 0.1 μM respectively). After recording, cells were detached with trypsin and harvested immediately. The number of cells per well was counted and used to normalize the corresponding OCR.

2.9. Proteomic analysis (TMT/iTRAQ scan)

Snap-frozen quadriceps muscle samples from three month-old Aifm1KI/c mice and three control littersates were used for proteomic analysis. DC Biosciences Ltd (Scotland, UK) performed lysis of the samples, protein precipitation, digestion and labeling with a TMT™ Mass Tag Labeling kit. Peptide samples were reconstituted, fractionated, and subjected to LC-MS/MS/MS analysis. Raw MS data were analyzed in MaxQuant. Data were then further reanalyzed, renormalized, and requantified in R.

2.10. Rapamycin treatment and grip strength

Rapamycin (LC Laboratories #R-5000) was dissolved in physiological saline solution supplemented with 5% PEG-400 and 5% Tween-80.

Figure 2: Aifm1 (R200 del) mice show pathological features associated with OXPHOS deficiency in skeletal muscle. (A) Modified Gomori trichrome staining on transverse quadriceps muscle sections in Aifm1 (R200 del) KI, Hq mutant, and respective control animals. Scale bar = 50 μm. (B) At 6 months of age, Aifm1 (R200 del) KI mice showed a significantly higher number of muscle fibers with cytosolic inclusions compared to age-matched wt littermates (mean ± SEM, Student’s t-test, n = 4–5 per genotype, **p < 0.01). (C) Schematic representation of the COX and SDH staining. Visualization of COX activity is based on the use of 3,3'-diaminobenzidine (DAB) as electron donor. The reaction product on oxidation of DAB occurs as brown pigmentation corresponding to the distribution of mitochondria. Visualization of SDH activity is based on the use of nitro blue tetrazolium (NBT) and rotenone/antimycin A (final concentrations were 1, 0.5 and 0.1 μM respectively). After recording, cells were detached with trypsin and harvested immediately. The number of cells per well was counted and used to normalize the corresponding OCR. (D) Immunoblot analyses were performed using quadriceps muscles from wt, Aifm1 (R200 del) KI and Hq mutant mice at (G) 3 and (H) 6 months of age. Densitometry is relative to wt littermates and reported as mean ± SEM, Student’s t-test, n = 4–5 per genotype, **p < 0.001, ***p < 0.01, *p < 0.05. Color code is: black = wt (for KI); red = KI; dark grey = wt (for Hq); green = Hq.
Mice were weighed daily and injected intraperitoneally (i.p.) with a dose of 8 mg/kg per day. Control animals received daily injections at a volume of 66 μl/10 g body weight. Treatment started when the animals were between 12 and 14 weeks of age and lasted for a total of 14 days. Twenty-four hours after the last injection, vehicle- and rapamycin-treated mice were tested for grip strength to assess muscle force. Here, animals were held at the tail, allowed to grasp onto the bar of a grip strength meter (TSE) with their forepaws, and then gently pulled backwards until they released their grip. Each mouse was tested three times and the average of these measurements was used.

2.11. Real-time PCR

Total RNA extraction was performed on snap frozen tissue samples using QIAzol, QiA shredder, and RNasey mini kit (Qiagen). DNase I digestion was carried out with the RNase-free DNase kit (Qiagen) and RNA concentrations were determined by spectrophotometry (Nano Drop, Thermo Fisher). RNA extracts (100 ng) were retrotranscribed using the qScript cDNA SuperMix (Quanta Biotechnology). Gene expression analysis was conducted with FastSYBR Green Master Mix (Applied Biosystems) on a Step One Plus Real Time PCR System (Applied Biosystems). Primers used for RT-PCR were as follows: Aifm1 (exon 1—2) F’ 5’-cgaggtctagtcgtcggag-3’ R’ 5’-gaggacacgcccgctgtc-3’; Aifm1 (exon 6—7) F’ 5’-tcacagctgatgttaagga-3’ R’ 5’-tagcagctgcgtgagcag-3’; Aifm1 (exon 12—13) F’ 5’-tcacagctgtaactcag-3’ R’ 5’-gcttgacaccacttatc-3’; Asns F’ 5’-gaggttcctcctcctcg-3’ R’ 5’-caagcttgctttgaatac-3’; Gdf15 F’ 5’-ctggggtctaccaagcata-3’ R’ 5’-tcggcgtctcgtagc-3’; Phgdh F’ 5’-ataagcttgctcaaatctgc-3’ R’ 5’-agttcagcatactctcctc-3’; Psat1 F’ 5’-ctggctagccagccataagatc-3’ R’ 5’-ctcttgcccttccaagctgg-3’; Stmrt F’ 5’-ttggagtagatactactcggg-3’ R’ 5’-cgagtctccacaccctgat-3’; ΔΔCt values were normalized to β-actin and represented as fold change compared to control mice.

2.12. SDS gel electrophoresis and western blot analysis

Cell pellets and snap frozen tissues were lysed and sonicated in ice-cold RIPA buffer (Sigma Aldrich) supplemented with protease and phosphatase inhibitors (Roche). Proteins were resolved on a 10—12% acrylamide gel and transferred onto nitrocellulose membranes (Bio-Rad). Following 1 h of blocking, membranes were incubated with primary antibodies overnight at 4 °C. On the next day, membranes were washed and incubated with appropriate HRP-conjugated secondary antibodies for 1 h at room temperature. Immunoblots were developed using the chemiluminescent analyzer Chemidoc imaging system (Bio-Rad) and quantified by densitometry (ImageLab software, Bio-Rad).

2.13. Statistics

Data are expressed as mean ± S.E.M. and statistical analyses were performed with Graph Pad Prism software. Unpaired t-tests were used to compare differences between genotype groups (e.g. Aifm1<sup>wt</sup>/<sup>wt</sup> vs. Aifm1<sup>fl/fl</sup>); wt vs. Hq). Data from rapamycin and vehicle treated mice were analyzed using a two-way analysis of variance (ANOVA) with genotype as the within-group and treatment as the between-groups factor. In the case of significant main effects, Bonferroni post-hoc pairwise comparisons were performed. The statistical significance was defined as p < 0.05.

3. RESULTS

3.1. Aifm1 (R200 del) knockin mice develop early-onset myopathy

Several disease-causing mutations in the AIFM1 gene have been identified in patients (Figure 1A). Based on prior biochemical analyses, recombinant human AIF protein lacking R201 shows conformational instability and altered redox properties [18]. To study the pathological implications of this mutation in vivo in rodents, we designed a targeting strategy that allowed both the generation of conditional Aifm1 (R200 del) knockin as well as Aifm1 knockout mice. The targeting vector included a loxP-flanked sequence encoding cDNA for exon 4 to 16, the sequence of 3 HA-tags and an additional polyadenylation tail (Figure 1B). The construct was inserted into intron 3 of the native Aifm1 locus, theoretically allowing the expression of a HA-tagged AIF protein. Exon 5 of the native Aifm1 gene carried a deletion for the amino acid R200 (R200 del). Both exon 4 and the mutated exon 5 were flanked with attP/attB sites, which allow the knockout of the Aifm1 gene upon PhiC31-driven recombination (Figure 1C). After transfection in male C57BL/6NTac ES cells, homologous recombinant clones were isolated using double positive Neomycin and Puromycin selection markers flanked by FRT and F3 sites, respectively. The correct genetic recombination was assessed by Southern blot analysis (data not shown). We tested the expression of HA-tagged AIF protein in the resulting positive ES cell clones. Surprisingly, we could not detect AIF expression at the protein and mRNA levels, suggesting that the mRNA splicing and/or maturation were somehow compromised (data not shown). Nevertheless, targeted ES cells were injected after recombinase-mediated in vitro deletion of the selection markers, and several chimeras were obtained. Ultimately, two females with a germline transmission for the transgene were identified as colony founders. Upon breeding with wild type mice, we obtained a very

Figure 3: Mutant AIF protein does not cause cerebellar degeneration but induces peripheral neuropathy. (A) Representative images of Nissl-stained sagittal brain sections and (B) corresponding quantification of the cerebellar size at 3 and 6 months of age. Scale bar = 500 μm, mean ± SEM, Student’s t-test, n = 3—4 per genotype. **p < 0.001, ***p < 0.001. (C) Representative images of cerebellar brain sections double-immunostained with calbindin (CALB1; red) and BAI1 (green). At 6 months of age, Hq mutant mice showed Purkinje cell degeneration and greatly enhanced BAI1 immunoreactivity. Scale bar = 100 μm. (D—E) Immunoblot analyses were performed using cerebella from wt, Aifm1 (R200 del) KI and Hq mutant animals at Do (3) and (E) 6 months of age. Densitometry is relative to wt littermates and reported as mean ± SEM. Student’s t-test, n = 4—9 per genotype. **p < 0.001, ***p < 0.001, ****p < 0.05. Color code is: black = wt (for KI); red = KI; dark grey = wt (for Hq); green = Hq (F—G) Cross-sections of the sciatic nerve from (F) 6 and (G) 12 month-old animals were stained with antibodies against Myelin Basic Protein (MBP, green) and Neurofilament (pan axonal, red). Scale bar = 50 μm.
Figure 4: AIF deficient mice exhibit aberrant 1-C metabolism. (A) Proteomic profiling using isobaric tags (TMT/iTRAQ) was performed in quadriceps muscle tissues from 6 month-old Aifm1 (R200del) KI mice and littermates (n = 3 per genotype). Volcano plot shows the median log2 ratio against −log10 (p-value). Dots represent individual proteins. Black dots are not significant; colored dots indicate differently expressed proteins. (B) Table of proteins differently expressed in KI mice compared to littermates. (C) Schematic representation of folate-driven 1C metabolism in mammalian cells. Enzymes involved in serine metabolism are in black solid box, whereas other enzymes analyzed in this study are in black dashed box. (D) RT-PCR analyses showing Mthfd2 expression levels in muscle and cerebellar tissues from 3 to 6 month-old mice (mean ± SEM, Student’s t-test, n = 3–5 per genotype, **p < 0.01, *p < 0.05 compared to littermates). (E) Immunoblot analysis for MTHFD2 and Diablo/SMAC protein expression levels in muscles from 6 month-old animals. (F) RT-PCR
limited number of heterozygous transgenic females, indicating an unexpected mortality of the mutation carriers despite the remaining wild type Aifm1 allele. We hypothesized that the inserted sequence affected mouse survival, perhaps interfering in trans with the maturation or translation of wild type Aifm1 mRNA. Thus, few original female founders were crossed with a male ubiquitously expressing the bacterial Cre-recombinase. Germline expression of the Cre recombinase resulted in genetic recombination of the floxed Aifm1 locus and expression of mutated Aifm1 (R200 del) (Figure 1B). DNA sequencing of Aifm1 exon 5 confirmed the correct recombination (data not shown). From further breeding, we recovered a certain number of viable heterozygous Aifm1 (R200 del) females and hemizygous Aifm1 (R200 del) males in a ratio slightly lower than the expected Mendelian inheritance pattern (Figure 1D). We tested Aifm1 protein expression levels in muscle, cerebellum, heart, and liver tissues from 3 month-old wild type, Hq mutant and Aifm1 (R200 del) males. Likewise, we measured Aifm1 mRNA expression across different organs using a set of validated primers for quantitative RT-PCR. Since Hq mutant animals and Aifm1 (R200 del) mice have different background strains, the relative wild type littermates were used as control animals in all experimental set-ups. Compared to wild type mice, both Hq mutant and Aifm1 (R200 del) males exhibited a similar reduction of the mature ~62 kDa AIF protein across different tissues (Figure 1E). However, Aifm1 mRNA expression did not differ between Aifm1 (R200 del) and wild type males, contrary to Hq mutant animals, where a significant reduction of Aifm1 transcripts occurred in all tested tissues (Figure 1F). In line with prior in vitro evidence [18], these findings further support that the loss of mutant AIF protein occurs posttranslationally due to its high instability in mammalian cells. As part of our in vivo characterization, we went on with phenotypical and biochemical assessments of Aifm1 (R200 del) mice, using wild type and Hq mutant animals as comparison. While Hq mutant males were highly variable in terms of body weight and baldness, Aifm1 (R200 del) males had normal fur, weighed less than wild type animals but with only slight differences across individuals of the same cohort (Figure 1G–J). Importantly, around 4–5 months of age, Aifm1 (R200 del) homozygous females and hemizygous males displayed hind limb claspimg and developed kyphosis (Figure 1G–H), indicating potential muscle atrophy and innervation defects. To provide additional evidence of abnormalities in the skeletal muscle, we performed a modified Golgi trichrome staining on quadriceps muscle sections. Consistent with the early development of myopathy-like features, Aifm1 (R200 del) males exhibited an increased number of nemaline rod-like structures in skeletal muscle fibers between 3 and 6 months of age (Figure 2A–B). Given these observations, we sought to define the biochemical and physiological effects of the mutant AIF protein. Cytochrome c oxidase (COX) and succinate dehydrogenase (SDH) staining (Figure 2C) is a widely used method to assess defects of mitochondrial respiratory complexes in model organisms as well as for diagnostic purposes in patients [42]. Compared to wild type animals, Aifm1 (R200 del) as well as Hq mutant mice exhibited a significantly decreased formation of the brown indamine polymer product in skeletal muscle sections. Notably, Aifm1 (R200 del) mice showed a more pronounced loss of COX-positive muscle fibers compared to Hq mutant animals at 3 months of age (Figure 2D–E), indicating reduced CV activity. SDH-mediated reduction of nitroblue tetrazolium to blue formazan was relatively similar throughout the different genotypes (Figure 2F). Since AIF deficiency induces tissue-dependent OXPHOS impairment according to the genetic manipulation [7,31–33], we performed comprehensive immunoblot analyses using a wide range of validated antibodies. Over time, we found that AIF loss altered CHCHD4 expression in skeletal muscle (Figure 2G–H). At 3 months of age, Aifm1 (R200 del) animals exhibited a clear trend towards a decreased expression of CI and CIV subunits, which became even more significant at 6 months of age (Figure 2G–H). Of note, Hq mutant mice displayed a milder reduction of CI and CIV subunits at 3 months of age, whereas many other respiratory complex subunits were altered significantly at a later stage (Figure 2G–H). Together, our in vivo data indicate that mutant AIF protein causes mitochondrial dysfunction and early-onset myopathy.

3.2. Aifm1 (R200 del) knockin mice do not exhibit cerebellar neurodegeneration
Hq mutant animals develop ataxia between 3 and 7 months of age [9]. Although tissue vulnerability in Hq mutant mice remains a matter of debate, the general consensus is that decreased Aifm1 expression and the consequent loss of AIF protein causes neurodegeneration within the cerebellum in an OXPHOS-dependent manner [9]. Since Aifm1 (R200 del) animals showed reduced cerebellar AIF expression levels akin to Hq mutant mice, we reasoned that related neurodegenerative processes might occur in the brains of our knockin animals. Thus, we performed immunohistochemical analysis and measured the cerebellar size in a group of 3 and 6 month-old wild type, Hq mutant and Aifm1 (R200 del) mice. Surprisingly, and contrary to our original hypothesis, Aifm1 (R200 del) animals did not show loss of Purkinje cells, nor did they exhibit any obvious signs of neurodegeneration within the cerebellum (Figure 3A–C). At 6 months of age, Hq mutant brains displayed a clear increase in immunoreactivity for the microglial marker IBA1, indicating a potential age-dependent microgliosis probably linked to inflammatory processes (Figure 3C). Conversely, the Aifm1 (R200 del) cerebella showed a limited number of IBA1-positive cells (Figure 3C). Despite the significant loss of the full length AIF protein in various brain areas (Figure 3D–E and Supplemental Fig. S1A), Aifm1 (R200 del) cerebella did not exhibit a significant decrease of CHCHD4 protein (Figure 3D–E), which instead was evident in Hq mutant brains as previously reported [10]. While Aifm1 (R200 del) mice showed a trend toward a reduction of mitochondrial CI subunits at 6 months of age, Hq mutant animals presented a marked CI and CIV deficiency at a much younger age, with a clear correlation between CHCHD4 loss and mitochondrial defects in the Hq cerebella (Figure 3D–E). Next, we sought to recapitulate some of our molecular findings in cultured cells. In primary cortical neurons (CNs), decreased AIF expression resulted in diminished CHCHD4 expression and partial OXPHOS impairment, with a significant downregulation of the CI1 subunit UQCRC2 (Supplemental Figs. S1B–S1C). Morphologically, Aifm1 (R200 del) knockin CNs displayed aberrant dendritic length;
however, they did not show any difference in the number of dendrites compared to wild type cells (Supplemental Fig. S1D). It is worth noting that we also tested the effect of mutant AIF protein in mouse embryonic fibroblast (MEFs). Unlike patient-derived fibroblasts [10], knockout MEFs did not show any difference in terms of OXPHOS subunits nor oxygen consumption rate (Supplemental Figs. S1E–S1F), although they exhibited enhanced glycolysis as revealed by an increased extracellular acidification rate (Supplemental Fig. S1G). It is not surprising that, under standard experimental conditions, cultured primary cells adopt a different metabolism, heavily relying on glycolysis that sufficiently compensates for subtle mitochondrial lesions. Since Aifm1 (R200 del) knockin mice displayed hind limb clamping starting from around 5 months of age (Figure 1G), we thought that this might be partially due to innervation defects. Therefore, we performed immunohistochemical analyses of myelin basic protein (MBP) and neurofilament in sciatic nerves from 6 to 12 month-old wild type and knockin mice. We observed axonal swelling around 6 months of age (Figure 3F), followed by an obvious loss of neurofilament and MBP staining in 12 month-old Aifm1 (R200 del) knockin mice (Figure 3G). These data suggest possible axonal neuropathy in adulthood as a secondary effect of muscle wasting. Together, our data indicate that mutant AIF protein induces OXPHOS impairment in a tissue-specific and age-dependent manner. Moreover, the onset and progression of the pathogenic processes are clearly diverse in Hq mutant and Aifm1 (R200 del) mice.

3.3. AIF deficiency induces MTHFD2 upregulation and aberrant glucose metabolism

To gain insights into the molecular processes associated with the expression of mutant AIF (R200 del) protein, we performed proteomic profiling using isobaric tags (TMT/TRAQ). Compared to wild type, Aifm1 (R200 del) muscles exhibited a significant dysregulation of ten proteins, with the expected diminished levels of AIF and NDUFB8 supporting the quality of our analysis (Figure 4A–B). We found that Collagen α-2, cytoskeletal-associated GTPase Septin-9 and mitochondrial FAM136A were downregulated, whereas mitochondrial stress-70 protein (HSPA9), Acyl-CoA thioesterase 2 (ACOT2), mitochondrial Diabolic Smac and mitochondrial bifunctional methylene-tetrahydrofolate dehydrogenase/cyclohydrolase (MTHFD2) were upregulated in Aifm1 (R200 del) mice. MTHFD2 is a mitochondrial protein regulating folate-mediated 1C metabolism (Figure 4C) [43], which has recently attracted much attention in the field of molecular medicine since it is highly upregulated in various models of mitochondrial diseases [38,39,44]. We set out to confirm this intriguing result using qRT-PCR and immunoblot analyses. In line with our proteomics, we found that MTHFD2 was significantly upregulated at both the transcriptional and protein levels in muscles from Aifm1 (R200 del) knockin and, to a much lower extent, in muscles and cerebella of Hq mice (Figure 4D–E). In the muscle of 6 month-old animals, the enhanced MTHFD2 expression was accompanied by an upregulation of phosphoglycerate dehydrogenase (Phgdh), phosphoserine amino-transferase (Psat1), and serine hydroxymethyltransferase (Shmt2), three enzymes involved in serine biosynthesis and, as a consequence, in folate-driven 1C metabolism (Figure 4C,F). Next, we tested the expression of fibroblast growth factor 21 (Fgf21), a hormone generally secreted in response to fasting, which is markedly upregulated in disorders resulting from mitochondrial lesions [45-46]. Consistent with other mouse models of mitochondrial diseases [39], we found Fgf21 overexpression in AIF deficient muscles starting from a young age (Figure 4G). Along with Mthfd2, Phgdh, Psat1, Shmt2, and Fgf21 [46–52], additional ATF4 target genes were differentially regulated in AIF deficient mice. Specifically, we found that growth differentiation factor 15 (Gdf15), asparaginase synthetase (AsnS) and phosphoserine phosphatase (Psph) mirrored Mthfd2 upregulation in affected organs of Aifm1 (R200 del) knockin and Hq mutant mice (Figure 4H), further supporting a tissue-specific regulation of ATF4 activity. Since mitochondrial lesions alter serine and folate-driven 1C metabolism, we assessed the expression levels of enzymes that contribute to compensatory cataplerotic reactions [53,54]. In the muscle of AIF deficient animals, we observed a significant upregulation of the mitochondrial phosphoenolpyruvate carboxykinase (PEPCK-M) and the cytosolic pyruvate kinase (PKM2) (Figure 4). These data suggest an increased conversion of the tricarboxylic acid (TCA) cycle intermediate oxaloacetate to phosphoenolpyruvate to pyruvate (Figure 4C), probably as a result of an enhanced glycolytic rate, ATP production and NADH oxidation through aerobic glycolysis. Finally, we tested the expression of glutathione reductase (GSR), an enzyme that converts oxidized glutathione (GSSH) to its reduced form (GSH) (Figure 4C). Our preliminary evidence indicates a tendency toward an enhanced glutathione synthesis (Figure 4), which may contribute to the oxidative stress tolerance of mitochondrial deficient muscle fibers. Overall, our findings reveal that AIF deficiency alters folate-driven 1C metabolism, induces cataplerotic reactions and stimulates gene expression patterns associated with the transcription factor ATF4.

3.4. Loss of AIF leads to sustained Akt/mTOR activity

Since serine metabolism and Mthfd2 expression is linked to mTOR activity [39] and since impaired mitochondrial function stimulates insulin/IGF-1 signaling [37,55], we tested the phosphorylation status of Akt and mTOR targets in AIF deficient mice and control littermates. We performed immunoblot analyses for the Akt target 40-kDa proline-rich Akt substrate (PRAS40) as well as mTOR substrates p70 S6 kinase (P70-S6K) and ribosomal protein S6 (RPS6). In the muscle and cerebellum, decreased AIF expression correlated with increased Akt and mTOR activity (Figure 5A–B). To further support our findings and address a current knowledge gap in the field, we sought to correlate mTOR activity with Mthfd2 expression in one of our mouse models of AIF deficiency. Similarly to other mitochondrial mutant mice

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rapamycin treatment attenuated mTOR activity and improved muscular strength in Hq mice (Figure 5C–D). Moreover, rapamycin-mediated inhibition of mTOR signaling led to a significant downregulation of Mthfd2 expression in the muscle and cerebellum of Hq mutant mice compared to vehicle-treated control littersmates (Figure 5E), further supporting the link between Akt/mTOR hyperactivity and aberrant 1C metabolism [38,39,47]. Taken together, AIF-dependent mitochondrial impairment stimulates Akt/mTOR signaling in a tissue-dependent manner, ultimately leading to a range of molecular defects and disease manifestations in mice (Figure 5F).

4. DISCUSSION

We describe here the tissue-dependent impairment of mitochondrial function in the first knockin mouse model of AIFM1-related mitochondrial disease. Mice carrying the disease-segregating deletion R200 display consistent phenotypes across individual animals. Pathologically, Aifm1 (R200 del) mice progressively accumulate nemaline rod-like structures in muscle fibers, show evident signs of muscle weakness, and develop severe myopathy within a few months. While at 6 months of age Hq mutant mice show extensive cerebellar neurodegeneration, Aifm1 (R200 del) knockin animals do not exhibit obvious brain pathology, loss of Purkinje cells or evidence of neuro-inflammation. Only at an advanced age, we observed defects of peripheral motor neurons (i.e., reduced size and myelination of the sciatic nerve). As in Hq mutant mice, Aifm1 (R200 del) knockin animals develop histological signs of progressive retinal degeneration (data not shown). Biochemically, Aifm1 (R200 del) muscle and cerebellar tissues show decreased expression of mutant AIF protein. In a tissue-, cell-, and time-dependent fashion, CHCHD4 deficiency seems to correlate with the status of the OPHOS system. Our mouse data indicate that the expression of a mutant AIF protein leads to significant loss of CI and CIV subunits as the most pronounced defects. We are rather surprised that Hq mutant and knockin animals do not show similar pathological profiles, given the comparable levels of residual full-length AIF protein. One explanation is that AIF expression varies considerably in Hq mutant cells during development until adulthood, leading to an irreversible compromised status that causes cerebellar degeneration. Alternatively, it is possible that other molecular mechanisms are sufficient to support mitochondrial bioenergetics in the brain, despite the expression of a mutant AIF (R200 del) protein. Finally, it may be that compensatory factors, which are lacking in Hq mutant mice due to their mixed background, contribute to the maintenance of the OPHOS system in Aifm1 (R200 del) mice. This would also explain the high variability between individual Hq mutant animals, as we observed in our animal cohort and in line with previous reports [31]. We believe that further work will be necessary to define an eventual degree of synthetic lethality between AIF deficiency and other deleterious alleles in model organisms, which may also be relevant for understanding the wide spectrum of clinical manifestations linked to AIFM1 mutations [18,20,21,24–29,57].

In an effort to gain insights into the mechanisms underlying AIFM1-linked pathologies, we found that Aifm1 (R200 del) knockin mice exhibit typical molecular hallmarks as observed in other forms of mitochondrial diseases. In this regard, an unbiased proteomic analysis supports that AIF deficiency induces an aberrant 1C metabolism, as revealed by a significantly increased expression of MTHFD2 in affected tissues. Folate-driven 1C metabolism is a series of evolutionarily conserved enzymatic reactions that support a large range of biosynthetic processes, including purine and thymidine synthesis, amino acid (e.g., glycine, serine and methionine) metabolism [43] and mitochondrial OXPHOS through the translation of mitochondrial DNA-encoded proteins [58]. Folate metabolism comprises distinct reactions that occur in the cytosol and in the mitochondria, with only a few intermediates that bridge the two compartments. Apart from glycine and serine, oxidized formate diffuses to the cytosol, whereas reduced tetrahydrofolate (THF) is shuttled into the mitochondria [43]. While the relationship between MTHFD2, ATF4, and mTOR is well established in physiological conditions [47,49,50], it remains unclear whether folate-dependent 1C metabolism is a driver of mitochondrial diseases or simply a consequence of aberrant signaling cascades [38,39]. In cultured cells [49] and in transgenic mice [38], isotope tracing indicates that OXPHOS defects lead to an increased abundance of methylene-THF and de-novo serine biosynthesis, parallel to a decreased production of formate. Based on this line of evidence, it may be that MTHFD2 upregulation stimulates the flux of 1C units toward reduced intermediates (i.e., THF) and serine production. In cells lacking a functional OXPHOS system, disturbed 1C metabolism alters serine-dependent formate synthesis and the usage of essential metabolites through cataplerotic reactions (e.g., conversion of oxaloacetate to phosphoenolpyruvate to pyruvate), which ultimately stimulate alternative routes for purine, methionine biosynthesis, and, eventually, ATP production. As part of an adaptive metabolic stress response, MTHFD2 upregulation depends on the mitochondrial deficiency-induced hyperactive Akt/mTOR signaling, which stimulates the transcriptional activity of ATF4, a stress response that seems to ameliorate protostasis in cells carrying mitochondrial lesions [50]. Based on our in vivo data using rapamycin, we confirm that mTOR participates in the transcriptional regulation of Mthfd2 in our models. In the future, it will be important to define which of these aforementioned processes are epigenetic adaptations that counteract mitochondrial dysfunction. This may lead to the identification of molecular targets relevant for the development of therapeutic options. Impaired mitochondrial bioenergetics is a common feature of inherited and sporadic forms of mitochondrial diseases. Over the past years, remarkable achievements in molecular medicine have helped shed light on mitochondrial disease pathophysiology. Yet, patient management and treatment options remain extremely challenging due to the poor correlation between genetic etiology and the wide spectrum of clinical manifestations, organ involvement, disease onset, and progression [16,17,59]. Given the heterogeneous clinical patterns of these disorders, it is not surprising that the development of effective therapies lags behind. In this regard, the use of mice is a critical aspect for proof-of-principle assessments of novel treatments and preclinical approaches, with some caveats that are worth mentioning. Among them, there is a growing awareness that findings from these model organisms need to be carefully evaluated due to the different pathophysiology of rodents compared to humans. Also, an increasing body of evidence has challenged the initial assumption that mice carrying OPHOS lesions are sufficient to mimic a wide spectrum of mitochondrial diseases. While traditional constitutive knockout mouse models have been undoubtedly instrumental for establishing the biological function of a specific targeted gene, their further characterization demonstrated that some of them do not fully recapitulate the biochemical traits and organ defects observed in human patients (reviewed in [80,61]). As in the case of the Hq mutant mice, striking phenotypic differences often exist across individual animals of the same model, perhaps due to their mixed genetic background or the incomplete penetrance of the hypomorphic mutation. In terms of drug development, such variability may undermine the feasibility even of hypothesis-driven screens of chemical compounds, since they would be extremely laborious and difficult to interpret in terms of their biological effects and meaning. Ultimately, it would be more helpful to compare...
Our study emphasizes the tissue-specific vulnerability due to a mutant AIF protein and delineates a pathological profile essentially different from the one linked to hypomorphic AIF expression. Mechanistically, AIF deficiency alters respiratory complexes, induces hyperactive Akt/mTOR signaling, and affects anabolic and catabolic processes, including folate-driven 1C-metabolism. Finally, our new knockin Aifm1 (R200 del) mouse model shows many pathological hallmarks that resemble those observed in patients.

5. CONCLUSION

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SUPPLEMENTARY DATA

Supplementary data related to this article can be found at https://doi.org/10.1016/j.molmet.2018.05.002.

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