



Metabolic autopsy with next generation sequencing in sudden unexpected death in infancy: Postmortem diagnosis of fatty acid oxidation disorders



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ABSTRACT

The recent introduction of metabolic autopsy in the field of forensic science has made it possible to detect hidden inherited metabolic diseases. Since the next generation sequencing (NGS) has recently become available for use in postmortem examinations, we used NGS to perform metabolic autopsy in 15 sudden unexpected death in infancy cases. Diagnostic results revealed a case of carnitine palmitoyltransferase II deficiency and some cases of fatty acid oxidation-related gene variants. Metabolic autopsy performed with NGS is a useful method, especially when postmortem biochemical testing is not available.

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1. Introduction

Sudden unexpected death in infancy (SUDI) is defined as a term that has been variably used to refer to all cases of sudden and unexpected deaths in infancy, and not just to those where the death has been attributed to sudden infant death syndrome [1]. The common causes of SUDI are accidental death, infection, cardiovascular anomaly, child abuse and metabolic diseases.

Fatty acid oxidation disorder (FAOD) is one type of the inherited metabolic diseases that can lead to patient death during situations such as long fasting or infection. Before the introduction of expanded newborn screening by tandem mass spectrometry, FAODs account for approximately 5% of sudden infant deaths [2–7] (Table 1). Some patients can now be screened before the symptom is apparent, others still may remain undetected because the screening has just started nationwide in Japan and some disorders including carnitine palmitoyltransferase (CPT) II deficiency are not included in the first target disease [8]. Since FAODs are functional diseases, they are not easy to diagnose, especially during postmortem examinations. Therefore, some

cases may remain undiagnosed or may be incorrectly classified as sudden infant death syndrome.

The recent introduction of metabolic autopsy in the field of forensic science has made it possible to detect hidden inherited metabolic diseases [7,9]. Metabolic autopsy is the autopsy which focuses on the inherited metabolic diseases [10]. The term metabolic autopsy includes microscopic examination of the liver, postmortem blood acylcarnitine analysis and genetic analysis [7]. Since liver steatosis is often seen as a nonspecific change in SUDI and the results of postmortem blood acylcarnitine analysis is often modified by postmortem changes, it is not easy to make a biochemical diagnosis [11]. Although successful genetic analysis has been reported in many cases, there are about 20 FAOD-related genes and thus, surveying all of the genes using Sanger's traditional method of "one gene, one exon at a time" is not an effective way for analyzing these types of cases.

The next generation sequencing (NGS) has recently become available for use in postmortem examinations [12,13]. This technique makes it possible to examine a much larger number of genes and exons at a lower cost in addition to requiring less time than that for the conventional Sanger's method. However, most of the studies using these new techniques have focused on cardiac diseases and thus, there has yet to be metabolic autopsy performed with NGS [13].

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Table 1
Proportion of inherited metabolic disorders among sudden unexpected death in infancy.

Number of cases	Number of diagnosis	Reference
58	6 (10.3%)	Bennett et al. [2]
79	3 (3.8%)	Lundemose et al. [3]
418	14 (3.3%)	Boles et al. [4]
7058	66 (0.93%)	Chace et al. [5]
247	3 (1.2%)	Wilcox et al. [6]
30	1 (3.3%)	Yamamoto et al. [7]

Therefore, the aim of our current study is to detect FAOD-related gene variants among sudden death cases. As far as we know, this is the first metabolic autopsy performed with NGS.

2. Materials and methods

2.1. Subjects and target sequence

A total of 15 SUDI cases, all of which did not have any characteristic appearance and remained undiagnosed after macroscopic examination, were analyzed at the Department of Forensic Pathology at Nagasaki University (Table 2; 11 males, 4 females, age range; 0 days to 11 months). All cases were born before 2014 and none of them were screened by tandem mass spectrometry.

2.2. Extraction of genomic DNA and genetic analysis

Genomic DNA was isolated from blood leukocytes with the QIAamp DNA Blood Mini Kit (Qiagen, Tokyo, Japan) in accordance with the manufacturer's standard methods. A custom-made HaloPlex Target Enrichment System (Agilent Technologies, Santa Clara, CA) was designed to capture the coding exons of the 13 genes targeted to the FAODs (Table 3). The sequencing was performed on an Illumina MiSeq (Illumina, San Diego, CA).

The sequencing reads were mapped on the hg19 human genome sequence using Novoalign version 3.02.12 software (Novocraft, Petaling Jaya, Selangor, Malaysia). Single nucleotide variations and small insertions/deletions were detected using the Genome Analysis Toolkit [14] and annotated using the ANNOVAR software package [15].

Filtering of the variant data was performed as described below. Using the gene information of the GENCODE version 19 [16], single nucleotide variations causing non-synonymous, splice site, or nonsense substitutions and insertions/deletions occurring in the coding regions

Table 2
Case summary.

Case	Age	Sex	Diagnosis	Postmortem acylcarnitine analysis	Fat staining
1	0 d	F	Unknown	None specific change	Negative
2	0 d	M	Unknown	None specific change	Negative
3	2 d	M	Pneumonia	Not analyzed	Negative
4	22 d	M	Unknown	None specific change	Negative
5	2 m	M	Acute respiratory infection	Not analyzed	Negative
6	3 m	M	SIDS	None specific change	Negative
7	4 m	M	SIDS	None specific change	Moderate
8	5 m	M	Pneumonia	Not analyzed	Negative
9	5 m	M	Unknown	Not analyzed	Negative
10	7 m	M	SIDS	Not analyzed	Negative
11	8 m	M	Reye's-like syndrome	Not analyzed	Moderate
12	8 m	M	SIDS	Not analyzed	Negative
13	10 m	F	Unknown	None specific change	Moderate
14	11 m	F	Acute encephalopathy	Not analyzed	Negative
15	11 m	F	Reye's-like syndrome	Long-chain fatty acid defect	Distinctive

SIDS; sudden infant death syndrome, d; day, m; month, M; male, F; female.

Table 3
Gene summary.

Gene	OMIM	Exon	Disease	OMIM
SLC22A5	603377	10	Primary carnitine deficiency	212140
CPT1A	600528	19	CPT I deficiency	255120
CPT2	600650	5	CPT II deficiency	608836
				600649
				255110
SLC25A20	613698	9	CACT deficiency	212138
ACADVL	609575	20	VLCAD deficiency	201475
ACADM	607008	12	MCAD deficiency	201450
ACADS	606885	10	SCAD deficiency	201470
HADHA	600890	20	LCHAD, MTP deficiency	609016 (LCHAD)
HADHB	143450	16	MTP, LCKAT deficiency	609015 (MTP)
HADH	601609	8	HAD deficiency	231530
ETFA	608053	12	MAD deficiency	231680
ETFB	130410	6		
ETFDH	231675	13		

CPT; carnitine palmitoyltransferase, CACT; carnitine-acylcarnitine translocase, VLCAD; very-long-chain acyl-CoA dehydrogenase, MCAD; medium-chain acyl-CoA dehydrogenase, SCAD; short-chain acyl-CoA dehydrogenase, LCHAD; long-chain 3-hydroxyacyl-CoA dehydrogenase, MTP; mitochondrial trifunctional protein, LCKAT; long-chain 3-ketoacyl-CoA thiolase, HAD; 3-hydroxyacyl-CoA dehydrogenase, MAD; multiple acyl-CoA dehydrogenase.

or the splice sites were retrieved. To identify putatively pathogenic variants, we retained variants with allele frequencies equal to or less than 0.5% in any of the ethnic subgroups found in the various databases. These included variants listed in the Japanese 1200 exomes from the Human Genetic Variation Database (<http://www.genome.med.kyoto-u.ac.jp/SnpDB/>), the 1000 Genomes Project [17] and the 6500 control exomes from the NHLBI GO Exome Sequencing Project (ESP) (<http://evs.gs.washington.edu/EVS/>).

The detected variants were confirmed by the traditional Sanger's method. Each of the exons was amplified, and then examined by polymerase chain reaction (PCR). All reactions were performed in a 25- μ L volume containing 12.5 μ L of PrimeSTAR Max Premix (2 \times) (Takara, Otsu, Japan), 0.4 μ M each of the primers and 200 ng of template DNA under the following conditions: 98.0 $^{\circ}$ C for 1 min, (98.0 $^{\circ}$ C for 10 s, 54.0 $^{\circ}$ C for 5 s, 72.0 $^{\circ}$ C for 30 s) for 30 cycles, and 72.0 $^{\circ}$ C for 5 min. The products were sequenced using the BigDye[®] Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Foster City, CA) on Applied Biosystems 3130 DNA Analyzer (Applied Biosystems) in accordance with the manufacturer's instructions. The sequence from both strands was visually inspected in order to confirm the substitution.

2.3. Analysis of the amino acid residues

SIFT (<http://sift.jcvi.org/>) and PolyPhen-2 (<http://genetics.bwh.harvard.edu/pph2/index.shtml/>) were used to predict whether each amino acid substitution would affect the function of each protein. These substitutions were also aligned across species (<https://genome.ucsc.edu/cgi-bin/hgGateway/>).

2.4. Postmortem blood acylcarnitine analysis by tandem mass spectrometry

Whole blood samples were blotted onto one spot on a Guthrie card and then subjected to acylcarnitine analysis by tandem mass spectrometry.

2.5. Extraction of genomic DNA and performance of mutational analysis in the other family members

Genomic DNA was purified from buccal cell swabs in accordance with standard methodology. PCR was performed using the previously discussed method. Genomic DNA samples from the parents and the sister were examined for the presence or absence of the *CPT2* mutation.

2.6. Ethics

This study was approved by the Ethics Committee of the Nagasaki University Graduate School of Medicine.

3. Case history in Case 15

The patient was a female carried to full-term and delivered via cesarean section. Her Apgar score was 6/9, birth weight was 2870 g, height was 49.0 cm and head circumference was 34.0 cm.

At 11 months of age, she was taken to a doctor's office because of fever and vomiting that had continued for several days. After examination, she was prescribed cephem antibiotics. During the morning of the

next day, however, she suddenly lost consciousness and an ambulance was requested. By the time the emergency service personnel arrived, she had already suffered cardiopulmonary arrest. Although cardiopulmonary resuscitation was initiated immediately and continued until she reached the hospital, she was pronounced dead.

The patient had never been ill until the time of her death. Family history was negative for seizures, arrhythmias and sudden death. Her parents were not consanguineous.

Histological examination of the patient led to the diagnosis of Reye's-like syndrome. The liver showed diffuse and distinctive vacuoles, which Oil-red O staining subsequently confirmed to be the accumulation of fatty acids. Oil-red O-positive vacuoles were also detected in the kidney and heart (Fig. 1).

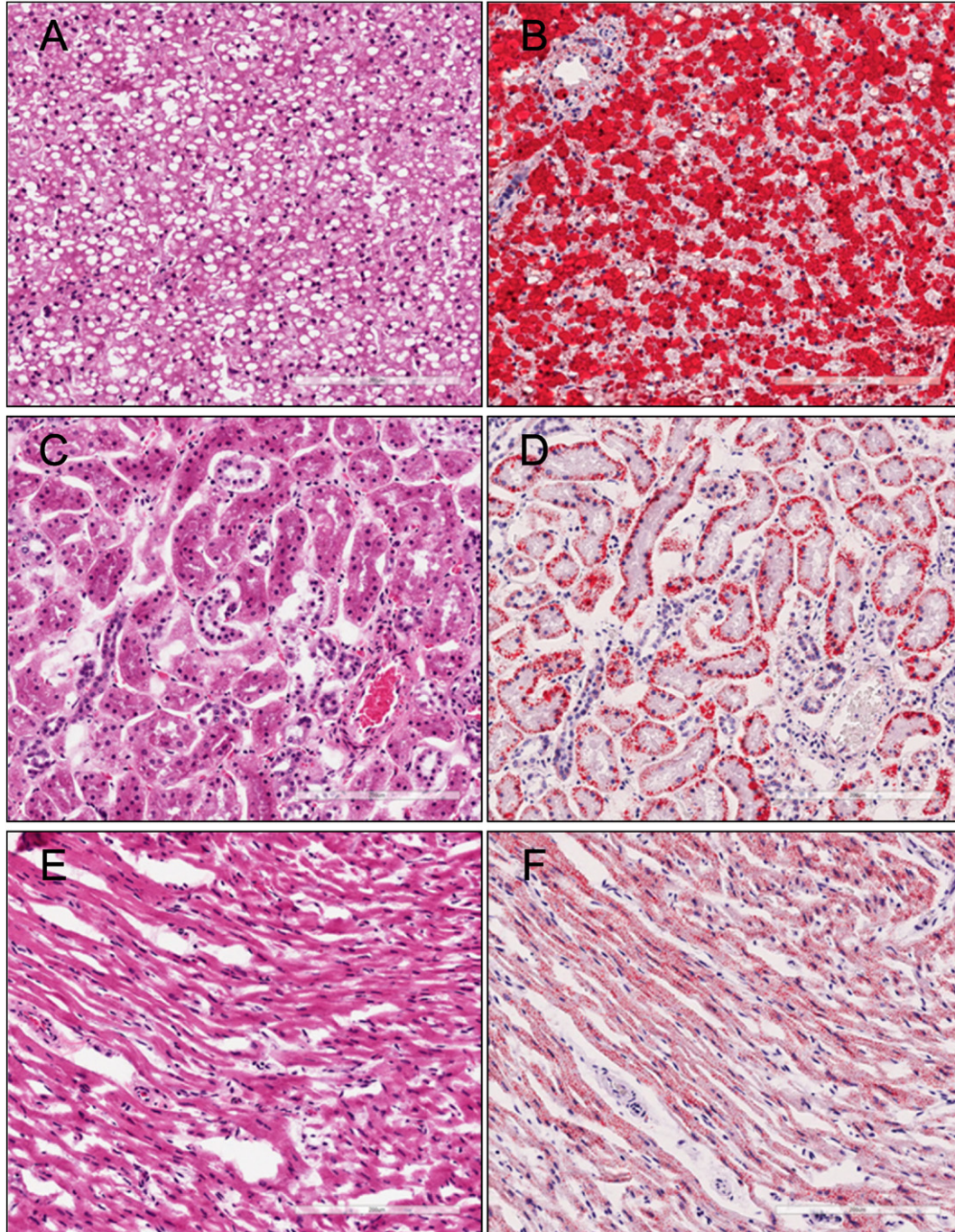


Fig. 1. Histological examination of Case 15. Steatosis was detected in the liver (A; hematoxylin–eosin (H.E.), B; Oil-red-O), kidney (C; H.E., D; Oil-red-O) and heart (E; H.E., F; Oil-red-O).

Table 4
Detected variants.

Case	Gene	AA	Substitution		SIFT		PolyPhen-2		HGVB	EXAC
5	ACADS	P55L	164C>T	Heterozygote	Damaging	0.0	Probably D	0.993	8/8654	3/1346
6	CPT2	F383Y	1148T>A	Heterozygote	Tolerated	0.61	Possibly D	0.932	3/8644	1/600
7	SLC22A5	D487N	1459G>A	Heterozygote	Tolerated	1.0	Benign	0.001	0/121,410	1/600
14	ACADS	V84M	250G>A	Heterozygote	Damaging	0.02	Probably D	0.997	0/6496	0/600
15	CPT2	F323fs	968_969 del TC	Heterozygote						
15	CPT2	V605L	1813G>C	Heterozygote	Damaging	0.004	Possibly D	0.885	3/8654	1/600

W; wild type, M; mutation type, AA; amino acid change, probably D; probably damaging, possibly D; possibly damaging, HGVB; Human Genetic Variation Browser, EXAC; The Exome Aggregation Consortium.

4. Results

4.1. Target sequence of sudden death cases

Targeted resequencing revealed the mean coverage of the coding sequence in the target genes was 155.4 reads, with an overall average gene level coverage at ≥ 10 reads of 90.9%.

Table 4 shows the detected variants found during the filtering steps. After the filtering, only six variants remained.

4.2. Genetic analysis in Case 15

Among the detected variants, only Case 15 was found to have two pairs of heterozygous deletion (c.968_969 del TC, p.F323fs) and substitution (c.1813G>C, p.V605L) in the CPT2 gene, all of which were confirmed by Sanger's sequencing (Fig. 2). Pedigree analysis confirmed that the deletion was transmitted from her father while the substitution was from her mother (Fig. 2). The c.1813G>C (p.V605L) substitution has been previously reported in a Japanese CPT II deficiency patient [21]. This was detected in 3 alleles among the 8654 East Asian control alleles (minor allele frequency: 0.0004, The Exome Aggregation Consortium) and in 1 allele out of the 600 Japanese control alleles (minor allele frequency: 0.002, Human Genetic Variation Browser). Results also predicted there would be an effect on the function of the protein, with a SIFT of 0.004, which indicated damaging and a PolyPhen-2 of 0.885,

which indicated possibly damaging. An examination of species ranging from zebrafish to human showed the substitution was conserved (Fig. 3).

Analysis also showed there were two homozygous substitutions (c.1055T>G, p.F352C and c.1102G>A, p.V368I) in the CPT2 gene. Since these two substitutions are common genetic polymorphisms [18–22], they were excluded from the targeted NGS analysis.

4.3. Other genetic substitutions

There were four other substitutions found in four different cases. Case 5 had the substitution ACADS-P55L (c.164C>T), Case 6 had CPT2-F383Y (c.1148T>A), Case 14 had ACADS-V84M (c.250G>A), and Case 7 had SLC22A5-D487N (c.1459G>A) (Table 4). The former three were heterozygous substitutions that according to SIFT or PolyPhen-2 were predicted to affect the function of the protein. An examination of species ranging from zebrafish to human showed the substitution was conserved (Fig. 3).

4.4. Acylcarnitine analysis in Case 15

We performed acylcarnitine analysis of the postmortem whole blood samples using tandem mass spectrometry. Free carnitine was 181.24 μM , which was increased as compared to the normal range (<60 μM), but which was within the postmortem reference value

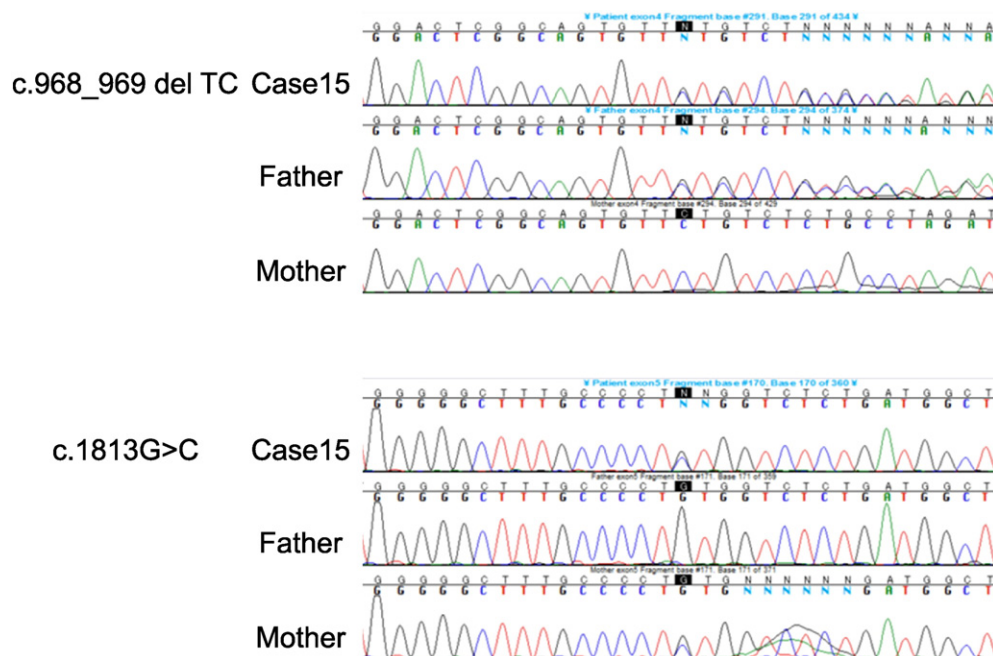


Fig. 2. Sequencing analysis in Case 15. Case 15 had two pairs of heterozygous deletions (c.968_969 del TC) and substitutions (c.1813G>C) in the CPT2 gene. The father had a heterozygous deletion (c.968_969 del TC) while the mother had a heterozygous substitution (c.1813G>C).

<i>CPT2</i>		605
Human	PAVNLLGGFAPV	VSDGFGVGYA
Chimp	PAVNLLGGFAPV	VSDGFGVGYA
Crab-eating macaque	PAVNLLGGFAPV	VSDGFGVGYA
Mouse	PAVSLGGFAPV	VPDGFGLIAYA
Rat	PAVSLGGFAPV	VPDGFGLIAYA
Pig	PAVNLLGGFAPV	VPDGFGLIAYA
Horse	PEVSLGGFAPV	VPDGFGLIAYA
Dog	STVNIIGGFAPV	VPDGFGLIAYA
Chicken	PAVQLGGFAPV	VPDGFGLIAYA
<i>X. Tropicalis</i>	PAVQLGGFAPV	VPDGFGLIAYA
Zebrafish	PAVSLGGFAPV	VPDGFGLIAYA

<i>CPT2</i>		383
Human	SWG DGVAVLR	RFNEVFKDSTQ
Chimp	SWG DGVAVLR	RFNEVFKDSTQ
Crab-eating macaque	SWG DGVAVLR	RFNEVFKDSTQ
Mouse	AWGDGVAVLR	RFNEVFRDSTQ
Rat	AWGDGVAVLR	RFNEVFRDSTQ
Pig	AWGDGVAVLR	RFNEVFKDSTQ
Horse	AWGDGVAVLR	RFHEVFKDSTQ
Dog	AWGDGVAVLR	RFNEVFKDSTQ
Chicken	SWG DGVAVLR	RFQNEVFKDSTE
<i>X. Tropicalis</i>	SWG DGVAVLR	RFQNEVFKDSTQ
Zebrafish	SWG DGVAVLR	RFQNEVFKDSTE

<i>SCAD</i>		55
Human	CRDFAEKELF	PPIAAQVDKEHL
Chimp	CRDFAEKELF	PPIAAQVDKEHL
Crab-eating macaque	CRDFAEKELF	PPIAAQVDKEQL
Mouse	CRDFAEKELV	PPIAAQVDREHL
Rat	CRDFAEKELV	PPIAAQVDKEHL
Pig	CRDFAEKELV	PPIAAQVDKEHR
Horse	CRDFAEKELV	PPIAAQVDREHL
Dog	CRDFAEKELV	PPIAAQVDKEHR
Chicken	CRDFAEKELM	PLAELDREHR
<i>X. Tropicalis</i>	CRDFAEKELQ	PPIAAGLDREHR
Zebrafish	CRDYAQKELA	PPIAAGLDREHR

<i>SCAD</i>		84
Human	MGGLGLLAMD	VPEELGGAGLD
Chimp	MGGLGLLAMD	VPEELGGAGLD
Crab-eating macaque	MGGLGLLAMD	VPEELGGAGLD
Mouse	MGELGLLAMD	VPEELSGAGLD
Rat	MGELGLLAMD	VPEELSGAGLD
Pig	MGELGMLAMD	VPEELSGAGLD
Horse	MGELGLLAMD	VPEELSGAGLD
Dog	MGELGLLAMD	VPEELSGAGLD
Chicken	MGSLGLLAVE	VPEQFKGAGLD
<i>X. Tropicalis</i>	MGQIGLLAVE	VPEELGGAGLD
Zebrafish	LGAMGVMAVE	VPEELSGAGMD

<i>SLC22A5</i>		487
Human	SPYFVYLGAY	DRFLPYILMGS
Chimp	SPYFVYLGAY	DRFLPYILMGS
Crab-eating macaque	SPYFVYLGAY	DRFLPYILMGS
Mouse	SPYFVYLGAY	DRFLPYILMGS
Rat	SPYFVYLGAY	DRFLPYILMGS
Pig	SPYFIYLGAY	DRFLPYILMGS
Horse	SPYFVYLGAY	DRFLPYILMGS
Dog	SPYFVYLGAY	DRFLPYILMGS
Chicken	SPYFAYLGAY	DRFLPYILMGS
<i>X. Tropicalis</i>	SPYFVYLGAY	NRLLPYILMGS
Zebrafish	APYIIFLGT	FNH-LPYVLMGS

Table 5

Acylcarnitine profile in Case 15.

	C0	C2	C5	C16	C18	C18:1	C18:2
Case 15	181.24	4.65	1.51	4.13	2.3	4.39	0.97
PRV	422.59	147.13	1.5	3.495	2.495	3.095	0.925
NR	60.0	45.0	1.0	7.0	2.1	3.2	0.8

PRV; postmortem reference value, NR; normal range.

(<422 μ M). C5-acylcarnitine was increased to 1.51 μ M (normal range: <1.0 μ M, postmortem reference value: <1.5 μ M). There was also an increase in the C16, C18, C18:1 and C18:2-acylcarnitine (Table 5). The ratio of [C16 + C18:1] to C2 was as high as 1.83, which suggests that Case 15 had either a CPT II or carnitine-acylcarnitine translocase deficiency.

5. Discussion

After many research studies and case reports examined postmortem samples [2–4,23–28], in 2001, Chace et al. performed a large-scale study of FAODs in which they analyzed postmortem blood samples by tandem mass spectrometry [5]. In our previous study, we also performed postmortem acylcarnitine analyses, which subsequently led to our discovery of other FAODs cases [7]. Due to postmortem changes, the interpretation of the postmortem acylcarnitine analysis is sometimes not easy. Table 6 shows our in-house data for our postmortem acylcarnitine analysis. Based on our analytical findings, it was possible to definitively diagnose a CPT II deficiency case, which we reported in our previously published study [7]. In the two false-positive cases that we observed, we found there were increases in the long-chain acylcarnitine in the absence of any genetic abnormality. The C16, C18, C18:1 and C18:2-acylcarnitine values in the present case were much lower than that of not only our definitively diagnosed case, but also the two false-positive cases.

Definite diagnoses of FAODs can be made by either a genetic or an enzyme analysis. The relationship between SUDI and FAODs was first discussed in detail in the 1990s [24,29,30]. After Bennett and Powell reported finding SUDI cases with an A985G mutation of the medium-chain acyl-CoA dehydrogenase (MCAD) deficiency, they recommended genetic analysis for SUDI be performed [2]. Unfortunately, this study only targeted one particular substitution and did not cover any of the other candidate genes. However, it should be noted that the number of candidate genes for FAODs is approximately 20 genes and thus, post-mortem genetic screening is not really practical.

Recently, NGS has been developed and is more widely used, especially in the field of sudden cardiac death [12,13]. This technique makes it possible to examine a larger number of genes and exons at a lower cost, in addition to requiring a smaller amount of time compared to the conventional Sanger's method [13]. Unlike that for clinical patients, there is a lack of information and no definitive clinical symptoms for sudden death cases. Thus, there are numerous candidate genes that could be responsible for sudden death cases.

In our current study, we used NGS to perform target exon sequencing, in addition to conducting postmortem comprehensive genetic screening for FAODs. As far as we know, this is the first study to examine metabolic autopsy performed with NGS.

In most of the cases, the sequence covered more than 90% of the targeted exons. False-positives and false-negatives were rare. After excluding the variants that have been reported elsewhere, there were six substitutions and deletions remaining. Because the majority of the FAODs are inherited in an autosomal recessive manner, we chose the one case that had at least two pairs of the heterozygous variant (Case

Fig. 3. Sequence alignment between species. Except for *SLC22A5*-D487N, the substitutions were highly conserved between the species.

Table 6

The comparison with other postmortem samples.

	C0	C2	C5	C16	C18	C18:1	C18:2
Case 15	181.24	4.65	1.51	4.13	2.3	4.39	0.97
DD	69.46	8.5	0.13	7.41	5.29	6.79	1.64
FP 1	147.82	96.45	4.29	13.65	6.74	8.99	1.23
FP 2	127.4	35.25	1.97	6.13	3.74	3.87	1.55

DD, definitively diagnosed case, FP; false-positive case.

15). This patient had a compound heterozygous deletion (c.968_969 del TC, p.F323fs) and substitution (c.1813G>C, p.V605L) in the *CPT2* gene. Sanger's method was used to confirm these variants. The former variant was inherited from her father and caused a frameshift, thereby resulting in an immature protein. The latter variant was inherited from her mother and has been previously found and reported in a Japanese CPT II deficiency patient [21]. SIFT and PolyPhen-2 classified the function of the protein as damaging. Our analyses additionally showed that the amino acid was conserved between the species examined. Thus, when taken together, these genetic analyses demonstrated that this patient had a CPT II deficiency.

There were four cases with other variants, each of which had a heterozygous substitution. The substitution in Case 5 was *ACADS*-P55L (c.164C>T), in Case 6 was *CPT2*-F383Y (c.1148T>A), in Case 14 was *ACADS*-V84M (c.259G>A) and in Case 7 was *SLC22A5*-D487N (c.1459G>A). Because the substitution of *CPT2*-F383Y has also been shown to cause decreases in the CPT II activity and been reported in a CPT II deficiency patient [8,19–21,31], even in the heterozygous F383Y mutation state [21,32,33], the heterozygous *CPT2*-F383Y mutation could be a cause of sudden death. While the postmortem acylcarnitine analysis in our current case did not suggest any CPT II deficiency, it is possible that Case 6 might have been affected by the mutation.

The substitutions of *ACADS* are controversial. *ACADS*-P55L was detected in 8 alleles among the 8654 East Asian control alleles (minor allele frequency: 0.0009, The Exome Aggregation Consortium) and in 3 alleles out of the 1346 Japanese control alleles that were examined (minor allele frequency: 0.002, Human Genetic Variation Browser). *ACADS*-V84M was neither detected in the 6496 East Asian control alleles (The Exome Aggregation Consortium) nor in the 600 Japanese control alleles (Human Genetic Variation Browser). The SIFT scores for these two *ACADS* substitutions were classified as damaging, with both substitutions conserved between species. It has been reported that *ACADS*-P55L decreases the enzyme activity of SCAD [34]. Although the final diagnoses in Case 14 and Case 5 were acute encephalopathy and respiratory infection, respectively, it cannot be denied that these substitutions could have potentially affected the enzyme activity to a greater or lesser extent. Thus, the possibility exists that individuals with rare variants are susceptible to environmental stress. However, MCAD can compensate for the SCAD enzyme deficiency because of the overlap in the substrate specificity [35] and the substitution may not have a major effect to the death. Further accumulation of the genetic data will be necessary in order to link these rare variants and SUDI.

Even though *SLC22A5*-D487N was not detected in the 121,410 control alleles (The Exome Aggregation Consortium), it was detected in 1 allele out of the 600 Japanese control alleles (minor allele frequency: 0.002, Human Genetic Variation Browser). The SIFT score was classified as tolerated while the PolyPhen-2 was classified as benign. Since amino acid position 487 is asparagine in *X. tropicalis* and zebrafish, this substitution might not affect the activity of this gene.

In the current study, our use of NGS led to finding a case of compound heterozygote CPT II deficiency. Furthermore, we additionally found a case of heterozygote CPT II deficiency-related gene variant and two cases of SCAD deficiency-related variants. It is true that the cost of NGS is still higher than postmortem blood acylcarnitine analysis, but these variants would not have been detected without the use of NGS. Thus, metabolic autopsy performed with NGS is a useful method,

especially when postmortem blood acylcarnitine analysis is not available. These findings suggest that metabolic autopsy should be performed in all cases of sudden death.

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