Leigh Syndrome: One Disorder, More Than 75 Monogenic Causes

Nicole J. Lake, MSc,[1,2] Alison G. Compton, PhD,[1,2]
Shamima Rahman, MD, PhD,[3] and David R. Thorburn, PhD[1,2,4]

Leigh syndrome is the most common pediatric presentation of mitochondrial disease. This neurodegenerative disorder is genetically heterogeneous, and to date pathogenic mutations in >75 genes have been identified, encoded by 2 genomes (mitochondrial and nuclear). More than one-third of these disease genes have been characterized in the past 5 years alone, reflecting the significant advances made in understanding its etiological basis. We review the diverse biochemical and genetic etiology of Leigh syndrome and associated clinical, neuroradiological, and metabolic features that can provide clues for diagnosis. We discuss the emergence of genotype–phenotype correlations, insights gleaned into the molecular basis of disease, and available therapeutic options.

ANN NEUROL 2016;79:190–203

Disorders of mitochondrial energy generation are the most frequent group of inherited metabolic disorders, with an estimated incidence of at least 1 in 5,000 live births.[1] The most common clinical presentation of mitochondrial disease in children is a progressive neurodegenerative disorder known as Leigh syndrome (LS; Mendelian Inheritance in Man [MIM] 25600). LS has an estimated prevalence of ~1 per 40,000 live births[2]; however, much higher incidences have been observed in specific populations owing to founder mutations.[3,4]

Since the identification of the first pathogenic mutation in an LS patient in 1991,[5] >75 disease genes have been identified, highlighting the remarkable heterogeneity underlying this disorder. Nearly 30 of these LS disease genes have been characterized in the past 5 years alone, reflecting how the introduction and greater utility of massively parallel sequencing (MPS) technology has transformed our ability to identify the genetic basis of disease. Beyond the identification of novel disease genes, MPS has also facilitated the identification of patients with mutations in known disease genes, enabling the emergence of genotype–phenotype relationships for this rare disorder. Advances in characterizing the genetic basis of LS have consolidated our understanding of the molecular basis of disease, revealing a diverse biochemical etiology consistent with the annotation of LS as a disorder of energy generation.[2]

Clinical and Neuroradiological Features

LS is clinically heterogeneous, with significant variation between patients with respect to age of onset, age of death, and symptomatology. Generally, onset occurs by 2 years of age,[6] with symptoms often presenting during infection or illness after an initial period of normal development. Patients develop neurological symptoms including developmental delay and regression, hypotonia, ataxia, dystonia, and ophthalmological abnormalities including nystagmus and optic atrophy.[2,6–8] The presentation can also be multisystemic; cardiac, hepatic, gastrointestinal, and renal tubular dysfunction have been observed.[9–12] Progression is often episodic, and typically results in death by 3 years of age.[2,7,8,13] Adult onset LS has been infrequently reported.[14]

View this article online at wileyonlinelibrary.com. DOI: 10.1002/ana.24551

Received Jun 30, 2015, and in revised form Oct 16, 2015. Accepted for publication Oct 18, 2015.

Address correspondence to Dr Thorburn, Murdoch Childrens Research Institute, Royal Children's Hospital, 50 Flemington Rd, Parkville, Victoria, 3052, Australia. E-mail: david.thorburn@mcri.edu.au

From the [1]Murdoch Childrens Research Institute, Royal Children's Hospital, Melbourne, Victoria, Australia; [2]Department of Paediatrics, University of Melbourne, Melbourne, Victoria, Australia; [3]Mitochondrial Research Group, Genetics and Genomic Medicine, Institute of Child Health, University College London and Metabolic Unit, Great Ormond Street Hospital, London, United Kingdom; and [4]Victorian Clinical Genetic Services, Royal Children's Hospital, Melbourne, Victoria, Australia.

Additional supporting information can be found in the online version of this article.

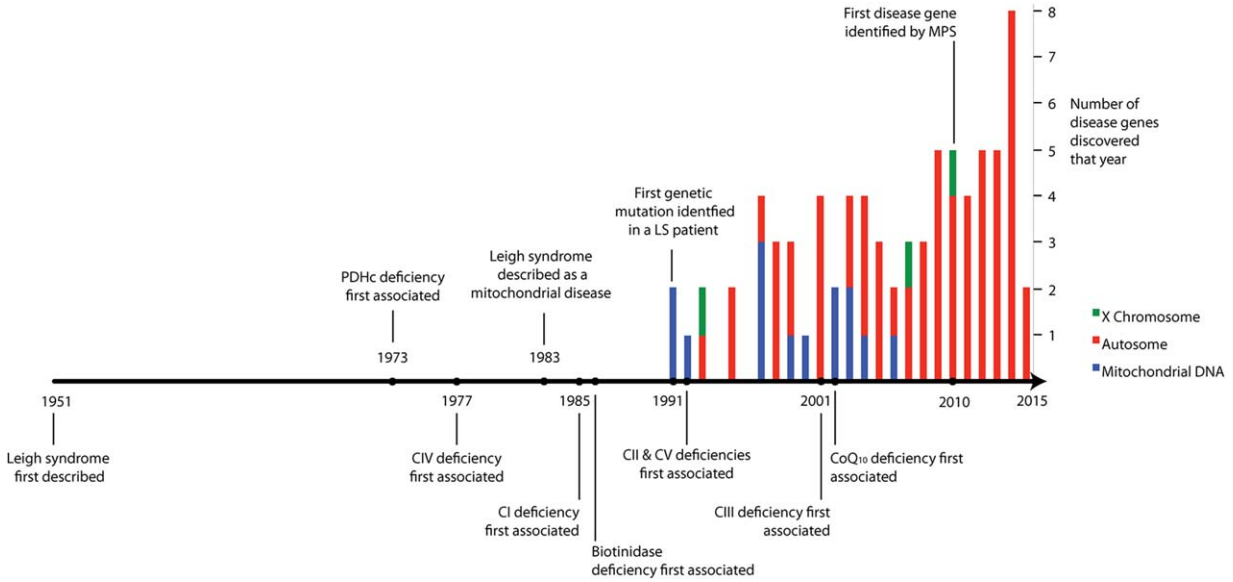

FIGURE 1: The development of our understanding of Leigh syndrome (LS). Timeline depicts significant advances in the understanding of the biochemical and genetic basis of LS. The graph represents the number of new LS disease genes identified in each year relative to the timeline. The coloring represents the location of the gene, either on the X-chromosome (green), autosome (red), or mitochondrial DNA (blue). CI–CV = oxidative phosphorylation complexes I–V; CoQ_{10} = coenzyme Q_{10}; MPS = massively parallel sequencing; PDHc = pyruvate dehydrogenase complex.

Neurological decline in LS patients is associated with the development of bilateral symmetrical lesions within the brainstem and basal ganglia structures, which characterize the disease.[13,15,16] These lesions are observed as regions of focal hyperintensity on T2-weighted magnetic resonance imaging (MRI), and elevated lactate may be detected by magnetic resonance spectroscopy. Additional neuroradiological abnormalities such as white matter involvement and cerebral atrophy may also be observed.[17] In 1996, we defined criteria for a stringent diagnosis of LS, requiring that characteristic neuropathology or neuroradiology must be accompanied by progressive neurodegeneration with (1) clinical evidence of brainstem and/or basal ganglia dysfunction, (2) intellectual and motor developmental delay, and (3) elevated serum or cerebrospinal fluid (CSF) lactate indicating abnormal energy metabolism.[2] In 2015, it would seem prudent to amend criterion (3) to "abnormal energy metabolism indicated by a severe defect in oxidative phosphorylation (OXPHOS) or pyruvate dehydrogenase complex (PDHc) activity, a molecular diagnosis in a gene related to mitochondrial energy generation, or elevated serum or CSF lactate." Where patients do not fulfill these stringent criteria, a diagnosis of Leigh-like syndrome can be considered, particularly in patients with atypical neuroradiology or normal lactate levels.[2]

The Development of Our Understanding of the Etiological Basis of LS

Since Denis Leigh's first description of LS in 1951,[18] there have been several key research milestones that have contributed to our understanding of the etiological basis of LS (Fig 1). The similarity of the neuropathology to Wernicke encephalopathy, a condition of thiamine deficiency, and findings of elevated blood lactate and pyruvate suggested that a metabolic abnormality was the underlying disease etiology.[19,20] Before the first genetic mutation was identified in 1991,[5] 40 years of clinical and biochemical investigation provided evidence that deficiency of the PDHc, and of nicotinamide adenine dinucleotide (NADH):ubiquinone oxidoreductase (complex I) and cytochrome *c* oxidase (complex IV) within the OXPHOS pathway, could cause LS.[21–23] Together with the finding of abnormal mitochondrial morphology in skeletal muscle tissue from patients, these abnormalities suggested a common theme of defective mitochondrial energy metabolism.[22] Subsequently LS was reannotated as a mitochondrial encephalopathy.

It has since been established that multiple other enzymatic deficiencies can underlie LS, mostly linked directly to OXPHOS or broader pathways of energy generation. The OXPHOS pathway of electron transfer, proton transport, and adenosine triphosphate (ATP) synthesis comprises 5 multiprotein complexes located in the mitochondrial inner membrane (Fig 2). Biochemical defects in each of the 5 OXPHOS complexes, and the electron carrier coenzyme Q_{10} (CoQ_{10}), have been observed in LS patients. PDHc enables the generation of electron donors for OXPHOS; hence PDHc deficiency also represents a disorder of energy generation. Complex I deficiency is the most common biochemical cause of

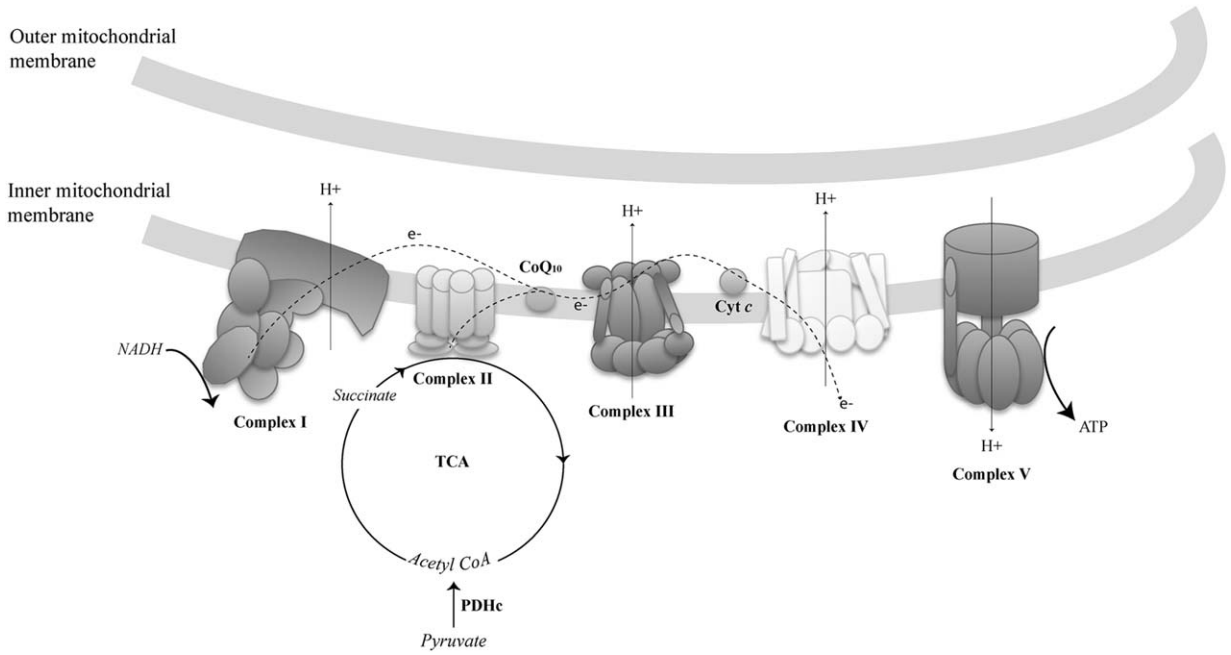

FIGURE 2: The biochemical basis of Leigh syndrome (LS). LS is caused by a genetic impairment of the mitochondrial pathways of energy generation. Briefly, pyruvate is metabolized by pyruvate dehydrogenase (PDHc) to produce acetyl coenzyme A (acetyl CoA), which is utilized by the citric acid cycle (TCA) to produce electron donors for the pathway of oxidative phosphorylation (OXPHOS). OXPHOS is performed within the mitochondrial inner membrane by 5 multiprotein complexes, known as complexes I to V, and electron carriers coenzyme Q (CoQ_{10}) and cytochrome *c* (Cyt *c*). Complexes I to IV, often referred to as the respiratory chain or electron transfer chain, direct the flow of electrons (e-) provided by the TCA cycle through the multiprotein complexes. CoQ_{10} mediates electron transfer between complex I and complex II to complex III, whereas Cyt *c* transfers electrons from complex III to complex IV. The respiratory chain utilizes the energy produced by this electron transfer to pump protons (H^+) through complexes I, III, and IV into the intermembrane space, generating a proton gradient that can be harnessed by adenosine triphosphate (ATP) synthase (complex V) to drive the synthesis of ATP. Deficiency of PDHc, complexes I to V, and CoQ_{10} can cause LS. NADH = nicotinamide adenine dinucleotide.

LS, with nearly one-third of all LS disease genes associated with complex I deficiency. Isolated complex IV deficiency and multiple OXPHOS defects are also frequently observed, whereas defects of complexes II, III, or V or of CoQ_{10} are relatively rare.[2,6,7] Measurement of OXPHOS and PDHc enzymes in a patient biopsy or cell line is often undertaken to provide evidence of a biochemical defect in these pathways to support a clinical diagnosis of LS.

The Heterogeneous Genetic Basis of LS

To date, pathogenic mutations in >75 genes have been identified in affected patients (Table 1, and see Supplementary Table for more detailed information). Most of these disease genes encode structural components of the OXPHOS complexes, or proteins required for their assembly, stability, and activity. As is the case for other mitochondrial diseases, there are several possible modes of inheritance including maternal (for mutations in mitochondrial DNA [mtDNA]) and autosomal recessive or X-linked (for nuclear-encoded genes). Despite the remarkable number of established disease genes, many LS patients remain without a genetic diagnosis, indicating that there are still more disease genes to be identified.

The aim of this article is not to provide an in-depth review of all known forms of LS and Leigh-like syndrome, but rather to discuss the most relevant biochemical and genetic etiologies, associated clinical and biochemical features relevant for diagnosis, and therapeutic options (where available, summarized in Table 2). We focus on the more common nuclear-encoded genetic causes, as well as describing types of LS and Leigh-like syndrome caused by mtDNA mutations.

Complex I Deficiency

The most frequent clinical presentation of complex I deficiency is LS,[24] and complex I deficiency is the leading biochemical basis of LS.[2,6,7] Mutations in the NADH dehydrogenase (ubiquinone) Fe-sulfur protein 4 (NDUFS4) subunit are the most frequent autosomal recessive cause of complex I–associated LS, with > 20 cases reported.[24] Interestingly, almost all patients reported with *NDUFS4* mutations had LS, in contrast to mutations in other nuclear-encoded complex I subunits, which may be associated with heterogeneous phenotypes. Patients with *NDUFS4* mutations display a characteristic LS presentation, experiencing onset and demise typically

TABLE 1. Genes in Which Mutations Cause Leigh Syndrome or Leigh-like Syndrome

Biochemical Deficiency	Genes
Pyruvate dehydrogenase	*PDHA1*,[a] *PDHB, PDHX, DLAT, DLD, LIPT1, LIAS, TPK1, SLC19A3, SLC25A19*
Complex I	*MTND1*,[b] *MTND2*,[b] *MTND3*,[b] *MTND4*,[b] *MTND5*,[b] *MTND6*,[b] *NDUFV1, NDUFV2, NDUFS1, NDUFS2, NDUFS3, NDUFS4, NDUFS7, NDUFS8, NDUFA1*,[a] *NDUFA2, NDUFA9, NDUFA10, NDUFA12, NDUFAF2, NDUFAF5, NDUFAF6, FOXRED1*
Complex II	*SDHA, SDHAF1*
Coenzyme Q_{10}	*PDSS2*
Complex III	*UQCRQ, BCS1L, TTC19*
Complex IV	*MTCO3*,[b] *NDUFA4, SURF1, COX10, COX15, SCO2, PET100, LRPPRC, TACO1, ETHE1*
Complex V	*MTATP6*[b]
Combined OXPHOS defects—pathway affected	
Mitochondrial DNA maintenance	*FBXL4, POLG, SUCLA2, SUCLG1*
Mitochondrial translation	ΔmtDNA,[c] *MTTI*,[b] *MTTK*,[b] *MTTL1*,[b] *MTTV*,[b] *MTTW*,[b] *MTFMT, GTPBP3, TRMU, EARS2, FARS2, IARS2, NARS2, GFM1, GFM2, TSFM, C12orf65, PNPT1*
Disease genes that cause secondary impairment of mitochondrial energy generation	
OXPHOS ± PDHc	*HIBCH, ECHS1, SERAC1, AIFM1*[a]
Biotinidase	*BTD*

Except as indicated, all genes are associated with autosomal recessive inheritance. Supplementary Table contains additional information on the role of each gene product.
[a]X-linked inheritance.
[b]Maternal inheritance.
[c]Sporadic inheritance.
OXPHOS = oxidative phosphorylation; PDHc = pyruvate dehydrogenase complex; ΔmtDNA = mtDNA deletion.

within the first 8 months of life and no later than 30 months. Neuroradiological features in these infants included bilateral symmetrical basal ganglia lesions in almost all cases, often extending down to the cerebral peduncles, pons, and medulla, and frequently with associated cerebral atrophy.[24,25] Approximately one-third of all reported cases also had hypertrophic cardiomyopathy.

Mutations in NADH dehydrogenase (ubiquinone) flavoprotein 1 (*NDUFV1*) and *NDUFS1* have also been widely reported to cause LS. *NDUFS1* mutations appear to be associated with an early age of death, with all reported patients presenting by 8.5 months and succumbing by 4 years.[24] Most patients with *NDUFV1* mutations also died in early childhood, although a few cases were alive in late childhood.[26,27] Thus, *NDUFS4*-, *NDUFV1*-, and *NDUFS1*-mediated LS appear to be particularly severe forms of the disease. Whereas all reported *NDUFS4* mutations except 1 predict complete loss-of-function alleles, no patients have been described with 2 null alleles of *NDUFV1* or *NDUFS1*, suggesting that complete loss of these 2 proteins may be incompatible with life.

Complex II, Complex III, and CoQ_{10} deficiencies

Deficiencies of complex II, complex III, or CoQ_{10} (ubiquinone) are rare causes of LS, and collectively underlie <10% of all cases.[2,6,7,28] Mutations in the complex II subunit SDHA were the first nuclear mutations identified to cause OXPHOS disease.[29] Some patients with *SDHA* mutations have a severe infantile presentation of LS with rapid demise,[29] but other patients may experience a mild LS course, with survival into late childhood years, preservation of cognitive abilities, and an "almost normal

TABLE 2. Available Therapeutic Options for LS Patients, and the Genetic and Biochemical Forms That Can Respond to Treatment

Gene or Biochemical Form	Treatment
Coenzyme Q_{10} deficiency (*PDSS2*)	Coenzyme Q_{10}
Ethylmalonic encephalopathy (*ETHE1)*	Metronidazole and N-acetylcysteine
Biotin/thiamine-responsive basal ganglia disease (*SLC19A3)*	Thiamine and high-dose biotin
TPK deficiency (*TPK1*)	Thiamine
Biotinidase deficiency (*BTD*)	Biotin
Pyruvate dehydrogenase deficiency (*PDHA1*)	Thiamine and high-fat diet

Apart from targeted therapies, all LS patients can be offered treatment for symptoms such as acidosis, seizures, dystonia, and cardiomyopathy. It is also important to ensure good nutrition, aggressive management of intercurrent illnesses, and caution with anesthesia.[113]
LS = Leigh syndrome; TPK = thiamine pyrophosphokinase.

school life."[28,30] Nearly all patients with mutations in the complex III assembly factor TTC19 develop neuroimaging abnormalities consistent with LS.[31] Occasional patients with LS and CoQ_{10} deficiency have been reported.[9,32] Prompt recognition of this subgroup of LS is imperative, because these patients may respond to CoQ_{10} supplementation and survive into adulthood,[32] although this has not been consistently observed.[33] One report described improvement of hepatic but not neurological symptoms,[34] and another patient with CoQ_{10}-deficient LS due to *PDSS2* mutations did not respond to treatment.[9]

Complex IV Deficiency

Complex IV deficiency underlies ~15% of LS cases.[2,6,7] Mutations in *SURF1*, encoding a complex IV assembly factor, are the most common cause of complex IV deficient LS and are among the most frequently reported causes of LS, with >200 cases described to date in the literature.[35] Our recent natural history study of a *SURF1* patient cohort highlighted the relatively homogenous clinical and biochemical presentation associated with SURF1 deficiency.[35] However, a minority of patients with *SURF1* mutations lack the neuroradiological hallmarks of LS or show atypical features such as leukodystrophy and atrophy.[35,36] Survival analysis of 142 *SURF1* patients revealed a median age of death at 5.4 years,[35] indicating longer survival in *SURF1*-associated LS than is observed for LS patients due to mutations in other complex IV disease genes *SCO2, LRPPRC*, and *ETHE1*.[37–39]

LRPPRC mutations were originally reported in an isolated French-Canadian population.[37,40] Characteristic clinical features associated with French-Canadian LS (LSFC; MIM 220111) include mild facial dysmorphism, liver pathology, and a clinical course punctuated by episodes of acute metabolic decompensation that contribute significantly to mortality.[3,37] Fifty-five of 56 reported cases inherited homozygous *LRPPRC* p.A354V mutations,[37] reflecting a founder effect that has resulted in an incidence of LSFC of ~1 in 2,000 live births (Table 3).[3] Broader effects of LRPPRC dysfunction on mitochondrial post-transcriptional and translation processes have recently been recognized, including deficiency of ATP synthase.[41] Despite presenting as an isolated complex IV deficiency, the pathogenesis of *LRPPRC* mutations may therefore be attributable to a global defect of mitochondrial translation.

Mutations in *ETHE1* cause ethylmalonic encephalopathy (EE; MIM 602473), a presentation that resembles LS clinically and neuroradiologically.[38,42] The characterization of a role for ETHE1 in sulfide detoxification revealed EE as a manifestation of sulfide toxicity, whereby the associated isolated complex IV deficiency is a consequence of sulfide accumulation.[43] Accordingly, therapeutic strategies that reduce sulfide accumulation resulted in clinical, biochemical, and neuroradiological improvement in patients with *ETHE1* mutations.[44]

The only complex IV subunit with mutations causing LS is the recently reassigned subunit NDUFA4, which was previously thought to be a subunit of complex I. *NDUFA4* mutations have been reported to cause childhood onset LS with prominent epilepsy, learning difficulties, and survival into adulthood.[45]

Combined OXPHOS Deficiencies

Because mtDNA encodes structural components of complexes I, III, IV, and V, a molecular defect that impairs mtDNA replication or translation can cause combined OXPHOS deficiency. Thus, mutations in various disease genes associated with mtDNA depletion or defective translation have been identified in patients with LS (see Table 1, see Supplementary Table, A for more detailed information). The predominant causes of LS associated with mtDNA depletion are mutations in *SUCLA2* or *SUCLG1*, encoding subunits of succinyl-CoA synthetase, which catalyzes the conversion of succinyl-CoA to succinate within the citric acid cycle. Methylmalonic aciduria is frequently observed in these patients due to an accumulation of succinyl-CoA, and can be used to screen for

TABLE 3. Characteristic LS Disease Features, Affected Ethnicities, and Founder Genotypes Associated with the Most Common Nuclear Disease Genes (All with ≥ 10 Patients Reported)

Gene	Biochemical Defect	Characteristic Disease Features	Ethnicities Notably Affected	Founder/Frequent Genotypes
NDUFS4	CI	"Typical" LS disease course with death by 3 years	Ashkenazi Jews	c.462delA with an estimated carrier frequency of 1:1,000[25]
SURF1	CIV	Hypertrichosis, cognitive sparing	Pan-ethnic	c.311_312insATdel10 in Caucasian Europeans[35]
LRPPRC	CIV	Mild facial dysmorphism, liver pathology, and a course punctuated by episodes of acute metabolic decompensation	Saguenay-Lac-Saint-Jean region of Quebec, Canada	c.1119C>T, p.A354V with an estimated carrier frequency of 1:23[3,37]
SCO2	CIV	Hypertrophic cardiomyopathy, spinal muscular atrophy pattern of histopathology in skeletal muscle	Pan-ethnic	c.1541G>A, p.E140K[39]
PET100	CIV	Seizures	Lebanese	c.3G>C, p.Met1?[114]
ETHE1	CIV	Ethylmalonic aciduria, acrocyanosis, petechiae, gastrointestinal involvement	Mediterranean basin and Arabian peninsula regions	c.487C>T, p.R163W[38]
SUCLA2	CI, CIII, CIV, CV	Methylmalonic aciduria, dystonia, deafness, often Leigh-like presentation, cerebral atrophy, onset in early infancy with long disease duration	Faroe Islanders	c.534 + 1G>A with an estimated carrier frequency of ~1:33 people[4,115]
MTFMT	CI, CIII, CIV, CV	Microcephaly frequently observed	Europeans	c.626C>T with an estimated carrier frequency of 1:100 in Europeans[51]
SERAC1	Multiple	Hypoglycemia, liver involvement, behavioral disturbance	Pan-ethnic	—
PDHA1	PDHc	Lactate:pyruvate ratio < 20, agenesis of corpus callosum frequently observed	Pan-ethnic	—
PDHX	PDHc	Lactic acidosis crisis in newborn or in early infancy, cerebral palsy–like presentation	Roma children from Bulgaria	c.1336C>T, p.R446*[116]

CI–CV = oxidative phosphorylation complexes I–V; LS = Leigh syndrome; PDHc = pyruvate dehydrogenase complex.

these 2 defects in LS patients.[46,47] Symptoms generally present in early infancy, and patients can survive into teenage years and young adulthood.[48,49] Although patients with mutations in *SUCLG1* and *SUCLA2* manifest similarly, they can be differentiated by liver involvement (*SUCLG1*) or deafness (more common with *SUCLA2* mutations).[49] The *SUCLA2* c.534 + 1G>A mutation has a high carrier frequency in the Faroe Islands owing to a founder effect, with an estimated LS incidence of 1 in 1,700 in that population (see Table 3).[4] An interaction between succinyl-CoA synthetase and nucleoside diphosphate kinase, an enzyme involved in regulating mitochondrial nucleotide supply, has been hypothesized to account for mtDNA depletion in patients with *SUCLA2* and *SUCLG1* mutations.[46]

Nuclear encoded mt-tRNA modifying enzymes are required for efficient mitochondrial translation, and mutations in these proteins represent a relatively new class of LS disease genes. Mitochondrial methionyl-tRNA formyltransferase (*MTFMT*) was the first LS disease gene of this type to be reported. *MTFMT* mutations were initially identified in 2 unrelated LS patients through targeted exome sequencing of the MitoExome,[50] and subsequently identified in multiple other LS patients.[51] Most cases carry at least 1 copy of the c.626C>T mutation, which has a carrier frequency of ~1 in 100 in the European population and so may account for a significant proportion of LS within this population.[51]

mtDNA Mutations Causing LS Associated with Complex I, Complex IV, Complex V, and Combined OXPHOS Deficiencies

Cohort studies have suggested that mtDNA mutations underlie approximately 10 to 20% of LS cases.[2,6,7] To date, mutations in 13 of the 37 mtDNA-encoded genes have been described to cause LS, with the majority in genes encoding subunits of complex I or V, or in mitochondrial tRNAs (see Table 1, and Supplementary Table, A for more detailed information). LS can also be caused by large-scale mtDNA deletions.[2] The percentage of mtDNA molecules that carry the pathogenic mutation, known as the level of heteroplasmy, is an important determinant of the clinical presentation. As a severe manifestation of mitochondrial disease, LS is typically associated with high mutant loads of ≥90%, although *MTND5* mutations associated with complex I deficiency are notable for their propensity to cause LS even when the mutant load is <50% in tissues including brain, where patients have been observed to survive into adulthood.[52–54]

Mutations in complex I subunits MTND3 and MTND5, and in the complex V subunit MTATP6, are the most frequent mtDNA causes of LS. *MTATP6* mutations represent the only established genetic basis of complex V–mediated LS, and mutations in this gene are estimated to underlie ~10% of all LS cases.[2,6,7,55] The majority of these patients carry either the *MTATP6* m.8993T>G or the less severe m.8993T>C mutation, which were among the first LS mutations described.[56,57] Although uncommon, mutations in 5 mt-tRNAs have been identified in LS patients, including the well-known m.3243A>G *MTTL1* mutation that is more commonly associated with the syndromes of mitochondrial encephalopathy with lactic acidosis and strokelike episodes (MELAS) and maternally inherited diabetes and deafness, and the m.8344A>G in *MTTK* that typically causes myoclonic epilepsy with ragged red fibers.[58,59]

Although mtDNA is inherited maternally, many patients with mtDNA mutations lack any maternal family history suggesting mtDNA disease. This can be because the heteroplasmic mutant load in other family members is below the pathogenic threshold for that mutation. De novo mutations in mtDNA are also relatively common, so a mutation present at high levels of heteroplasmy in the proband can be undetectable in the mother and other maternal relatives.[60,61]

Pyruvate Dehydrogenase Complex Deficiency

Evidence of elevated pyruvate and a lactate:pyruvate ratio of < 20 can indicate PDHc deficiency in LS patients, with agenesis of the corpus callosum another common finding.[62] Mutations in *PDHA1*, encoding the E1 alpha subunit, are the predominant cause of PDHc-associated LS.[62,63] *PDHA1* is an X-chromosome gene, but approximately equal numbers of boys and girls are diagnosed with *PDHA1* mutations.[62] This pseudodominant inheritance is not surprising given that random X-inactivation means that typically ~50% of cells will express the mutant allele. Skewed X-inactivation means that the biochemical diagnosis of PDHc deficiency in females can be challenging.[64] Cohort studies of PDHc-deficient individuals support previous observations that *PDHA1* likely has a high de novo mutation rate.[62,63]

Mutations in genes related to the PDHc cofactors lipoic acid and thiamine pyrophosphate (TPP) have more recently been described to cause LS. The *LIPT1* and *LIAS* genes encode enzymes responsible for synthesis and transfer of the lipoic acid cofactor, and the *DLD* gene encodes the PDHc subunit E3 dihydrolipoamide dehydrogenase. Patients with PDHc deficiency due to mutations in these genes present with a recognizable metabolic profile that reflects additional deficiency of α-ketoglutarate dehydrogenase and branched-chain α-keto acid dehydrogenase.[65–67] PDHc deficiency due to

mutations in genes associated with TPP availability (*TPK1, SLC19A3*, and *SLC25A19*) can be missed because of the presence of TPP in routine PDHc enzymatic assays, but may be identifiable when measuring PDHc activity in the absence of TPP.[68,69] Mutations in the thiamine transporter *SLC19A3* are well known to cause biotin/thiamine-responsive basal ganglia disease (BTBGD; MIM 607483), which phenocopies LS as a progressive encephalopathy with similar neuroimaging and episodic decline.[70] Unlike typical LS, patients with BTBGD can show significant clinical and neuroradiological improvement following administration of thiamine and high-dose biotin, particularly when commenced early in the disease course.[71] Patients with *SLC19A3* mutations have been described as having "treatable" or "reversible" LS.[71,72]

Disease Genes Associated with Leigh-like Syndrome

A diagnosis of Leigh-like syndrome usually refers to patients presenting with atypical neuropathology or neuroradiology, but can also reflect an atypical clinical presentation or course.[2] Leigh-like presentations can display overlap with other mitochondrial encephalopathies, and many cases are caused by mutations in the same genes associated with LS. *MTND5* and *MTND3* mutations have been described to underlie a rare clinical presentation of an LS/MELAS overlap syndrome where patients simultaneously display neuroradiological and clinical characteristics of both syndromes,[73] and large-scale mtDNA deletions can cause Pearson syndrome with Leigh-like neuropathology.[74,75] Furthermore, Leigh-like patients with *POLG* mutations generally lie on a spectrum between Alpers–Huttenlocher syndrome (MIM 203700) and LS, where the neuropathology exhibits features characteristic of both syndromes and hepatic dysfunction is present.[76,77] Disease genes that predominantly underlie a Leigh-like presentation that may not fit a stringent LS diagnosis also include *SERAC1*, which causes 3-methylglutaconic aciduria with deafness, encephalopathy, and Leigh-like syndrome associated with isolated or combined OXPHOS enzyme deficiency.[78] These patients often present with atypical neuroradiology, or with unusual additional symptoms including abnormal behavior.[79]

The Emergence of Genotype–Phenotype Relationships

Historically, strong correlations between a molecular defect and clinical features could not be identified among LS patients,[2] in part reflecting the low numbers of patients for most disease genes. However, the increasing utilization of MPS technology has facilitated the identification of multiple LS patients with mutations in the same gene, enabling the recognition of emerging genotype–phenotype correlations (see Table 3 for examples). The presence of these signature features in combination with a biochemical deficiency and knowledge of the patient's ethnicity may suggest a specific genetic basis. Beyond having characteristic symptoms, different LS disease genes can underlie distinct disease courses, where differences in median age of onset, and length of disease course, can be observed (illustrated in Fig 3). For example, *NDUFS4* mutations appear to be associated with early onset and death, whereas patients with mutations in *SUCLA2* or the complex IV assembly factor PET100 experience early onset but a more variable lifespan including survival into adolescence.

The accumulation of additional patients with an established genetic basis of disease and thorough phenotyping may reveal more LS genotype–phenotype correlations. More research is required to determine the molecular basis of such relationships, although they may be expected to in part reflect tissue-specific effects relating to expression levels, function, and/or responses to the genetic defect. Being able to recognize the genetic or biochemical basis of disease has important utility for guiding treatment options, and in some cases can enable life-saving intervention for the genetic forms that are most responsive to treatment such as *SLC19A3* or *BTD* mutations (outlined in Table 2).

Established Molecular Defects Indicate a Common Disorder of Energy Generation

Our current understanding of the genetic basis of LS supports impairment in mitochondrial energy generation being the key to pathogenesis. However, it appears that the specific enzyme or process that is disrupted is not as relevant to molecular pathogenesis, given the remarkably diverse range of molecular defects causing LS. These include defects of catalytic activity, stability, or assembly of individual OXPHOS complexes, of mtDNA maintenance and expression, and of PDHc activity and cofactors required for enzyme activity (see Table 1, and Supplementary Table, A for more detailed information).

The identification of several disease genes that are not known to encode proteins with a direct role in OXPHOS or PDHc activity raises new questions about the pathogenesis of LS (see Table 1, and Supplementary Table, B for more detailed information). Some of these defects appear to cause secondary defects of PDHc or OXPHOS enzymes, which may show variability across patients and tissues.[78,80–82] Such secondary defects have not been reported in patients with biotinidase deficiency due to *BTD* mutations, a treatable condition that can

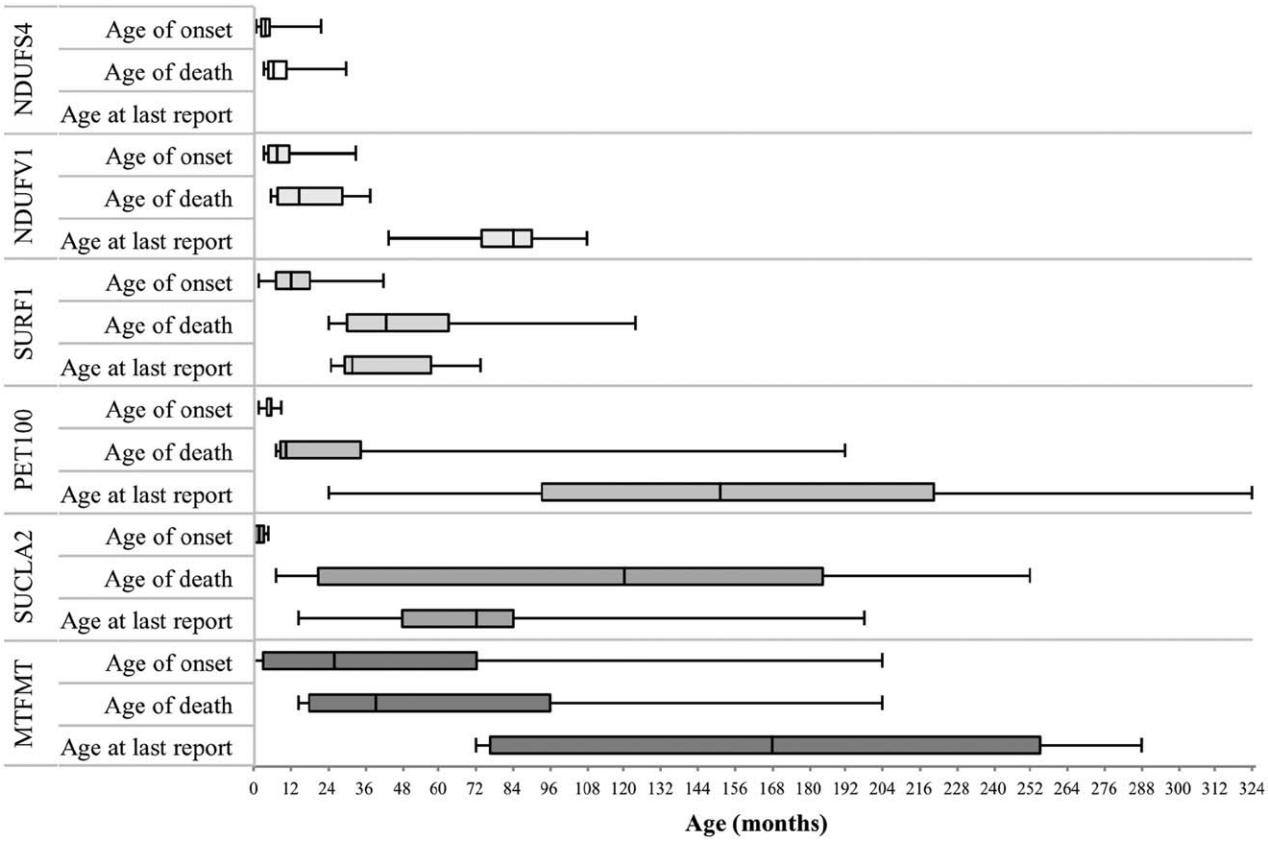

FIGURE 3: Genotype–phenotype correlations with respect to disease course. Box and whisker plot representation of the ages of onset, death, or last report for patients with mutations in *NDUFS4*, *NDUFV1* (complex I deficiency), *SURF1*, *PET100* (complex IV deficiency), *SUCLA2*, and *MTFMT* (combined oxidative phosphorylation deficiency) as reported in the literature. Genotype–phenotype differences in disease course can be observed between the genetic and biochemical forms of disease. Data points are represented as error bars depicting minimum and maximum, the box edges depicting the 1st and 3rd quartiles, with the line within the box representing the median. Number of patients for whom information was available: *NDUFS4*, 21; *NDUFV1*, 12; *SURF1*, 21; *PET100*, 10; *SUCLA2*, 31; *MTFMT*, 12.

manifest as LS (see Table 2),[83,84] although there is evidence of ATP deficiency and complex IV inhibition from animal and cellular models.[85,86]

Mutations in the phospholipid remodeling protein SERAC1 and apoptosis-inducing factor AIFM1 may impair OXPHOS by reducing the stability of the mitochondrial membrane.[78,82] However, the mechanism by which mutations in enzymes involved in valine catabolism (ECHS1, HIBCH) and biotin recycling (BTD) impair OXPHOS and PDHc activity remains to be determined. These enzymes facilitate pathways that can produce substrates for the citric acid cycle,[81,87] an important source of electrons for OXPHOS. However, the relevance of this to pathogenesis is unclear, as is the contribution of primary effects of these disorders such as perturbed valine catabolism.[80,81] Instead, an accumulation of toxic reactive metabolites has been suggested to be the mechanism by which *ECHS1* and *HIBCH* mutations impair OXPHOS and PDHc activity,[81,88] similar to the toxic accumulation of sulfide due to *ETHE1* mutations described above.[43] Although it may not be the primary consequence of mutation, an indirect effect on mitochondrial energy generation can therefore be sufficient to cause the development of LS.

Our understanding of cerebral energy metabolism further supports the central role of a diminished energy supply to the pathogenesis of LS. Brain metabolism accounts for ~20 to 25% of resting energy expenditure in adults.[89] The metabolic requirements of the brain increase during infancy and peak in early childhood, where it uses glucose at a rate of up to 66% of the body's resting metabolism.[90] Therefore, it is not surprising that defects in OXPHOS and energy generation can cause early onset neurodegeneration in the form of LS. Studies indicating that the brain's metabolic requirements are highest at ~5 years of age[90] are relevant to observations suggesting that survival past periods of increased vulnerability in infancy and early childhood may predict a lifespan into and beyond late childhood for patients with LS. This is supported by the cohort study of *LRPPRC*

patients, where no metabolic crises were observed in patients after the age of 7 years,[37] and suggested by the notably later median age at last report relative to the median age of death observed across patients with either *PET100, NDUFV1*, or *MTFMT* mutations in Figure 3.

The particular vulnerability of the basal ganglia and brainstem structures to neurodegeneration in LS patients is unexplained. Positron emission tomography studies examining the cerebral metabolic rate for glucose in infants and children suggested that the brainstem and basal ganglia/thalamus do not necessarily have the highest energy requirement of all examined brain structures in conditions of basal metabolism.[91] Furthermore, the capacity for patients with inherited mitochondrial energy generation disorders to develop neuropathological abnormalities distinct from LS, including in infancy and early childhood,[92] suggests that other factors beyond a reduced energy supply must contribute to pathogenesis. Previous studies demonstrating differences in mitochondrial protein expression across mouse tissues, including between different brain regions,[93] imply that cell- and tissue-specific responses to a molecular defect of mitochondrial energy generation will also contribute to pathogenesis. This is supported by transcriptomic studies of cells and tissues from mitochondrial disease patients demonstrating tissue-specific patterns of transcriptional dysregulation.[94]

Updating Diagnostic Strategies to Incorporate New Knowledge of Molecular Etiologies

Detailed approaches to diagnosis of LS have been published elsewhere.[19,55] The initial steps remain a detailed medical and family history, physical examination including determining extent of multiorgan involvement, measurement of laboratory parameters such as lactic acid in blood and CSF, and imaging (MRI and magnetic resonance spectroscopy).[19] In patients such as those described in Table 3, the phenotype may prompt investigation of a specific gene, such as *SURF1* in a child with hypertrichosis and relative cognitive sparing.[35] However, in most patients the next step has traditionally been to measure OXPHOS and PDHc enzyme activities in a muscle biopsy and cultured skin fibroblasts, respectively, the results of which can guide subsequent gene-by-gene analysis. Although enzyme testing may often still be required for diagnosis, the diagnostic paradigm is increasingly shifting to using MPS first, to potentially avoid the need for muscle biopsy. Testing gene panels of perhaps a few hundred genes is a popular approach, although the rate of discovery of novel disease genes means that such panels can become outdated quite quickly. Whole exome sequencing can potentially detect mutations in any nuclear gene but typically is not a sensitive test for mtDNA mutations, so it may need to be accompanied by a separate test for mtDNA mutations. Whole genome sequencing can detect mutations in nuclear and mtDNA genes, but is less widely available than exome sequencing. Each of these approaches has specific advantages and disadvantages,[95,96] but in our experience they can enable molecular diagnosis of LS in >60% of patients with a stringent LS diagnosis, as defined by the original criteria of Rahman et al.[2]

Insights into Broader Cellular Dysfunction: An Emerging Area for Therapeutic Intervention

There is a growing body of evidence supporting the contribution of broader cellular dysfunction in disorders of mitochondrial energy generation. Recent studies have demonstrated that PDHc and OXPHOS defects can induce transcriptional dysregulation of multiple cellular pathways including those that regulate RNA and protein metabolism.[94] These disturbances in cellular metabolism appear to be primarily mediated by effects on pathways responsible for sensing and responding to nutrient availability, including effects on the expression and activity of regulator of cellular growth mTORC1.[94] Treatment with rapamycin, an inhibitor of mTORC1, improved lifespan and attenuated neurodegeneration in the *Ndufs4* knockout mouse model of LS,[97] supporting the notion that dysregulation of these pathways contributes to pathogenesis. More recently, improvement in mitochondrial cristae morphology was observed to modestly but significantly improve motor performance, lifespan, and complex I activity in *Ndufs4* knockout mice,[98] suggesting that effects on mitochondrial morphology may additionally contribute to disease pathology.

Molecular defects of PDHc and OXPHOS may furthermore impair normal cell function through mechanisms distinct from energy generation per se. PDHc and OXPHOS enzyme defects can produce a cellular environment more conducive for the production of reactive oxygen species (ROS). Increased ROS have been observed in cellular models of PDHc and OXPHOS enzyme deficiencies,[99,100] and there is evidence of increased oxidative damage to proteins in affected brain regions of the *Ndufs4* knockout mice.[101] However, these results have been inconsistent,[102,103] and increases in ROS production do not always correlate with neurodegeneration.[104] A possible alternative explanation could be that elevated ROS production is simply reflecting a highly reduced state of the respiratory chain. This typically leads to a partial block in NADH oxidation, with a concomitant decrease in the NAD^+/NADH ratio.[105] This redox

imbalance may lead to dysregulation of the signaling pathways related to nutrient sensing referred to earlier.[94,105] NAD metabolism varies in different brain regions[106] and could potentially contribute to different susceptibility of brainstem and basal ganglia in conditions such as LS. Drugs such as nicotinamide riboside that can boost NAD synthesis or poly(adenosine diphosphate ribose) polymerase inhibitors that can block NAD degradation are thus promising agents for treating mitochondrial diseases.[107,108]

Alleviation of oxidative stress has therefore emerged as a promising avenue of therapy for LS and other mitochondrial diseases, including the development of antioxidants EPI-743 and RP103, which are currently being examined in clinical trials.[109] Increased ROS are also implicated in the activation of inflammatory pathways that may in turn alter mitochondrial function and produce a state of chronic stress that further compromises cellular function.[110,111] The contribution of oxidative stress to disease pathogenesis may therefore be multifaceted.

Another relevant consequence of the molecular defects observed to cause LS is elevation of lactate.[2] Increased lactate levels reflect a greater utilization of glycolysis for energy generation, and may contribute to lesion development in LS patients, including through alterations of pH when lactic acidosis ensues.[16] An observed correlation between CSF lactate levels and disease severity in LS patients[6] supports the pathological significance of lactate. Interestingly, attenuation of lesion development and neurological decline in *Ndufs4* knockout mice following rapamycin treatment was suggested to in part reflect a reduction in toxic glycolytic metabolites within the brain.[97] Significantly, this study also demonstrated that neurological improvement and an increase in lifespan could be achieved independently of an effect on the primary defect in complex I assembly. This supports the role of broader cellular dysfunction in disease pathogenesis, and the validity of targeting these pathways therapeutically. Characterization of the precise molecular mechanisms driving disease pathology could therefore have great utility for the development of new therapies.

Conclusion

Like other mitochondrial diseases, there is currently no effective treatment for LS as a group.[112] However, there are several genetic and biochemical forms of LS that can benefit from therapeutic intervention, emphasizing the importance of determining the molecular basis of disease in LS patients. Furthermore, confirmation of the genetic basis of disease enables access to accurate genetic counseling and assisted reproductive technologies. MPS has transformed the approach for determining the genetic basis of LS, and therefore has the potential to markedly improve diagnostic and clinical outcomes for patients. Consolidating our understanding of the cellular mechanisms underlying disease pathology is important for enabling the development of novel therapeutics.

Acknowledgment

This work was supported by grants from the Australian National Health and Medical Research Council (NHMRC) (1068409 to D.R.T.), the Australian Mitochondrial Disease Foundation, an NHMRC Principal Research Fellowship (1022896 to D.R.T.), an Australian Postgraduate Award (N.J.L.), the Victorian Government's Operational Infrastructure Support Program, and Great Ormond Street Hospital Children's Charity (S.R.).

Author Contributions

All authors contributed to reviewing publications on the genetic, clinical, and pathological features of LS and on mechanisms of disease causation. All authors contributed to drafting and review of the manuscript.

Potential Conflicts of Interest

S.R.: grant support, Vitaflo International.

References

1. Skladal D, Halliday J, Thorburn DR. Minimum birth prevalence of mitochondrial respiratory chain disorders in children. Brain 2003; 126:1905–1912.
2. Rahman S, Blok RB, Dahl HH, et al. Leigh syndrome: clinical features and biochemical and DNA abnormalities. Ann Neurol 1996; 39:343–351.
3. Morin C, Mitchell G, Larochelle J, et al. Clinical, metabolic, and genetic aspects of cytochrome C oxidase deficiency in Saguenay-Lac-Saint-Jean. Am J Hum Genet 1993;53:488–496.
4. Ostergaard E, Hansen FJ, Sorensen N, et al. Mitochondrial encephalomyopathy with elevated methylmalonic acid is caused by SUCLA2 mutations. Brain 2007;130:853–861.
5. Hammans SR, Sweeney MG, Brockington M, et al. Mitochondrial encephalopathies: molecular genetic diagnosis from blood samples. Lancet 1991;337:1311–1313.
6. Sofou K, De Coo IF, Isohanni P, et al. A multicenter study on Leigh syndrome: disease course and predictors of survival. Orphanet J Rare Dis 2014;9:52.
7. Ma YY, Wu TF, Liu YP, et al. Genetic and biochemical findings in Chinese children with Leigh syndrome. J Clin Neurosci 2013;20: 1591–1594.
8. van Erven PM, Cillessen JP, Eekhoff EM, et al. Leigh syndrome, a mitochondrial encephalo(myo)pathy. A review of the literature. Clin Neurol Neurosurg 1987;89:217–230.
9. Lopez LC, Schuelke M, Quinzii CM, et al. Leigh syndrome with nephropathy and CoQ10 deficiency due to decaprenyl diphosphate synthase subunit 2 (PDSS2) mutations. Am J Hum Genet 2006;79:1125–1129.

10. Langes K, Frenzel H, Seitz R, et al. Cardiomyopathy associated with Leigh's disease. Virchows Arch A Pathol Anat Histopathol 1985;407:97–105.
11. Monlleo-Neila L, Toro MD, Bornstein B, et al. Leigh syndrome and the mitochondrial m.13513G>A mutation: expanding the clinical spectrum. J Child Neurol 2013;28:1531–1534.
12. Broide E, Elpeleg O, Lahat E. Type IV 3-methylglutaconic (3-MGC) aciduria: a new case presenting with hepatic dysfunction. Pediatr Neurol 1997;17:353–355.
13. Montpetit VJ, Andermann F, Carpenter S, et al. Subacute necrotizing encephalomyelopathy. A review and a study of two families. Brain 1971;94:1–30.
14. McKelvie P, Infeld B, Marotta R, et al. Late-adult onset Leigh syndrome. J Clin Neurosci 2012;19:195–202.
15. Cavanagh JB, Harding BN. Pathogenic factors underlying the lesions in Leigh's disease. Tissue responses to cellular energy deprivation and their clinico-pathological consequences. Brain 1994;117(pt 6):1357–1376.
16. Lake NJ, Bird MJ, Isohanni P, et al. Leigh syndrome: neuropathology and pathogenesis. J Neuropathol Exp Neurol 2015;74:482–492.
17. Arii J, Tanabe Y. Leigh syndrome: serial MR imaging and clinical follow-up. AJNR Am J Neuroradiol 2000;21:1502–1509.
18. Leigh D. Subacute necrotizing encephalomyelopathy in an infant. J Neurol Neurosurg Psychiatry 1951;14:216–221.
19. Baertling F, Rodenburg RJ, Schaper J, et al. A guide to diagnosis and treatment of Leigh syndrome. J Neurol Neurosurg Psychiatry 2014;85:257–265.
20. Worsley HE, Brookfield RW, Elwood JS, et al. Lactic acidosis with necrotizing encephalopathy in two sibs. Arch Dis Child 1965;40:492–501.
21. Farmer T, Veath L, Miller A, et al. Pyruvate decarboxylase deficiency in a patient with subacute necrotizing encephalomyelopathy. Neurology 1973;23:429.
22. Willems JL, Monnens LA, Trijbels JM, et al. Leigh's encephalomyelopathy in a patient with cytochrome c oxidase deficiency in muscle tissue. Pediatrics 1977;60:850–857.
23. Van Erven PM, Gabreels FJ, Ruitenbeek W, et al. Subacute necrotizing encephalomyelopathy (Leigh syndrome) associated with disturbed oxidation of pyruvate, malate and 2-oxoglutarate in muscle and liver. Acta Neurol Scand 1985;72:36–42.
24. Fassone E, Rahman S. Complex I deficiency: clinical features, biochemistry and molecular genetics. J Med Genet 2012;49:578–590.
25. Assouline Z, Jambou M, Rio M, et al. A constant and similar assembly defect of mitochondrial respiratory chain complex I allows rapid identification of NDUFS4 mutations in patients with Leigh syndrome. Biochim Biophys Acta 2012;1822:1062–1069.
26. Marin SE, Mesterman R, Robinson B, et al. Leigh syndrome associated with mitochondrial complex I deficiency due to novel mutations in NDUFV1 and NDUFS2. Gene 2013;516:162–167.
27. Laugel V, This-Bernd V, Cormier-Daire V, et al. Early-onset ophthalmoplegia in Leigh-like syndrome due to NDUFV1 mutations. Pediatr Neurol 2007;36:54–57.
28. Ma YY, Wu TF, Liu YP, et al. Two compound frame-shift mutations in succinate dehydrogenase gene of a Chinese boy with encephalopathy. Brain Dev 2014;36:394–398.
29. Bourgeron T, Rustin P, Chretien D, et al. Mutation of a nuclear succinate dehydrogenase gene results in mitochondrial respiratory chain deficiency. Nat Genet 1995;11:144–149.
30. Pagnamenta AT, Hargreaves IP, Duncan AJ, et al. Phenotypic variability of mitochondrial disease caused by a nuclear mutation in complex II. Mol Genet Metab 2006;89:214–221.
31. Koch J, Freisinger P, Feichtinger RG, et al. Mutations in TTC19: expanding the molecular, clinical and biochemical phenotype. Orphanet J Rare Dis 2015;10:40.
32. Van Maldergem L, Trijbels F, DiMauro S, et al. Coenzyme Q-responsive Leigh's encephalopathy in two sisters. Ann Neurol 2002;52:750–754.
33. Rahman S, Clarke CF, Hirano M. 176th ENMC International Workshop: diagnosis and treatment of coenzyme Q_{10} deficiency. Neuromuscul Disord 2012;22:76–86.
34. Leshinsky-Silver E, Levine A, Nissenkorn A, et al. Neonatal liver failure and Leigh syndrome possibly due to CoQ-responsive OXPHOS deficiency. Mol Genet Metab 2003;79:288–293.
35. Wedatilake Y, Brown R, McFarland R, et al. SURF1 deficiency: a multi-centre natural history study. Orphanet J Rare Dis 2013;8:96.
36. Rahman S, Brown RM, Chong WK, et al. A SURF1 gene mutation presenting as isolated leukodystrophy. Ann Neurol 2001;49:797–800.
37. Debray FG, Morin C, Janvier A, et al. LRPPRC mutations cause a phenotypically distinct form of Leigh syndrome with cytochrome c oxidase deficiency. J Med Genet 2011;48:183–189.
38. Mineri R, Rimoldi M, Burlina AB, et al. Identification of new mutations in the ETHE1 gene in a cohort of 14 patients presenting with ethylmalonic encephalopathy. J Med Genet 2008;45:473–478.
39. Pronicka E, Piekutowska-Abramczuk D, Szymanska-Debinska T, et al. The natural history of SCO2 deficiency in 36 Polish children confirmed the genotype-phenotype correlation. Mitochondrion 2013;13:810–816.
40. Mootha VK, Lepage P, Miller K, et al. Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics. Proc Natl Acad Sci U S A 2003;100:605–610.
41. Mourier A, Ruzzenente B, Brandt T, et al. Loss of LRPPRC causes ATP synthase deficiency. Hum Mol Genet 2014;23:2580–2592.
42. Garcia-Silva MT, Ribes A, Campos Y, et al. Syndrome of encephalopathy, petechiae, and ethylmalonic aciduria. Pediatr Neurol 1997;17:165–170.
43. Tiranti V, Viscomi C, Hildebrandt T, et al. Loss of ETHE1, a mitochondrial dioxygenase, causes fatal sulfide toxicity in ethylmalonic encephalopathy. Nat Med 2009;15:200–205.
44. Viscomi C, Burlina AB, Dweikat I, et al. Combined treatment with oral metronidazole and N-acetylcysteine is effective in ethylmalonic encephalopathy. Nat Med 2010;16:869–871.
45. Pitceathly RD, Rahman S, Wedatilake Y, et al. NDUFA4 mutations underlie dysfunction of a cytochrome c oxidase subunit linked to human neurological disease. Cell Rep 2013;3:1795–1805.
46. Elpeleg O, Miller C, Hershkovitz E, et al. Deficiency of the ADP-forming succinyl-CoA synthase activity is associated with encephalomyopathy and mitochondrial DNA depletion. Am J Hum Genet 2005;76:1081–1086.
47. Van Hove JL, Saenz MS, Thomas JA, et al. Succinyl-CoA ligase deficiency: a mitochondrial hepatoencephalomyopathy. Pediatr Res 2010;68:159–164.
48. Navarro-Sastre A, Tort F, Garcia-Villoria J, et al. Mitochondrial DNA depletion syndrome: new descriptions and the use of citrate synthase as a helpful tool to better characterise the patients. Mol Genet Metab 2012;107:409–415.
49. Valayannopoulos V, Haudry C, Serre V, et al. New SUCLG1 patients expanding the phenotypic spectrum of this rare cause of mild methylmalonic aciduria. Mitochondrion 2010;10:335–341.
50. Tucker EJ, Hershman SG, Kohrer C, et al. Mutations in MTFMT underlie a human disorder of formylation causing impaired mitochondrial translation. Cell Metab 2011;14:428–434.
51. Haack TB, Gorza M, Danhauser K, et al. Phenotypic spectrum of eleven patients and five novel MTFMT mutations identified by

exome sequencing and candidate gene screening. Mol Genet Metab 2014;111:342–352.

52. Taylor RW, Morris AA, Hutchinson M, et al. Leigh disease associated with a novel mitochondrial DNA ND5 mutation. Eur J Hum Genet 2002;10:141–144.
53. Kirby DM, Boneh A, Chow CW, et al. Low mutant load of mitochondrial DNA G13513A mutation can cause Leigh's disease. Ann Neurol 2003;54:473–478.
54. Ruiter EM, Siers MH, van den Elzen C, et al. The mitochondrial 13513G>A mutation is most frequent in Leigh syndrome combined with reduced complex I activity, optic atrophy and/or Wolff-Parkinson-White. Eur J Hum Genet 2007;15:155–161.
55. Thorburn DR, Rahman S. Mitochondrial DNA-associated Leigh syndrome and NARP. In: Pagon RA, Adam MP, Ardinger HH, et al, eds. GeneReviews. Seattle, WA: University of Washington, 1993.
56. Tatuch Y, Christodoulou J, Feigenbaum A, et al. Heteroplasmic mtDNA mutation (T----G) at 8993 can cause Leigh disease when the percentage of abnormal mtDNA is high. Am J Hum Genet 1992;50:852–858.
57. de Vries DD, van Engelen BG, Gabreels FJ, et al. A second missense mutation in the mitochondrial ATPase 6 gene in Leigh's syndrome. Ann Neurol 1993;34:410–412.
58. Koga Y, Koga A, Iwanaga R, et al. Single-fiber analysis of mitochondrial A3243G mutation in four different phenotypes. Acta Neuropathol 2000;99:186–190.
59. Hammans SR, Sweeney MG, Brockington M, et al. The mitochondrial DNA transfer RNA(Lys)A-->G(8344) mutation and the syndrome of myoclonic epilepsy with ragged red fibres (MERRF). Relationship of clinical phenotype to proportion of mutant mitochondrial DNA. Brain 1993;116(pt 3):617–632.
60. Tulinius MH, Houshmand M, Larsson NG, et al. De novo mutation in the mitochondrial ATP synthase subunit 6 gene (T8993G) with rapid segregation resulting in Leigh syndrome in the offspring. Hum Genet 1995;96:290–294.
61. White SL, Shanske S, McGill JJ, et al. Mitochondrial DNA mutations at nucleotide 8993 show a lack of tissue- or age-related variation. J Inherit Metab Dis 1999;22:899–914.
62. Patel KP, O'Brien TW, Subramony SH, et al. The spectrum of pyruvate dehydrogenase complex deficiency: clinical, biochemical and genetic features in 371 patients. Mol Genet Metab 2012;106:385–394.
63. DeBrosse SD, Okajima K, Zhang S, et al. Spectrum of neurological and survival outcomes in pyruvate dehydrogenase complex (PDC) deficiency: lack of correlation with genotype. Mol Genet Metab 2012;107:394–402.
64. Willemsen M, Rodenburg RJ, Teszas A, et al. Females with PDHA1 gene mutations: a diagnostic challenge. Mitochondrion 2006;6:155–159.
65. Soreze Y, Boutron A, Habarou F, et al. Mutations in human lipoyltransferase gene LIPT1 cause a Leigh disease with secondary deficiency for pyruvate and alpha-ketoglutarate dehydrogenase. Orphanet J Rare Dis 2013;8:192.
66. Quinonez SC, Leber SM, Martin DM, et al. Leigh syndrome in a girl with a novel DLD mutation causing E3 deficiency. Pediatr Neurol 2013;48:67–72.
67. Baker PR Jr, Friederich MW, Swanson MA, et al. Variant non ketotic hyperglycinemia is caused by mutations in LIAS, BOLA3 and the novel gene GLRX5. Brain 2014;137:366–379.
68. Gerards M, Kamps R, van Oevelen J, et al. Exome sequencing reveals a novel Moroccan founder mutation in SLC19A3 as a new cause of early-childhood fatal Leigh syndrome. Brain 2013;136:882–890.
69. Mayr JA, Freisinger P, Schlachter K, et al. Thiamine pyrophosphokinase deficiency in encephalopathic children with defects in the pyruvate oxidation pathway. Am J Hum Genet 2011;89:806–812.
70. Zeng WQ, Al-Yamani E, Acierno JS Jr, et al. Biotin-responsive basal ganglia disease maps to 2q36.3 and is due to mutations in SLC19A3. Am J Hum Genet 2005;77:16–26.
71. Ortigoza-Escobar JD, Serrano M, Molero M, et al. Thiamine transporter-2 deficiency: outcome and treatment monitoring. Orphanet J Rare Dis 2014;9:92.
72. Fassone E, Wedatilake Y, DeVile CJ, et al. Treatable Leigh-like encephalopathy presenting in adolescence. BMJ Case Rep 2013;2013:200838.
73. Wang Z, Qi XK, Yao S, et al. Phenotypic patterns of MELAS/LS overlap syndrome associated with m.13513G>A mutation, and neuropathological findings in one autopsy case. Neuropathology 2010;30:606–614.
74. Santorelli FM, Barmada MA, Pons R, et al. Leigh-type neuropathology in Pearson syndrome associated with impaired ATP production and a novel mtDNA deletion. Neurology 1996;47:1320–1323.
75. Yamadori I, Kurose A, Kobayashi S, et al. Brain lesions of the Leigh-type distribution associated with a mitochondriopathy of Pearson's syndrome: light and electron microscopic study. Acta Neuropathol 1992;84:337–341.
76. Scalais E, Francois B, Schlesser P, et al. Polymerase gamma deficiency (POLG): clinical course in a child with a two stage evolution from infantile myocerebrohepatopathy spectrum to an Alpers syndrome and neuropathological findings of Leigh's encephalopathy. Eur J Paediatr Neurol 2012;16:542–548.
77. Taanman JW, Rahman S, Pagnamenta AT, et al. Analysis of mutant DNA polymerase gamma in patients with mitochondrial DNA depletion. Hum Mutat 2009;30:248–254.
78. Wortmann SB, Vaz FM, Gardeitchik T, et al. Mutations in the phospholipid remodeling gene SERAC1 impair mitochondrial function and intracellular cholesterol trafficking and cause dystonia and deafness. Nat Genet 2012;44:797–802.
79. Wortmann S, Rodenburg RJ, Huizing M, et al. Association of 3-methylglutaconic aciduria with sensori-neural deafness, encephalopathy, and Leigh-like syndrome (MEGDEL association) in four patients with a disorder of the oxidative phosphorylation. Mol Genet Metab 2006;88:47–52.
80. Loupatty FJ, Clayton PT, Ruiter JP, et al. Mutations in the gene encoding 3-hydroxyisobutyryl-CoA hydrolase results in progressive infantile neurodegeneration. Am J Hum Genet 2007;80:195–199.
81. Peters H, Buck N, Wanders R, et al. ECHS1 mutations in Leigh disease: a new inborn error of metabolism affecting valine metabolism. Brain 2014;137(pt 11):2903–2908.
82. Ghezzi D, Sevrioukova I, Invernizzi F, et al. Severe X-linked mitochondrial encephalomyopathy associated with a mutation in apoptosis-inducing factor. Am J Hum Genet 2010;86:639–649.
83. Baumgartner ER, Suormala TM, Wick H, et al. Biotinidase deficiency: a cause of subacute necrotizing encephalomyelopathy (Leigh syndrome). Report of a case with lethal outcome. Pediatr Res 1989;26:260–266.
84. Mitchell G, Ogier H, Munnich A, et al. Neurological deterioration and lactic acidemia in biotinidase deficiency. A treatable condition mimicking Leigh's disease. Neuropediatrics 1986;17:129–131.
85. Hernandez-Vazquez A, Wolf B, Pindolia K, et al. Biotinidase knockout mice show cellular energy deficit and altered carbon metabolism gene expression similar to that of nutritional biotin deprivation: clues for the pathogenesis in the human inherited disorder. Mol Genet Metab 2013;110:248–254.
86. Atamna H, Newberry J, Erlitzki R, et al. Biotin deficiency inhibits heme synthesis and impairs mitochondria in human lung fibroblasts. J Nutr 2007;137:25–30.

87. Depeint F, Bruce WR, Shangari N, et al. Mitochondrial function and toxicity: role of the B vitamin family on mitochondrial energy metabolism. Chem Biol Interact 2006;163:94–112.

88. Ferdinandusse S, Waterham HR, Heales SJ, et al. HIBCH mutations can cause Leigh-like disease with combined deficiency of multiple mitochondrial respiratory chain enzymes and pyruvate dehydrogenase. Orphanet J Rare Dis 2013;8:188.

89. Leonard WR, Robertson ML, Snodgrass JJ, et al. Metabolic correlates of hominid brain evolution. Comp Biochem Physiol A Mol Integr Physiol 2003;136:5–15.

90. Kuzawa CW, Chugani HT, Grossman LI, et al. Metabolic costs and evolutionary implications of human brain development. Proc Natl Acad Sci U S A 2014;111:13010–13015.

91. Chugani HT, Phelps ME, Mazziotta JC. Positron emission tomography study of human brain functional development. Ann Neurol 1987;22:487–497.

92. Filosto M, Tomelleri G, Tonin P, et al. Neuropathology of mitochondrial diseases. Biosci Rep 2007;27:23–30.

93. Pagliarini DJ, Calvo SE, Chang B, et al. A mitochondrial protein compendium elucidates complex I disease biology. Cell 2008;134: 112–123.

94. Zhang Z, Tsukikawa M, Peng M, et al. Primary respiratory chain disease causes tissue-specific dysregulation of the global transcriptome and nutrient-sensing signaling network. PloS One 2013; 8:e69282.

95. Carroll CJ, Brilhante V, Suomalainen A. Next-generation sequencing for mitochondrial disorders. Br J Pharmacol 2014;171:1837–1853.

96. Wortmann SB, Koolen DA, Smeitink JA, et al. Whole exome sequencing of suspected mitochondrial patients in clinical practice. J Inherit Metab Dis 2015;38:437–443.

97. Johnson SC, Yanos ME, Kayser EB, et al. mTOR inhibition alleviates mitochondrial disease in a mouse model of Leigh syndrome. Science 2013;342:1524–1528.

98. Civiletto G, Varanita T, Cerutti R, et al. Opa1 overexpression ameliorates the phenotype of two mitochondrial disease mouse models. Cell Metab 2015;21:845–854.

99. Glushakova LG, Judge S, Cruz A, et al. Increased superoxide accumulation in pyruvate dehydrogenase complex deficient fibroblasts. Mol Genet Metab 2011;104:255–260.

100. Distelmaier F, Koopman WJ, van den Heuvel LP, et al. Mitochondrial complex I deficiency: from organelle dysfunction to clinical disease. Brain 2009;132:833–842.

101. Quintana A, Kruse SE, Kapur RP, et al. Complex I deficiency due to loss of Ndufs4 in the brain results in progressive encephalopathy resembling Leigh syndrome. Proc Natl Acad Sci U S A 2010;107:10996–11001.

102. Choi WS, Palmiter RD, Xia Z. Loss of mitochondrial complex I activity potentiates dopamine neuron death induced by microtubule dysfunction in a Parkinson's disease model. J Cell Biol 2011;192:873–882.

103. Bird MJ, Wijeyeratne XW, Komen JC, et al. Neuronal and astrocyte dysfunction diverges from embryonic fibroblasts in the Ndufs4fky/fky mouse. Biosci Rep 2014;34:e00151.

104. Lin AL, Pulliam DA, Deepa SS, et al. Decreased in vitro mitochondrial function is associated with enhanced brain metabolism, blood flow, and memory in Surf1-deficient mice. J Cereb Blood Flow Metab 2013;33:1605–1611.

105. Lightowlers RN, Chrzanowska-Lightowlers ZM. Salvaging hope: is increasing NAD(+) a key to treating mitochondrial myopathy? EMBO Mol Med 2014;6:705–707.

106. Braidy N, Poljak A, Grant R, et al. Mapping NAD(+) metabolism in the brain of ageing Wistar rats: potential targets for influencing brain senescence. Biogerontology 2014;15:177–198.

107. Cerutti R, Pirinen E, Lamperti C, et al. NAD(+)-dependent activation of Sirt1 corrects the phenotype in a mouse model of mitochondrial disease. Cell Metab 2014;19:1042–1049.

108. Khan NA, Auranen M, Paetau I, et al. Effective treatment of mitochondrial myopathy by nicotinamide riboside, a vitamin B3. EMBO Mol Med 2014;6:721–731.

109. Rahman S. Emerging aspects of treatment in mitochondrial disorders. J Inherit Metab Dis 2015;38:641–653.

110. Lopez-Armada MJ, Riveiro-Naveira RR, Vaamonde-Garcia C, et al. Mitochondrial dysfunction and the inflammatory response. Mitochondrion 2013;13:106–118.

111. Olsen RK, Cornelius N, Gregersen N. Redox signalling and mitochondrial stress responses; lessons from inborn errors of metabolism. J Inherit Metab Dis 2015;38:703–719.

112. Pfeffer G, Majamaa K, Turnbull DM, et al. Treatment for mitochondrial disorders. Cochrane Database Syst Rev 2012;4: CD004426.

113. Niezgoda J, Morgan PG. Anesthetic considerations in patients with mitochondrial defects. Paediatr Anaesth 2013;23:785–793.

114. Lim SC, Smith KR, Stroud DA, et al. A founder mutation in PET100 causes isolated complex IV deficiency in Lebanese individuals with Leigh syndrome. Am J Hum Genet 2014;94:209–222.

115. Carrozzo R, Dionisi-Vici C, Steuerwald U, et al. SUCLA2 mutations are associated with mild methylmalonic aciduria, Leigh-like encephalomyopathy, dystonia and deafness. Brain 2007;130:862–874.

116. Ivanov IS, Azmanov DN, Ivanova MB, et al. Founder p.Arg 446* mutation in the PDHX gene explains over half of cases with congenital lactic acidosis in Roma children. Mol Genet Metab 2014; 113:76–83.