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New mitochondrial disorders

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A H V Schapira

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It is now clear that mitochondria serve two fundamental biological roles: the provision of ATP by aerobic respiration, and the mediation of cell death by apoptosis. Production of ATP is achieved primarily by oxidative phosphorylation and also through the tricarboxylic acid cycle and β -oxidation of fatty acids. The oxidative phosphorylation system comprises the respiratory chain and ATP synthase and consists of five multisubunit proteins, termed complexes I to V (table 1), embedded in the inner mitochondrial membrane. Electrons are passed down the chain and protons are pumped from the matrix side to the space between the inner and outer mitochondrial membranes. This creates an electrochemical gradient (membrane potential) which is used to drive ATP production via ATPase (complex V). The operation of the mitochondrial respiratory chain and oxidative phosphorylation (MITOX) system is responsible for the production of more than 95% of a cell's superoxide ions.

Mitochondria contain their own DNA, which is present in multiple copies. Human mitochondrial DNA (mtDNA) is a circular double stranded molecule 16 493 bases long encoding two ribosomal RNAs (rRNA), 22 transfer RNAs (tRNA), and 13 proteins. These proteins are all part of the oxidative phosphorylation system. MtDNA remains dependent on the nucleus for the proteins that undertake and regulate its transcription, translation, replication, and repair. Indeed the nucleus encodes more than 98% of mitochondrial proteins, including 70 of the 83 proteins of complexes I to V.

The MtDNA encoded proteins are translated on mitochondrial ribosomes and incorporated directly into complexes I, III, IV, and V on the inner membrane. By contrast, nuclear encoded proteins

are translated on cytosolic ribosomes and must be imported into the mitochondrion. This import system is highly complex and includes, for most proteins, a targeting sequence at the N-terminus that interacts with membrane receptors before being cleaved.¹ The protein is transported through the membrane and then folded and sorted to its correct intramitochondrial location.

There is now ample evidence that mitochondria play an important part in determining apoptotic cell death.² Apoptosis is important in embryological development, immune cell regulation, and several other physiological functions. Numerous factors may induce apoptosis, many of which seem to act through mitochondria by opening of the megapore thereby decreasing the electrochemical gradient (permeability transition) and releasing apoptosis initiating factors. The megapore is located at inner/outer membrane junctions and comprises several components including the peripheral benzodiazepine receptor, voltage dependent anion channel, and cyclophilin D. The pore is opened by proapoptotic molecules such as Bax and Bak, and by free radicals and respiratory chain defects, and is closed by antiapoptotic agents—for example, Bcl_x and cyclosporine. The voltage dependent anion channel seems to play an important part in mediating the modulatory effects of Bcl₂ proteins. Bax and Bak bind to the voltage dependent anion channel and accelerate opening of its channel, thereby allowing the release of cytochrome c. Bcl_x binds to and closes the voltage dependent anion channel, preventing cytochrome c release.³ Cytochrome c is an integral part of the respiratory chain and is released from the mitochondrial intermembranous space during the preapoptotic phase. Cytochrome c binds to Apaf-1 and activates

procaspase 9 to initiate the caspase cascade, which in turn induces the changes that constitute the final events in apoptosis. The critical role of mitochondria in the pathway to apoptotic cell death adds an additional dimension to the possible mechanisms that may be involved in the pathogenesis of mitochondrial diseases.

Numerous disorders have now been described in which mutations of mtDNA, or nuclear genes encoding respiratory chain subunits, have been identified. These have been the subject of several recent reports and reviews⁴⁻¹¹ and will not be discussed further. This review focuses on a separate group of "new" mitochondrial diseases in which defective oxidative phosphorylation is due to mutations of *nuclear genes* that encode *non-respiratory chain proteins* that are involved in mitochondrial biogenesis and, directly or indirectly, cause defective mitochondrial energy metabolism and neurological disease.

DEFECTS OF MITOCHONDRIAL DNA BIOGENESIS

Multiple deletions of mtDNA

Several families have been described with autosomal dominant or recessive inheritance of mitochondrial myopathy. The families with the dominantly inherited disorder usually have chronic progressive external ophthalmoplegia and proximal limb myopathy with ragged red fibres on biopsy, deficiency of oxidative phosphorylation on biochemical analysis, and multiple mtDNA deletions on Southern blotting. These mtDNA mutations are secondary to a nuclear gene defect and contrast with the single deletions that characterise primary mitochondrial diseases such as the Kearns-Sayre syndrome.

Abbreviations: MITOX, mitochondrial oxidative phosphorylation system; mtDNA, mitochondrial DNA; rRNA, ribosomal RNA; tRNA, transfer RNA; ANT-1, gene for the heart/skeletal muscle isoform of the adenine nucleotide translocator; MNGIE, mitochondrial neurogastrointestinal encephalomyopathy; GAA, guanine-adenine-adenine; YFH1, yeast frataxin homologue 1; CAG, cytosine-adenine-guanine; SOD-1, superoxide dismutase 1; OH⁸dG, 8-hydroxy-2-deoxyguanosine, ³¹P-MRS, ³¹phosphorus magnetic resonance spectroscopy

Table 1 The respiratory chain and oxidative phosphorylation system

Complex	Enzyme activity	No of subunits	MtDNA encoded subunits
Complex I	NADH ubiquinone reductase	41	7
Complex II	Succinate ubiquinone reductase	4	—
Complex III	Ubiquinol cytochrome c reductase	11	1
Complex IV	Cytochrome c oxidase	13	3
Complex V	ATP synthase	14	2

There are at least three chromosomal loci for the autosomal dominant disorder (chromosomes 4, 10, and other(s)).¹²⁻¹⁴ A mutation on chromosome 3 was subsequently excluded on re-evaluation of the data available.¹⁵ The mutation on chromosome 4 lies within the gene for the heart/skeletal muscle isoform of the adenine nucleotide translocator (ANT-1), responsible for the exchange of ADP and ATP across the inner mitochondrial membrane.¹⁵ One type of autosomal recessive mitochondrial disease with multiple mtDNA deletions—mitochondrial neurogastrointestinal encephalomyopathy (MNGIE)—has recently been linked to chromosome 22¹⁶ and found to be caused by a mutation of the thymidine phosphorylase gene.¹⁷ Patients with MNGIE typically present with chronic progressive external ophthalmoplegia, sensorimotor peripheral neuropathy, recurrent nausea, vomiting, and diarrhoea. A leukodystrophy may be seen on MRI. Thymidine phosphorylase activity is severely decreased and blood thymidine concentrations are high.

Depletion of mtDNA

Many patients with depletion of mtDNA present in the first few days or weeks of life with hypotonia and lactic acidosis or progressive hepatorenal failure.^{18, 19} Most die before the age of 12 months, although occasional less severely affected infants have been reported. In affected tissues, the concentrations of mtDNA are usually less than 30% but can be as low as less than 1% of age matched normal subjects. In some cases, the depletion is expressed in culture,^{20, 21} the mtDNA depleted cells being capable of growing and dividing in specially supplemented medium. Genomic transplantation studies have shown that the mtDNA remaining in these patients' cells can be restored to normal by replacement of the nucleus with the nucleus from a normal cell, indicating that mtDNA depletion in these patients is caused by a nuclear gene defect.

DISEASES DUE TO NUCLEAR GENE MUTATIONS IN NON-MITOX MITOCHONDRIAL PROTEINS

Friedreich's ataxia

Friedreich's ataxia is an autosomal recessive disorder with an incidence of 1 in 30 000 to 50 000 live births. The disorder usually becomes evident in childhood or adolescence, with ataxia, skeletal deformities, hyporeflexia, pyramidal tract deficits, and a hypertrophic cardiomyopathy. Most patients become wheelchair bound 10 to 15 years after diagnosis and die 5 to 10 years later from progressive cardiac failure. In 98% of patients Friedreich's ataxia is caused by an expanded guanine-adenine-adenine

(GAA) repeat in intron 1 of the gene on chromosome 9 which encodes frataxin and results in an abnormality of RNA processing.²² Frataxin is a widely expressed 18 kDa protein of unknown function.²³ The frataxin gene has close homology to a yeast gene (now termed yeast frataxin homologue 1, YFH1) which when deleted results in defective energy metabolism, intramitochondrial iron accumulation, induction of the high affinity iron transport system, and low mtDNA concentrations.²⁴ Frataxin was subsequently found to have a mitochondrial targeting sequence and to be a mitochondrial protein.²⁵ Mitochondrial function studies have disclosed severe deficiencies in the activities of complexes I, II, and III, and aconitase in cardiac and skeletal muscle.^{26, 27} Furthermore, there is histological evidence for iron accumulation in these tissues. Thus, there is a striking parallel between the yeast knockout model and the human disease. Of particular interest is the demonstration in vivo in patients with Friedreich's ataxia of a defect of oxidative phosphorylation in skeletal muscle by ³¹P magnetic resonance spectroscopy (³¹P-MRS) correlating with the length of the patient's GAA repeat.²⁸

Complexes I, II, and III and aconitase are all iron-sulphur containing enzymes, and their combined deficiency in Friedreich's ataxia, coupled with tissue iron accumulation, suggests that frataxin deficiency may result in a defect of iron-sulphur protein construction. Iron is a pro-oxidant, and the pattern of enzyme defect in patients with Friedreich's ataxia is identical to that seen in the manganese superoxide dismutase knockout mouse model of oxidative stress²⁹ supporting an important role for free radicals in the pathogenesis of Friedreich's ataxia. This raises the possibility that effective antioxidants may have a disease modifying role in this neurodegenerative disorder.

Two recent studies have shown objective improvement in patients with Friedreich's ataxia given antioxidants. In one, 10 patients took high dose ubiquinone (coenzyme Q₁₀) and vitamin E and significant improvements in their skeletal and cardiac muscle biochemical defects, as determined by ³¹P-MRS, were noted at 3 and 6 months³⁰ and 24 months (R Lodi *et al*, unpublished results). In another study, three patients were given idebenone with improvements in cardiac hypertrophy over 3 to 6 months.³¹ Whether antioxidant therapy in Friedreich's ataxia will modify the course of the neurological dysfunction is not yet known, but this issue is currently the subject of a long term study.

Leigh syndrome

Leigh syndrome usually presents in infancy or childhood with failure to

thrive, hypotonia, recurrent vomiting, lactic acidosis, psychomotor retardation, and evidence of brain stem or basal ganglia dysfunction. Magnetic resonance spectroscopy shows bilateral and symmetric high signal in the thalamus and brain stem on T2 weighted images. Leigh syndrome is heterogeneous at the biochemical and molecular levels; defects of pyruvate dehydrogenase and respiratory chain complexes have been described, and mutations have been identified in pyruvate dehydrogenase or mtDNA genes in some patients.

Interest has recently focused on a group of patients with Leigh syndrome with non-maternally inherited cytochrome oxidase (complex IV) deficiency. Somatic cell genetics demonstrated the nuclear basis of complex IV deficient Leigh syndrome,³² and mutations in the SURF-1 gene were subsequently identified in a high proportion of these patients.^{33, 34} SURF-1 is a nuclear encoded mitochondrial protein involved in the maintenance of complex IV activity and mitochondrial respiration in yeast³⁵ and is probably important in holoenzyme assembly. SURF-1 mutations in complex IV-deficient Leigh syndrome result in a severe decrease in enzyme activity.³⁶ Mutations in other nuclear encoded genes encoding proteins involved in COX assembly have been identified including SCO1, SCO2,^{37, 38} and COX 10.³⁹ These mutations were associated with infantile onset of features that included hepatic failure, cardiomyopathy and lactic acidosis.

Hereditary spastic paraplegia

Hereditary spastic paraplegia results in the gradual onset and slow progression of leg spasticity, and sometimes also a distal predominantly sensory neuropathy, mental retardation, retinitis, optic atrophy, and amyotrophy. Prevalence is estimated at 1 in 10 000. Autosomal dominant, recessive, and X linked forms have been described. A new locus on 16q24.3 has recently been described with a 9.5 kb deletion in one family and different frameshift mutations in a further two families.⁴⁰ The gene product, paraplegin, has significant sequence homology to a class of yeast metalloproteases.⁴¹ Paraplegin was found to carry a mitochondrial N-terminal targeting sequence, the mature protein colocalising with, and being internalised by, mitochondria. Muscle biopsies from two patients with hereditary spastic paraplegia and paraplegin deficiency showed several ragged red, succinate dehydrogenase positive, complex IV negative fibres. Biopsies from a further two less severely affected patients had occasional ragged red fibres only. The finding of mitochondrial changes in the muscle of patients with hereditary spastic paraplegia provides another example

of a nuclear gene mutation causing apparently widespread mitochondrial abnormalities.

Dystonia

Movement disorders, and dystonia in particular, are known to occur more often than expected in patients with primary mitochondrial diseases.⁴² Several families with maternally inherited Leber's hereditary optic neuropathy with dystonia and mutations in mtDNA genes encoding complex I subunits have been described.⁴³⁻⁴⁵ A specific and reproducible deficiency of complex I activity in patients with sporadic focal dystonia⁴⁶⁻⁴⁷ has been identified, but not in patients with generalised dystonia linked or not to the dystonia-1 gene.⁴⁸

A nuclear encoded mitochondrial protein defect has now been identified in one particular type of dystonia. Deafness dystonia (Mohr-Tranebjaerg) syndrome is an X linked disorder characterised by progressive sensorineural deafness, cortical blindness, dystonia, dysphagia, and paranoia.⁴⁹ Deafness dystonia syndrome is due to deletion or truncation of a gene (DFN-1) encoding a 11 kDa protein termed DDPI. This protein has recently been identified, through homology studies, as a component of the mitochondrial import system.⁵⁰ It is not yet known which proteins are affected by this import defect, nor whether oxidative phosphorylation is compromised—although the clinical phenotype is reminiscent of other mitochondrial encephalopathies.

DISEASES DUE TO NUCLEAR GENE DEFECTS IN NON-MITOCHONDRIAL PROTEINS

Huntington's disease

Huntington's disease is an autosomal dominant neurodegenerative disorder characterised clinically by chorea, ataxia, and dementia and pathologically by the loss of neurons of the striatum containing γ -aminobutyric acid and enkephalin. It usually presents in early to middle adult life, although both juvenile and late onset forms are recognised. The mutation responsible is an abnormally expanded (>36) cytosine-adenine-guanine (CAG) repeat in the huntingtin gene on chromosome 4. Knockout of the huntingtin gene results in early fetal death in mice, implying a critical role in embryogenesis.⁵¹ The gene product, huntingtin, is a widely expressed 349 kDa protein of unknown function.⁵² Cultured cells expressing mutant huntingtin molecules have intranuclear inclusions,⁵³ which are also seen in the brains of patients with Huntington's disease⁵⁴ and in Huntington transgenic mice.⁵⁵

Excitotoxicity has been suggested to play an important part in neuronal cell

death in Huntington's disease.⁵⁶ This is dependent on glutamate excitation of N-methyl-D-aspartate receptors, inward flow of calcium, activation of nitric oxide synthase, and nitric oxide generation. Nitric oxide, and particularly peroxynitrite, the product of the reaction of nitric oxide with superoxide O_2^- are free radicals that can damage tissues. An important factor in this sequence is the release of the energy dependent magnesium blockade of NMDA receptors, thus rendering ambient concentrations of glutamate excitotoxic. Evidence for a defect of energy metabolism in Huntington's disease arises from various sources, including reduced striatal and cerebral cortical glucose utilisation as detected by positron emission tomography and increased lactic acid concentrations as detected by magnetic resonance spectroscopy,⁵⁷⁻⁵⁸ although the latter is not a universal finding.⁵⁹ Biochemical analyses by several groups have shown a severe MITOX defect: deficiency of complexes II and III and IV⁶⁰⁻⁶¹ in addition to a 90% decrease in aconitase activity.⁶² R6/2 HD transgenic mice also show evidence of striatal deficiencies of complex IV and aconitase.⁶³

The mitochondrion plays a central part in cell biology in maintaining life through ATP generation and in determining cell death through its role in apoptosis.

The development of such severe defects of mitochondrial respiratory chain and aconitase function must be secondary to the primary huntingtin gene defect. The question arises as to whether this is a causal relation or the consequence of alternative biochemical and pharmacological events. Huntingtin is expressed in muscle and, at a low level, in fibroblasts and lymphoblasts. Mitochondrial respiratory chain and aconitase activities were normal in fibroblasts and platelets from patients with Huntington's disease.⁶⁰ Magnetic resonance spectroscopy in muscle of patients with Huntington's disease has been reported to be abnormal.⁵⁸ This finding has recently been confirmed and also decreased rates of ATP synthesis (which correlated with the length of the CAG repeat—that is, the longer the repeat, the worse the defect) were found in the muscle of both symptomatic and presymptomatic patients.⁶⁴

The presence of mitochondrial defects in Huntington's disease brain and skeletal muscle, in particular the correlation of the latter with the length of the CAG repeats, suggests that mutant huntingtin

may have a direct role in inducing mitochondrial abnormalities. These findings are supported by the protective effects of creatine in the R6/2 transgenic mouse⁶⁵ and have been the basis for a trial in the United States of ubiquinone therapy in Huntington's disease.

Wilson's disease

Wilson's disease is an autosomal recessive disorder which results in liver disease in 40% of affected patients, neurological dysfunction (dystonia, rigidity, parkinsonism) in 40%, and psychiatric disease in 20% of patients. The Wilson's disease gene on 13q14.3 codes for a protein that functions as a P-type ATPase localised in both the Golgi network⁶⁶ and possibly in mitochondria.⁶⁷ We have recently identified severe defects of MITOX function, particularly complexes I, II, and III, and aconitase deficiency in liver samples from patients with Wilson's disease.⁶⁸ This pattern of enzyme defect, identical to that seen in Friedreich's ataxia and to that found in the superoxide dismutase 2 knockout mouse,²⁹ suggests that free radical formation and oxidative damage may contribute to the pathogenesis of cirrhosis in Wilson's disease. This might be expected as copper, which accumulates in the liver in Wilson's disease, may substitute for iron in free radical generating reactions. The results suggest that effective antioxidant therapy may be helpful in patients with Wilson's disease.

DISEASES WITH UNDEFINED MITOCHONDRIAL CONTRIBUTION TO AETIOLOGY AND PATHOGENESIS

There are a group of neurodegenerative diseases where there is clear evidence of mitochondrial dysfunction. However, the role of mitochondria in aetiology and pathogenesis as yet remains undefined—and may be primary or secondary. Indeed it is increasingly likely that in Parkinson's disease in particular, the mitochondrial abnormality may be primary in some patients, secondary in others, but still plays an important contributory part in pathogenesis in many. The position with respect to Alzheimer's disease and motor neuron disease is less clear.

Parkinson's disease

The cause of dopaminergic cell death in Parkinson's disease is not known. However, during the past 2 years several mutations have been identified in both autosomal dominant and recessive Parkinson's disease.⁶⁹⁻⁷² Environmental agents—for example, 1-methyl-4-phenyl 1,2,3,6 tetrahydropyridine, manganese, and carbon monoxide—have also been associated with the development of parkinsonism. A rat model of parkinsonism

has been produced by parenteral infusion of rotenone—a naturally occurring pesticide and complex I inhibitor.⁷³ It seems increasingly likely that idiopathic, sporadic Parkinson's disease may be the clinical, pathological, and possibly biochemical end point common to various different aetiological agents.

There is evidence of a mitochondrial complex I defect in the substantia nigra of patients with Parkinson's disease (see Schapira *et al*⁷⁴ for review), and this defect is also detectable in platelets in some patients with sporadic Parkinson's disease.⁷⁵ Genomic transplantation studies have demonstrated that the complex I defect in this subgroup is determined by mtDNA.^{76 77} Whether this defect is caused by mtDNA mutations or a series of polymorphisms that render cells susceptible to damage by, for instance, an environmental agent, is not yet known, nor whether such mtDNA abnormalities are somatic or inherited. Any mtDNA mutation may be systemically distributed but, as with primary mtDNA mutations, may be heteroplasmic (present in varying proportions of wild-type and mutant genomes) and therefore, for instance, be present in higher concentration in certain tissues—for example, the substantia nigra. In addition, the biochemical (oxidative stress, increased iron) and pharmacological (dopamine oxidation, excitotoxicity) characteristics of the substantia nigra may exacerbate the complex I defect. Some or all of these processes may influence complex I function and respiratory (proton pumping) activity such as to decrease membrane potential, thereby lowering the cell's threshold to undergo apoptosis. These events and their effects may vary from one cell type to another, and could particularly affect neurons in view of their dependence on oxidative phosphorylation. These findings suggest that, in some patients with Parkinson's disease, mtDNA defects may be primary, whereas in others the mitochondrial abnormalities may be secondary to, for instance, free radical generation or possibly exogenous toxins.

Alzheimer's disease

Evidence for mitochondrial dysfunction in Alzheimer's disease is derived from several different but complementary studies. A specific deficiency in the activity of complex IV (cytochrome oxidase) has been described in Alzheimer's disease brain^{78–80} and in platelet mitochondria.⁸¹ A decrease in the expression of nuclear and mtDNA encoded COX subunits has been found in Alzheimer's disease brain.⁸² The complex IV defect may be transferred to recipient cells using mtDNA derived from patients with Alzheimer's disease,⁸³ implying that an mtDNA defect is the cause of the complex IV deficiency. Indeed a group of

mtDNA "mutations" were identified, but subsequently found to be amplifications of nuclear pseudogenes.^{84 85} Down regulation of COX gene expression is known to occur in association with decreased neuronal activity or degeneration.⁸⁶ Complex IV deficiency has also been reported in Friedreich's ataxia and spinocerebellar ataxia-1 brains⁸⁷ and so is not specific to Alzheimer's disease—unlike the complex I deficiency in Parkinson's disease. At present, therefore, there remains uncertainty about the relevance of complex IV deficiency in Alzheimer's disease and whether it may represent a primary phenomenon in some, or a secondary epiphenomenon in all.

Motor neuron disease

The evidence for mitochondrial dysfunction in motor neuron disease (amyotrophic lateral sclerosis) is compelling and fits well with our current understanding of the pathogenesis of this disorder. Mutations in the gene for superoxide dismutase 1 (SOD-1) are found in about 20% of patients with familial forms of motor neuron disease⁸⁸ and may induce neuronal damage by enhanced peroxidation.⁸⁹ There have been several reports of free radical induced damage to proteins, lipid, and DNA in postmortem tissue from patients with motor neuron disease.^{90–95} Increased concentrations of 8-hydroxy-2-deoxyguanosine (OH⁸dG)—an indicator of oxidatively damaged DNA—have also been found in plasma, urine, and CSF from patients with motor neuron disease, and to increase with progression of the disease.⁹⁶ Changes have been seen in both sporadic and familial forms of the disease, as well as in a transgenic mouse model with a SOD-1 mutation (G93A).⁹⁷ Furthermore, fibroblasts from patients with sporadic and familial motor neuron disease are more susceptible to damage by free radicals.⁹⁸ Increased activities of respiratory chain complexes I–III were seen in postmortem brain tissue from familial but not sporadic patients. Complex I activity was increased in the forebrain of the G93A transgenic SOD-1 mouse model but complex I and IV activities were decreased in the spinal cord.⁹⁹ Complex I activity has been found to be decreased in skeletal muscle from patients with motor neuron disease¹⁰⁰ and respiratory defects were associated with the presence of mtDNA deletions¹⁰¹ which in turn were correlated with negative staining for complex IV in single fibres.¹⁰² Mitochondrial morphological changes have been found in anterior horn cells from patients¹⁰³ and the G37R transgenic mouse model.^{104 105} Complex IV was decreased in motor neuron disease motor neurons¹⁰⁶ and an excess of the 4977 "common" mtDNA deletion was found in motor neuron disease motor cortex.¹⁰⁷

The mitochondrial abnormalities in motor neuron disease are most easily explained as a secondary phenomenon to free radical mediated damage. The pattern of respiratory chain deficiency is consistent with excitotoxicity and peroxynitrite mediated protein dysfunction. This is supported by evidence for increased free nitrotyrosine in patients¹⁰⁸ and a transgenic mouse model with a SOD-1 mutation.¹⁰⁹ Whether the mitochondrial dysfunction is merely an epiphenomenon, or whether it also contributes to disease pathogenesis, is not clear. However, the recent demonstration that creatine significantly prolongs life in a SOD-1 transgenic model suggests that improving mitochondrial function may be of benefit to patients with motor neuron disease.¹¹⁰ This may be achieved for instance with either carnitine or ubiquinone—or both—and could be used in conjunction with other potentially disease modifying therapies including NMDA antagonists. A double blind placebo controlled trial to address these issues is currently being initiated.

CONCLUSIONS

The mitochondrion plays a central part in cell biology in maintaining life through ATP generation and in determining cell death through its role in apoptosis. It is hardly surprising, therefore, that mitochondrial dysfunction, both primary and secondary, is associated with disease. The dependence of nervous tissue, in particular, on intact mitochondrial activity means that neurological dysfunction will be a frequent consequence of both primary and secondary respiratory chain defects. Evidence is emerging that there may be common pathogenetic features in several of the neurodegenerative diseases. These may include defects of intracellular protein handling, protein damage with consequent aggregation and accumulation, and mitochondrial dysfunction. The development of therapeutic strategies to intervene in the cascade of events that involves these processes and terminates in cell death may provide disease modifying drugs not only for neurodegenerative disorders, but also for the primary mitochondrial defects.

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