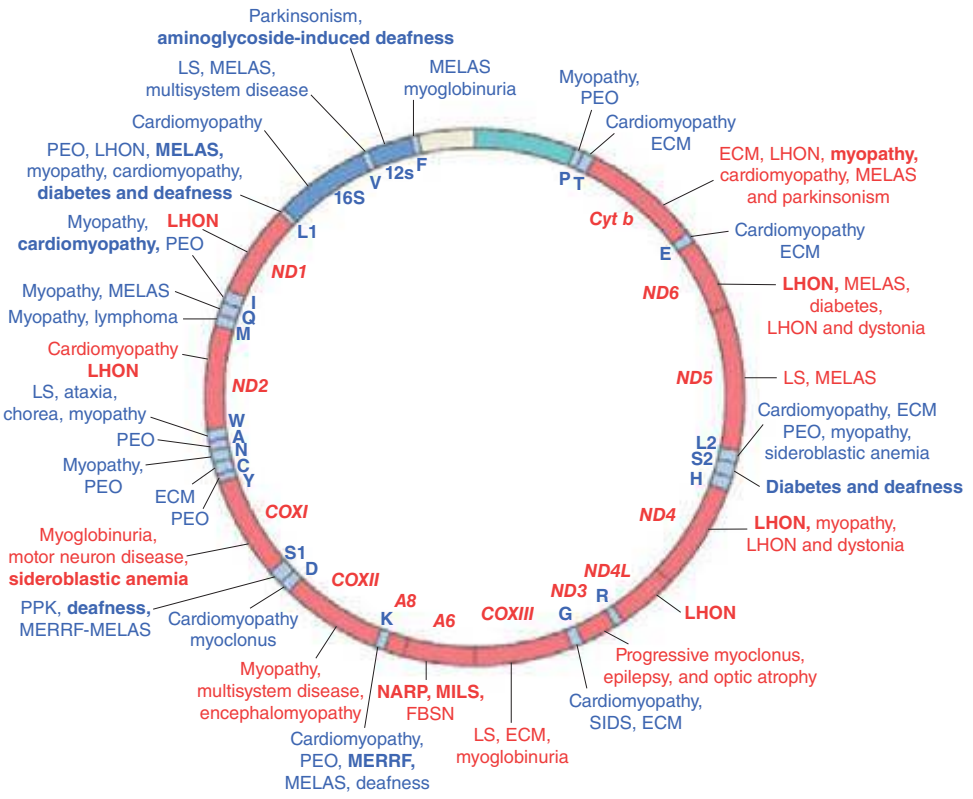

FIGURE 85e-4 Mutations in the human mitochondrial genome known to cause disease. Disorders that are frequently or prominently associated with mutations in a particular gene are shown in *boldface*. Diseases due to mutations that impair mitochondrial protein synthesis are shown in *blue*. Diseases due to mutations in protein-coding genes are shown in *red*. ECM, encephalomyopathy; FBSN, familial bilateral striatal necrosis; LHON, Leber's hereditary optic neuropathy; LS, Leigh syndrome; MELAS, mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes; MERRF, myoclonic epilepsy with ragged red fibers; MILS, maternally inherited Leigh syndrome; NARP, neuropathy, ataxia, and retinitis pigmentosa; PEO, progressive external ophthalmoplegia; PPK, palmoplantar keratoderma; SIDS, sudden infant death syndrome. *(Reproduced with permission from S DiMauro, E Schon: Mitochondrial respiratory-chain diseases. N Engl J Med 348:2656, 2003.)*

(or with the somatic accumulation of mtDNA mutations, see below) can show a mosaic pattern of reduced histochemical staining in comparison with histochemical staining for the complex II enzyme, succinate dehydrogenase (Fig. 85e-5). Heteroplasmy can also be detected at the genetic level through direct Sanger-type mtDNA genotyping under special conditions, although clinically significant low levels of heteroplasmy can escape detection in genomic samples extracted from whole blood using conventional genotyping and sequencing techniques.

The emerging next-generation sequencing (NGS) techniques and their rapid penetration and recognition as useful clinical diagnostic tools are expected to also dramatically improve the clinical genetic diagnostic evaluation of mitochondrial diseases at the level of both the nuclear genome and mtDNA. In the context of the larger nuclear genome, the ability of NGS techniques to dramatically increase the speed at which DNA can be sequenced at a fraction of the cost of conventional Sanger-type sequencing technology is particularly beneficial. Low sequencing costs and short turnaround time expedite "first-tier" screening of panels of hundreds of previously known or suspected mitochondrial disease genes or screening for the entire exome or genome in an attempt to identify novel genes and mutations affecting different patients or families. In the context of the mtDNA, NGS approaches hold the particular promise for rapid and reliable detection of heteroplasmy in different affected tissues. Although Sanger sequencing allows for complete coverage of the mtDNA, it is limited by the lack of deep coverage and low sensitivity for heteroplasmy detection when it is much less than 50%. In contrast, NGS technology is an excellent tool for rapidly and accurately obtaining a patient's predominant mtDNA sequence and also lower frequency heteroplasmic variants. This is enabled by deep coverage of the genome through multiple independent sequence reads. Accordingly, recent studies making use of NGS techniques have demonstrated sequence accuracy equivalent to Sanger-type sequencing, but also have uncovered heretofore unappreciated heteroplasmy rates ranging between 10 and 50% and detection of single-nucleotide heteroplasmy down to levels of <10%.

Clinically, the most striking overall characteristic of mitochondrial genetic disease is the phenotypic heterogeneity associated with mtDNA mutations. This extends to intrafamilial phenotypic heterogeneity for the same mtDNA pathogenic mutation and, conversely, to the overlap of phenotypic disease manifestations with distinct mutations. Thus, although fairly consistent and well-defined "classic" syndromes have been attributed to specific mutations, frequently "nonclassic" combinations of disease phenotypes ranging from isolated myopathy to extensive multisystem disease are often encountered, rendering genotype-phenotype correlation challenging. In both classical and nonclassical mtDNA disorders, there is often a clustering of some combination of abnormalities affecting the neurologic system (including optic nerve atrophy, pigment retinopathy, and sensorineural hearing loss), cardiac and skeletal muscle (including extraocular muscles), and endocrine and metabolic systems (including diabetes mellitus). Additional organ systems that may be affected include the hematopoietic, renal, hepatic, and gastrointestinal systems, although these are more frequently involved in infants and children. Disease-causing mtDNA coding region mutations can affect either one of the 13 protein encoding genes or one of the 24 protein synthetic genes. Clinical manifestations do not readily distinguish these two categories, although lactic acidosis and muscle pathologic findings tend to be more prominent in the latter. In all cases, either defective ATP production due to disturbances in the ETC or enhanced generation of ROS has been invoked as the mediating biochemical mechanism between mtDNA mutation and disease manifestation.

MTDNA DISEASE PRESENTATIONS

The clinical presentation of adult patients with mtDNA disease can be divided into three categories: (1) clinical features suggestive of mitochondrial disease (Table 85e-2), but not a well-defined classic syndrome; (2) classic mtDNA syndromes; and (3) clinical presentation confined to one organ system (e.g., isolated sensorineural deafness, cardiomyopathy, or diabetes mellitus).

Table 85e-3 provides a summary of eight illustrative classic mtDNA syndromes or disorders that affect adult patients and highlights some of the most interesting features of mtDNA disease in terms of molecular pathogenesis, inheritance, and clinical presentation. The first five of these syndromes result from heritable point mutations in either protein-encoding or protein synthetic mtDNA genes; the other three result from rearrangements or deletions that usually do not involve the germline.