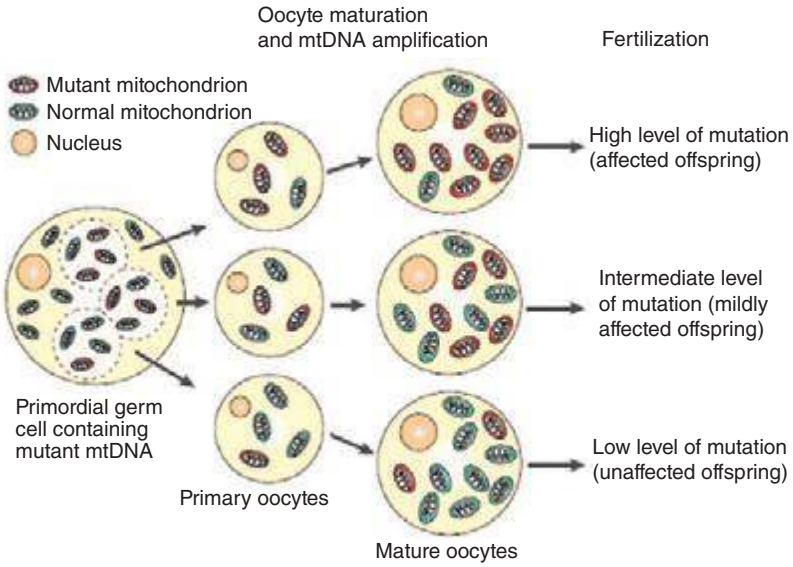

FIGURE 85e-3 Heteroplasmy and the mitochondrial genetic bottleneck. During the production of primary oocytes, a selected number of mitochondrial DNA (mtDNA) molecules are transferred into each oocyte. Oocyte maturation is associated with the rapid replication of this mtDNA population. This restriction-amplification event can lead to a random shift of mtDNA mutational load between generations and is responsible for the variable levels of mutated mtDNA observed in affected offspring from mothers with pathogenic mtDNA mutations. Mitochondria that contain mutated mtDNA are shown in *red*, and those with normal mtDNA are shown in *green*. *(Reproduced with permission from R Taylor, D Turnbull: Mitochondrial DNA mutations in human disease. Nat Rev Genetics 6:389, 2005.)*

and eventually exclusive, version of the mtDNA for that particular nucleotide site. All of the offspring of a woman bearing an mtDNA sequence variant or mutation that has become homoplasmic will also be homoplasmic for that variant and will transmit the sequence variant forward in subsequent generations.

Considerations of reproductive fitness limit the evolutionary or population emergence of homoplasmic mutations that are lethal or cause severe disease in infancy or childhood. Thus, with a number of notable exceptions (e.g., mtDNA mutations causing Leber's hereditary optic neuropathy; see below), most homoplasmic mutations are considered to be neutral markers of human evolution, which are useful and interesting in the population genetics analysis of shared maternal ancestry but which have little significance in human phenotypic variation or disease predisposition.

More importantly is the understanding that this accumulation of homoplastic mutations occurs at a genetic locus that is transmitted only through the female germline and that lacks recombination. In turn, this enables reconstruction of the sequential topology and radiating phylogeny of mutations accumulated through the course of human evolution since the time of the most recent common mtDNA ancestor of all contemporary mtDNA sequences, some 200,000 years ago. The term haplogroup is usually used to define major branching points in the human mtDNA phylogeny, nested one within the other, which often demonstrate striking continental geographic ancestral partitioning. At the level of the complete mtDNA sequence, the term haplotype is usually used to describe the sum of mutations observed for a given mtDNA sequence and as compared to a reference sequence, such that all haplotypes falling within a given haplogroup share the total sum of mutations that have accumulated since the most recent common ancestor and the bifurcation point they mark. The remaining observed variants are private to each haplotype. Consequentially, human mtDNA sequence is an almost perfect molecular prototype for a nonrecombining locus, and its variation has been extensively used in phylogenetic studies. Moreover, the mtDNA mutation rate is considerably higher than the rate observed for the nuclear genome, especially in the control region, which contains the displacement, or D-loop, in turn comprising two adjacent hypervariable regions (HVR-I and HVR-II). Together with the absence of recombination, this amplifies drift to high frequencies of novel haplotypes. As a result, mtDNA haplotypes are more highly partitioned across geographically defined populations than sequence variants in other parts of the genome. Despite extensive research, it has not been well established that such haplotype-based partitioning has a significant influence on human health conditions. However, mtDNA-based phylogenetic analysis can be used both as a quality assurance tool and as a filter in distinguishing neutral mtDNA variants comprising human mtDNA phylogeny from potentially deleterious mutations.

MITOCHONDRIAL DNA DISEASE

The true prevalence of mtDNA disease is difficult to estimate because of the phenotypic heterogeneity that occurs as a function of heteroplasmy, the challenge of detecting and assessing heteroplasmy in different affected tissues, and the other unique features of mtDNA function and inheritance described above. It is estimated that at least 1 in 200 healthy humans harbors a pathogenic mtDNA mutation with the potential to causes disease, but that heteroplasmic germline pathogenic mtDNA mutations actually affect up to approximately 1 in 8500 individuals.

The true disease burden relating to mtDNA sequence variation will only be known when the following capabilities become available: (1) ability to distinguish a completely neutral sequence variant from a true phenotype-modifying or pathogenic mutation, (2) accurate assessment of heteroplasmy that can be determined with fidelity, and (3) a systems biology approach **(Chap. 87e)** to determine the network of epistatic interactions of mtDNA sequence variations with mutations in the nuclear genome.

OVERVIEW OF CLINICAL AND PATHOLOGIC FEATURES OF HUMAN MTDNA DISEASE

Given the vital roles of mitochondria in all nucleated cells, it is not surprising that mtDNA mutations can affect numerous tissues with pleiotropic effects. More than 200 different disease-causing, mostly heteroplasmic mtDNA mutations have been described affecting ETC function. **Figure 85e-4** provides a partial mtDNA map of some of the better characterized of these disorders. A number of clinical clues can increase the index of suspicion for a heteroplasmic mtDNA mutation as an etiology of a heritable trait or disease, including (1) familial clustering with absence of paternal transmission; (2) adherence to one of the classic syndromes (see below) or paradigmatic combinations of disease phenotypes involving several organ systems that normally do not fit together within a single nuclear genomic mutation category; (3) a complex of laboratory and pathologic abnormalities that reflect disruption in cellular energetics (e.g., lactic acidosis and neurodegenerative and myodegenerative symptoms with the finding of ragged red fibers, reflecting the accumulation of abnormal mitochondria under the muscle sarcolemmal membrane); or (4) a mosaic pattern reflecting a heteroplasmic state.

Heteroplasmy can sometimes be elegantly demonstrated at the tissue level using histochemical staining for enzymes in the oxidative phosphorylation pathway, with a mosaic pattern indicating heterogeneity of the genotype for the coding region for the mtDNA-encoded enzyme. Complex II, CoQ, and cytochrome c are exclusively encoded by nuclear DNA. In contrast, complexes I, III, IV, and V contain at least some subunits encoded by mtDNA. Just 3 of the 13 subunits of the ETC complex IV enzyme, cytochrome c oxidase, are encoded by mtDNA, and, therefore, this enzyme has the lowest threshold for dysfunction when a threshold level of mutated mtDNA is reached. Histochemical staining for cytochrome c oxidase activity in tissues of patients affected with heteroplasmic inherited mtDNA mutations