populations with a societal or environmental difference or with different allele frequencies at other genomic loci, which are actually causally related to the heritable trait or disease of interest. The difficulty in generating cellular or animal models to test the functional influence of homoplasmic sequence variants (as a result of mtDNA polyploidy) further compounds the challenge. The most likely formulation is that the risk conferred by different mtDNA haplogroup–defining homoplasmic mutations for common diseases depends on the concomitant nuclear genomic background, together with environmental influences. Progress in minimizing potentially misleading associations in mtDNA heritable trait and disease studies should include ensuring adequate sample size taken from a large sample recruitment base, using carefully matched controls and population structure determination, and performing analysis that takes into account epistatic interactions with other genomic loci and environmental factors.

IMPACT OF ACQUIRED SOMATIC MTDNA MUTATION ON HUMAN HEALTH AND DISEASE

Studies on aging humans and animals have shown a potentially important correlation of age with the accumulation of heterogeneous mtDNA mutations, especially in those organ systems that undergo the most prominent age-related degenerative tissue phenotype. Sequencing of PCR-amplified single mtDNA molecules has demonstrated an average of two to three point mutations per molecule in elderly subjects when compared with younger ones. Point mutations observed include those responsible for known heritable heteroplasmic mtDNA disorders, such as the m.3344A>G and m.3243A>G mutations responsible for the MERRF and MELAS syndromes, respectively. However, the cumulative burden of these acquired somatic point mutations with age was observed to remain well below the threshold expected for phenotypic expression (<2%). Point mutations at other sites not normally involved in inherited mtDNA disorders have also been shown to accumulate to much higher levels in some tissues of elderly individuals, with the description of tissue-specific "hot spots" for mtDNA point mutations. Along the same lines, an age-associated and tissue-specific accumulation of mtDNA deletions has been observed, including deletions involved in known heritable mtDNA disorders, as well as others. The accumulation of functional mtDNA deletions in a given tissue is expected to be associated with mitochondrial dysfunction, as reflected in an age-associated patchy and reduced COX activity on histochemical staining, especially in skeletal and cardiac muscle and brain. A particularly well-studied and potentially important example is the accumulation of mtDNA deletions and COX deficiency observed in neurons of the substantia nigra in Parkinson's disease patients.

The progressive accumulation of ROS has been proposed as the key factor connecting mtDNA mutations with aging and age-related disease pathogenesis (Fig. 85e-8). As noted above, ROS are a by-product of oxidative phosphorylation and are removed by detoxifying antioxidants into less harmful moieties; however, exaggerated production of ROS or impaired removal results in their accumulation. One of the main targets for ROS-mediated injury is DNA, and mtDNA is particularly vulnerable because of its lack of protective histones and less efficient injury repair systems compared with nuclear DNA. In turn, accumulation of mtDNA mutations results in inefficient oxidative phosphorylation, with the potential for excessive production of ROS, generating a "vicious cycle" of cumulative mtDNA damage. Indeed, measurement of the oxidative stress biomarker 8-hydroxy-2-deoxyguanosine has been used to measure age-dependent increases in mtDNA oxidative damage at a rate exceeding that of nuclear DNA. It should be noted that mtDNA mutation can potentially occur in postmitotic cells as well, because mtDNA replication is not synchronized with the cell cycle. Two other proposed links between mtDNA mutation and aging, besides ROS-mediated tissue injury, are the perturbations in efficiency of oxidative phosphorylation with disturbed cellular aerobic function and perturbations in apoptotic pathways, whose execution steps involve mitochondrial activity.

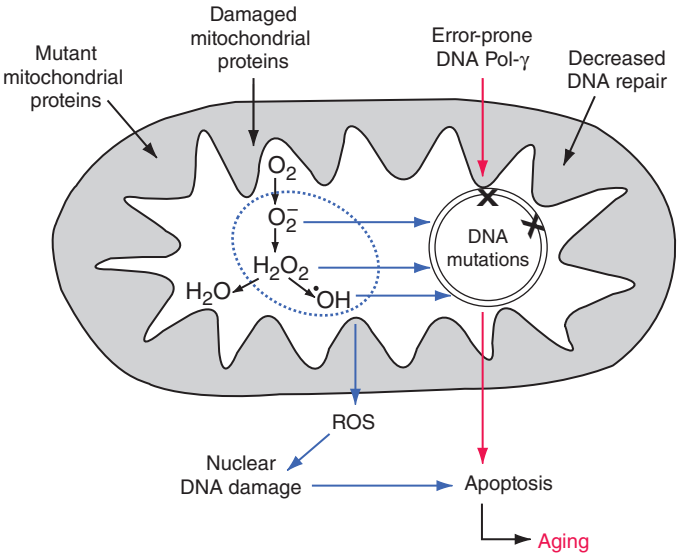

FIGURE 85e-8 Multiple pathways of mitochondrial DNA (mtDNA) damage and aging. Multiple factors may impinge on the integrity of mitochondria that lead to loss of cell function, apoptosis, and aging. The classic pathway is indicated with *blue arrows*; the generation of reactive oxygen species (ROS; superoxide anion, hydrogen peroxide, and hydroxyl radicals), as a by-product of mitochondrial oxidative phosphorylation, results in damage to mitochondrial macromolecules, including the mtDNA, with the latter leading to deleterious mutations. When these factors damage the mitochondrial energy-generating apparatus beyond a functional threshold, proteins are released from the mitochondria that activate the caspase pathway, leading to apoptosis, cell death, and aging. *(Reproduced with permission from L Loeb et al: The mitochondrial theory of aging and its relationship to reactive oxygen species damage and somatic mtDNA mutations. Proc Natl Acad Sci USA 102:18769, 2005.)*

Genetic intervention studies in animal models have sought to clarify the potential causative relationship between acquired somatic mtDNA mutation and the aging phenotype, and the role of ROS in particular. Replication of the mitochondrial genome is mediated by the activity of the nuclear-encoded polymerase gamma gene. A transgenic homozygous mouse knock-in mutation of this gene renders the polymerase enzyme deficient in proofreading and results in a three- to fivefold increase in mtDNA mutation rate. Such mice develop a premature aging phenotype, which includes subcutaneous lipoatrophy, alopecia, kyphonia, and weight loss with premature death. Although the finding of increased mtDNA mutation and mitochondrial dysfunction with age has been solidly established, the causative role and specific contribution of mitochondrial ROS to aging and age-related disease in humans has yet to be proved. Similarly, although many tumors display higher levels of heterogeneous mtDNA mutations, a causal relationship to tumorigenesis has not been proved.

Besides the age-dependent acquired accumulation in somatic cells of heterogeneous point mutations and deletions, a quite different effect of nonheritable and acquired mtDNA mutation has been described affecting tissue stem cells. In particular, disease phenotypes attributed to acquired mtDNA mutation have been observed in sporadic and apparently nonfamilial cases involving a single individual or even tissue, usually skeletal muscle. The presentation consists of decreased exercise tolerance and myalgias, sometimes progressing to rhabdomyolysis. As in the case of the sporadic, heteroplasmic, large-scale deletion, classic syndromes of chronic PEO, Pearson syndrome, and KSS, the absence of a maternal inheritance pattern, together with the finding of limited tissue distribution, suggests a molecular pathogenic mechanism emanating from mutations arising de novo in muscle stem cells after germline differentiation (somatic mutations that are