

Mitochondrial DNA Mutations and Their Impact on Aging

Prof. Lucas Reinhardt

Heidelberg Academy of Life Sciences, Heidelberg, Germany

Submission: 26.11.2025| Acceptance: 06.03.2026| Publication: 04.06.2026

Abstract

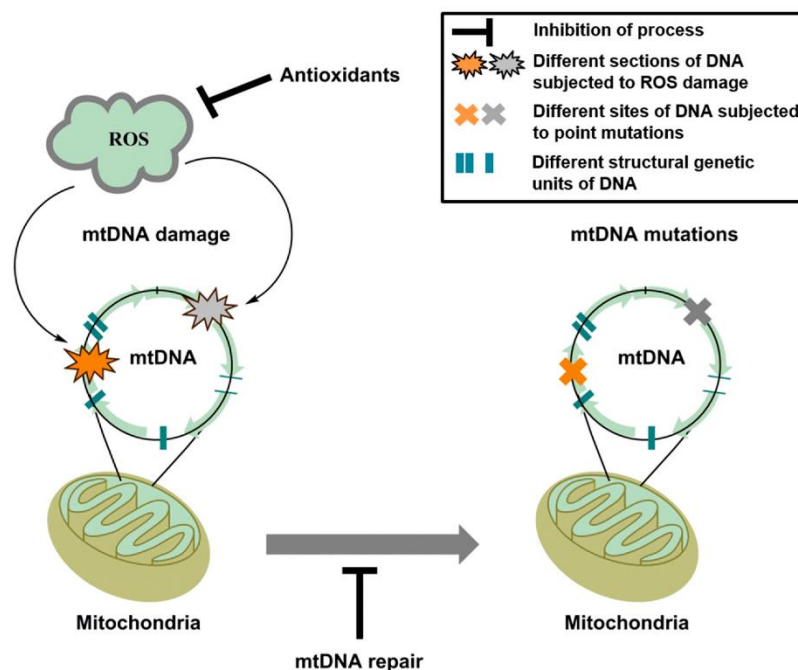
Deterioration of mitochondria has long been linked to aging and age-related disorders; they are essential for cellular energy production, metabolism, and apoptosis. Because of its close proximity to reactive oxygen species (ROS), restricted repair mechanisms, and fast replication rate, mitochondrial DNA (mtDNA) is far more prone to mutations than nuclear DNA. Cellular senescence and tissue degeneration are caused by metabolic imbalance, reduced ATP synthesis, increased ROS production, and the disruption of oxidative phosphorylation caused by the accumulation of mtDNA mutations over time. Research in both humans and animals points to mtDNA mutations as a key player in the aging process, with the potential to trigger oxidative stress and mitochondrial malfunction. Neurodegenerative illnesses, cardiovascular diseases, sarcopenia, and metabolic syndromes are just some of the age-related conditions that have been linked to these changes. Heteroplasmy, in which wild-type and mutant mitochondrial DNA reside in the same cell, also plays a significant role in how mitochondrial dysfunction develops and how quickly it manifests in aged tissues. Our knowledge of the role of certain point mutations, deletions, and copy number changes in mtDNA in the aging phenotype has been enhanced by developments in mitochondrial biology and next-generation sequencing. New therapeutic techniques, including gene editing, mitochondrial replacement therapy, and antioxidants targeted to mitochondria, show promise in reducing the harmful consequences of mtDNA mutations and postponing the start of age-related deterioration. delves into the molecular pathways that connect mtDNA mutations to aging, investigates their function in age-related illnesses, and addresses possible therapies that aim at mitochondrial health to encourage healthy aging and increase lifespan.

Keywords: Mitochondrial DNA (mtDNA), aging, oxidative phosphorylation, reactive oxygen species (ROS), heteroplasmy

Introduction

One of the most compelling theories to explain aging, which gradually declines cellular and physiological functions and increases vulnerability to disease and mortality, is mitochondrial dysfunction. The cell's powerhouse, mitochondria, generates ATP through oxidative phosphorylation, regulates calcium homeostasis, initiates apoptosis, and produces ROS as metabolic byproducts. Mitochondrial DNA (mtDNA) is small, circular, maternally inherited, and encodes essential respiratory chain components, but its proximity to ROS, lack of protective histones, limited DNA repair capacity, and high replication rate make it vulnerable to damage. Mutations in mtDNA cause structural and functional electron transport chain deficiencies, lower ATP synthesis, and increased ROS formation, creating a cycle of oxidative

stress and mitochondrial decline. Studies show that mtDNA mutation burdens rise in aged organs such skeletal muscle, heart, and brain, causing functional deterioration and age-related illnesses. Experiments in mice with proofreading-deficient mitochondrial DNA polymerase (Poly) have shown that elevated mtDNA mutations accelerate aging phenotypes, such as hair loss, osteoporosis, reduced fertility, and shorter lifespan, supporting the role of mitochondrial genome instability in aging. Heteroplasmy, where both wild-type and mutant mtDNA coexist in a cell, also affects mitochondrial dysfunction severity because the proportion of mutant genomes can vary across tissues and increase with age. The systemic impact of mitochondrial decline is shown by clinical evidence linking mtDNA mutations to aging and many age-related diseases, including neurodegenerative disorders like Parkinson's and Alzheimer's, cardiovascular diseases, metabolic syndromes, sarcopenia, and even cancer. MtDNA mutations disrupt electron transport complexes, causing electron leakage and increased ROS generation, which destroys proteins, lipids, and nucleic acids, increasing cellular stress and senescence. These mechanisms support the free radical theory of aging by stressing mitochondria's dual role as ROS generators and targets, with mtDNA mutations amplifying oxidative damage. High-throughput sequencing, bioinformatics, and imaging technologies have improved our understanding of the mtDNA mutation spectrum, revealing patterns of deletions, point mutations, and copy number variations associated with aging tissues and suggesting biological age markers. Additionally, mitochondria-targeted antioxidants like MitoQ and SkQ1 to reduce oxidative damage, pharmacological or lifestyle interventions to improve mitochondrial biogenesis and dynamics, and cutting-edge genetic techniques like mitochondrial gene editing and replacement therapies to correct or bypass mutant genomes are gaining popularity. Many of these approaches are experimental, but they show mitochondrial medicine's potential to delay aging and prevent age-related illnesses. Importantly, exercise, calorie restriction, and diet improve mitochondrial function and reduce mtDNA mutations, suggesting that environmental and behavioral therapies may complement future medicinal techniques. After significant advances, it is still unclear whether mtDNA mutations are primary drivers of aging or secondary consequences of metabolic decline. However, the evidence increasingly supports a bidirectional relationship in which mtDNA instability both contributes to and is exacerbated by aging. As research on mitochondrial genetics, cellular metabolism, and systemic aging develops, mtDNA mutations are crucial to understanding aging biology and creating ways to enhance lifespan and health.

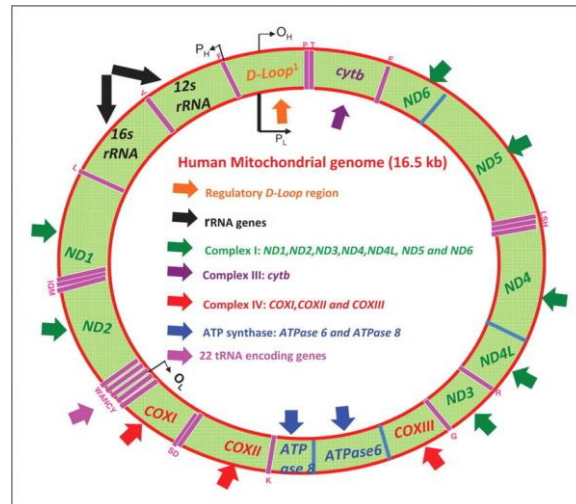


Mitochondrial DNA (mtDNA) mutations play a crucial role in the biological process of aging by affecting cellular energy production and increasing oxidative damage. Unlike nuclear DNA, mtDNA is more vulnerable to mutations due to its proximity to the electron transport chain, where reactive oxygen species (ROS) are continuously generated. Over time, the accumulation of these mutations impairs mitochondrial function, leading to reduced efficiency in ATP production, which is essential for cellular activities. One of the central mechanisms linking mtDNA mutations to aging is oxidative stress. As mitochondria produce energy, they also generate ROS as byproducts. These highly reactive molecules can damage mtDNA, proteins, and lipids, creating a cycle where mitochondrial damage leads to more ROS production, further accelerating cellular aging. This phenomenon contributes to the gradual decline in cellular function observed in aging tissues. Additionally, mtDNA mutations can disrupt apoptosis regulation and cellular homeostasis. Damaged mitochondria may trigger abnormal cell death or, conversely, allow dysfunctional cells to persist. This imbalance contributes to tissue degeneration and age-related diseases such as neurodegenerative disorders, cardiovascular diseases, and metabolic syndromes. Another important aspect is the heteroplasmy effect, where both normal and mutated mtDNA coexist within a cell. As the proportion of mutated mtDNA increases over time, cellular function progressively declines. This threshold effect explains why symptoms of mitochondrial dysfunction often appear later in life.

Mitochondrial DNA and Its Unique Features

Mitochondrial DNA (mtDNA) is a unique component of the eukaryotic genome, originating from a proto-eukaryotic cell and an α -proteobacterium. Its unique characteristics distinguish it from nuclear DNA and make it crucial for aging and disease. In humans, mtDNA is a small, circular, double-stranded molecule that encodes 37 genes necessary for mitochondrial function, including 13 polypeptides that form critical subunits of the oxidative phosphorylation (OXPHOS) complexes, 22 transfer RNAs, and 2 ribosomal RNAs needed for mitochondrial protein synthesis. Unlike nuclear DNA, mtDNA has no introns and a high coding density, with

little noncoding sequence except for the D-loop, which controls replication and transcription. Mutations can have major functional effects, so even small regions are vulnerable. After fertilization, sperm mitochondria are actively degraded, resulting in the exclusive transmission of maternal mtDNA to offspring. This allows tracing of maternal lineages but limits the corrective influence of recombination, leading to deleterious mutations across generations. MtDNA exists in hundreds to thousands of copies per cell, depending on tissue type and energy demand, resulting in heteroplasmy, where the proportion of mutant genomes determines whether mitochondrial dysfunction becomes clinically apparent. Unlike nuclear DNA, mtDNA is packaged with proteins like TFAM (mitochondrial transcription factor A), but this protection is weak, exposing it to a high level of damage, especially from reactive oxygen species (ROS) generated in close proximity during electron transport chain activity. Despite some base excision repair mechanisms, mitochondria lack nucleotide excision repair and mismatch repair, resulting in a ten-fold higher mutation rate in mtDNA than nuclear DNA. MtDNA replication is distinct in its replication mechanism, independent of the cell cycle and carried out by DNA polymerase gamma (Poly γ), which is prone to errors and leads to point mutations and deletions with age. MtDNA encodes proteins directly involved in ATP production, and OXPHOS subunit disruption impairs energy metabolism, increases ROS production, and triggers apoptotic pathways, which are essential to cellular aging and tissue degeneration. Brain, heart, and skeletal muscle, which use more energy, have more mtDNA mutations and deletions, which correlate with functional decrease with age. Importantly, mtDNA copy number fluctuates in response to stress, age, and disease, and both depletion and uncontrolled expansion have been linked to pathological states, highlighting its potential as a mitochondrial health diagnostic. Sequencing technologies have revealed a variety of mtDNA mutations, including point mutations, large-scale deletions, duplications, and copy number variations, many of which are found at low heteroplasmic levels in young people but expand clonally with age, causing mosaic mitochondrial dysfunction across tissues. The maternal inheritance pattern of mtDNA allows pathogenic mutations to pass from mother to child, resulting in inherited mitochondrial diseases that often manifest as neuromuscular disorders, but somatic mutations accumulate over time and appear to be a stronger predictor of functional decline in aging. In addition to bioenergetics, damaged mtDNA fragments released into the cytoplasm or extracellular space can activate innate immune responses and contribute to chronic inflammation, a phenomenon increasingly known as “inflammaging.” Maternal inheritance, high copy number and heteroplasmy, lack of protective histones, elevated mutation rate, limited repair capacity, and essential role in energy metabolism make mtDNA a key player in cellular homeostasis and aging biology. Understanding these traits helps explain how mtDNA mutations accumulate, how they affect cellular function, and why they are such a key target for therapies to promote healthy aging and prevent age-related illnesses.



Mitochondrial DNA (mtDNA) is a small, circular genome located within the mitochondria, distinct from the linear DNA found in the cell nucleus. In humans, mtDNA consists of approximately 16,569 base pairs and encodes 37 genes essential for mitochondrial function, including 13 proteins involved in oxidative phosphorylation, along with transfer RNAs (tRNAs) and ribosomal RNAs (rRNAs). These genes are crucial for energy production, as mitochondria are responsible for generating adenosine triphosphate (ATP), the primary energy currency of the cell.

One of the most unique features of mtDNA is its maternal inheritance. Unlike nuclear DNA, which is inherited from both parents, mtDNA is almost exclusively passed down from the mother because the mitochondria in sperm are typically destroyed after fertilization. This characteristic makes mtDNA particularly useful in evolutionary biology and ancestry studies. Another distinctive aspect is the high mutation rate of mtDNA. Due to its close proximity to the electron transport chain and limited DNA repair mechanisms, mtDNA is more susceptible to damage from reactive oxygen species (ROS). This leads to a faster accumulation of mutations compared to nuclear DNA, which has important implications for aging and mitochondrial diseases. mtDNA also exhibits heteroplasmy, meaning that a single cell can contain a mixture of normal and mutated mitochondrial genomes. The proportion of mutated mtDNA can influence the severity of mitochondrial dysfunction and disease expression. Additionally, mtDNA lacks protective histone proteins and has a compact structure with little non-coding DNA, making it more exposed to environmental and metabolic damage.

mtDNA Mutations and Cellular Aging

Increasing evidence shows that mitochondrial genome instability disrupts cellular homeostasis, accelerates senescence, and causes tissue functional decline. This link is based on mitochondria's role in oxidative phosphorylation (OXPHOS), which requires mtDNA-encoded proteins that comprise key respiratory chain complex subunits. When mtDNA mutations accumulate, they impede complex assembly and efficiency, reducing ATP synthesis, electron leakage, and increase ROS. This cycle worsens mitochondrial dysfunction and cellular stress as ROS produce mtDNA mutations. Cellular aging results from these alterations through numerous interrelated pathways. Cells are more susceptible to stress and less able to maintain homeostasis due to energy shortages caused by defective OXPHOS, which impairs biosynthesis, repair, and signaling. ROS-induced damage to proteins, lipids, and nucleic acids

increases molecular deterioration, while mitochondrial failure activates intrinsic apoptotic pathways, increasing cell death in energy-intensive tissues like the heart, brain, and skeletal muscle. Moreover, mtDNA mutations activate cellular senescence programs, which cause cells to permanently exit the cell cycle while remaining metabolically active and secreting pro-inflammatory cytokines, chemokines, and growth factors. This pro-inflammatory milieu hinders tissue regeneration and increases systemic low-grade inflammation, known as “inflammaging,” which is increasingly recognized as a characteristic of aging and a cause of age-related diseases. Heteroplasmic mtDNA mutations complicate matters because the ratio of mutant to wild-type genomes in a cell defines the clinically significant malfunction threshold. Mutant mtDNA can clonally grow in some cells as people age, causing a mosaic pattern of mitochondrial failure across tissues, with some cells totally functional and others significantly affected. It may explain why aging affects individuals and tissues differently and causes patchy decrease in aged organs, such as isolated impairments in skeletal muscle fibers or neurons. Experimental evidence clearly suggests mtDNA mutations cause cellular aging. Mice lacking proofreading-deficient DNA polymerase gamma (Poly), responsible for mtDNA replication, show increased mutations leading to premature aging phenotypes like osteoporosis, anemia, reduced fertility, hair loss, and shorter lifespans, linking mtDNA instability to organismal aging. Human studies also show higher mtDNA deletions and point mutations in aged tissues, especially in post-mitotic cells like neurons and muscle fibers, where cell division cannot mitigate cumulative damage. Sarcopenia, cognitive decline, and cardiovascular aging are linked to mtDNA mutation-induced respiratory chain deficits in these organs. MtDNA mutations also affect mitochondrial activity in hematopoietic and mesenchymal stem cells, limiting their ability to self-renew and differentiate and aging organisms' regenerative capacity. Impact on cellular signaling and nuclear-mitochondrial communication is another important relationship between mtDNA mutations and aging. Damage-associated molecular patterns (DAMPs) from dysfunctional mitochondria activate innate immune pathways like the cGAS-STING axis and cause chronic inflammation. In addition, mitochondrial dysfunction alters NAD⁺/NADH balance and sirtuin activity, affecting epigenetic control and increasing nuclear aging.

Conclusion

Mitochondrial DNA mutations are a hallmark of cellular damage and a driver of the steady loss in physiological function that defines aging. Due to its proximity to reactive oxygen species generated by oxidative phosphorylation, lack of protective histones, and limited repair capacity, mtDNA has a much higher mutation rate and becomes more consequential over time. Mutations weaken mitochondrial respiratory chain complexes, reduce ATP synthesis, and increase reactive oxygen species formation, creating a loop of oxidative stress and mitochondrial malfunction that worsens cellular and tissue damage. Reduced energy availability, increased molecular damage, cellular senescence pathways, apoptosis, and chronic inflammation all contribute to “inflammaging.” Heteroplasmy, where mutant and wild-type mtDNA coexist in the same cell, is crucial to this process because clonal expansion of mutations can cause cell and tissue dysfunction, explaining the mosaic nature of organ aging phenotypes. Experiments on proofreading-deficient Poly mice show that excessive mtDNA

mutation burdens accelerate aging and cause premature phenotypes, mirroring human age-associated decline. Human studies also show that mtDNA deletions and point mutations in post-mitotic tissues, including brain, heart, and skeletal muscle, are linked to cognitive decline, sarcopenia, and cardiovascularitis. In addition to bioenergetics, fragmented mtDNA released into the cytosol can activate innate immune responses and perpetuate chronic inflammation, linking mitochondrial dysfunction with immune aging. Importantly, the discovery that mtDNA mutations are reversible contributors to aging has spurred the development of therapies that preserve mitochondrial integrity, reduce oxidative damage, and restore energy metabolism. In experimental animals, regular exercise, calorie restriction, and nutritional manipulation promote mitochondrial biogenesis and function, lowering mtDNA mutations and increasing healthspan. Pharmaceuticals like mitochondria-targeted antioxidants like MitoQ and SkQ1, sirtuin activators, and AMPK agonists have shown promise in mitigating ROS-induced damage and improving tissue function, while cutting-edge genetic approaches like mitochondrial gene editing and mitochondrial replacement therapies may directly correct or circumvent pathogenic mtDNA mutations. These efforts show that mitochondrial health can delay aging and prevent or treat age-related illnesses. Many obstacles remain, including technological difficulties in modifying the mitochondrial genome, heteroplasmic dynamics, and the need to determine the causal vs consequential role of mtDNA mutations in aging. Germline mitochondrial therapies, including mitochondrial replacement therapy, present ethical problems about heredity and long-term safety. Despite these challenges, current evidence supports a model in which mtDNA mutations synergistically interact with genomic instability, telomere attrition, and deregulated nutrient sensing to reinforce the multifactorial nature of aging. The research of mtDNA mutations has increased our mechanistic understanding of aging and opened practical intervention paths, making mitochondrial medicine a viable geroscience frontier. Integrating advances in molecular biology, genetics, pharmacology, and lifestyle research and approaching mitochondrial dysfunction with scientific rigor and ethical responsibility may help extend human life and reduce age-related diseases. In conclusion, mitochondrial DNA mutations are both a reflection and an active participant in aging, making them a key topic for study into the molecular basis of aging and interventions to address its causes. Their study emphasizes mitochondria's importance in cellular and organismal health and suggests a technique to make aging manageable and changeable.

Bibliography

- Alexeyev, M., Shokolenko, I., Wilson, G., & LeDoux, S. (2013). The maintenance of mitochondrial DNA integrity—critical analysis and update. *Cold Spring Harbor Perspectives in Biology*, 5(5), a012641. <https://doi.org/10.1101/cshperspect.a012641>
- Barja, G., & Herrero, A. (2000). Oxidative damage to mitochondrial DNA is inversely related to maximum life span in the heart and brain of mammals. *FASEB Journal*, 14(2), 312–318. <https://doi.org/10.1096/fasebj.14.2.312>
- Bratic, A., & Larsson, N. G. (2013). The role of mitochondria in aging. *Journal of Clinical Investigation*, 123(3), 951–957. <https://doi.org/10.1172/JCI64125>

- Greaves, L. C., & Turnbull, D. M. (2009). Mitochondrial DNA mutations and ageing. *Biochimica et Biophysica Acta (BBA) - Bioenergetics*, 1790(10), 1015–1020. <https://doi.org/10.1016/j.bbagen.2009.04.018>
- Harman, D. (1972). The biologic clock: The mitochondria? *Journal of the American Geriatrics Society*, 20(4), 145–147. <https://doi.org/10.1111/j.1532-5415.1972.tb00787.x>
- Kauppila, T. E. S., Kauppila, J. H. K., & Larsson, N. G. (2017). Mammalian mitochondria and aging: An update. *Cell Metabolism*, 25(1), 57–71. <https://doi.org/10.1016/j.cmet.2016.09.017>
- Krishnan, K. J., Reeve, A. K., Samuels, D. C., Chinnery, P. F., Blackwood, J. K., Taylor, R. W., ... & Turnbull, D. M. (2008). What causes mitochondrial DNA deletions in human cells? *Nature Genetics*, 40(3), 275–279. <https://doi.org/10.1038/ng.f.94>
- Kujoth, G. C., Hiona, A., Pugh, T. D., Someya, S., Panzer, K., Wohlgemuth, S. E., ... & Prolla, T. A. (2005). Mitochondrial DNA mutations, oxidative stress, and apoptosis in mammalian aging. *Science*, 309(5733), 481–484. <https://doi.org/10.1126/science.1112125>
- Larsson, N. G. (2010). Somatic mitochondrial DNA mutations in mammalian aging. *Annual Review of Biochemistry*, 79, 683–706. <https://doi.org/10.1146/annurev-biochem-060408-093701>
- Nunnari, J., & Suomalainen, A. (2012). Mitochondria: In sickness and in health. *Cell*, 148(6), 1145–1159. <https://doi.org/10.1016/j.cell.2012.02.035>
- Payne, B. A. I., & Chinnery, P. F. (2015). Mitochondrial dysfunction in aging: Much progress but many unresolved questions. *Biochimica et Biophysica Acta (BBA) - Bioenergetics*, 1847(11), 1347–1353. <https://doi.org/10.1016/j.bbabi.2015.05.022>
- Shokolenko, I. N., Wilson, G. L., & Alexeyev, M. F. (2013). Aging: A mitochondrial DNA perspective, critical analysis, and update. *Antioxidants & Redox Signaling*, 19(9), 904–917. <https://doi.org/10.1089/ars.2012.4805>
- Trifunovic, A., Wredenberg, A., Falkenberg, M., Spelbrink, J. N., Rovio, A. T., Bruder, C. E., ... & Larsson, N. G. (2004). Premature ageing in mice expressing defective mitochondrial DNA polymerase. *Nature*, 429(6990), 417–423. <https://doi.org/10.1038/nature02517>
- Wallace, D. C. (2005). A mitochondrial paradigm of metabolic and degenerative diseases, aging, and cancer: A dawn for evolutionary medicine. *Annual Review of Genetics*, 39, 359–407. <https://doi.org/10.1146/annurev.genet.39.110304.095751>
- Yusoff, A. A. M., Khair, S. Z., & Khairuddin, S. (2021). Mitochondrial DNA mutations and aging: Recent developments and future perspectives. *Frontiers in Aging*, 2, 656961. <https://doi.org/10.3389/fragi.2021.656961>