



Energy transduction in mitochondria

Organelle in eukaryotic cells responsible for respiration Two mitochondria from mammalian lung tissue displaying their matrix and membranes as shown by electron microscopy Cell biologyAnimal cell diagramComponents of a typical animal cell. Nucleous Ribosome (dots as part of 5) Vesicle Rough endoplasmic reticulum Golgi apparatus (or, Golgi body) Cytoskeleton Smooth endoplasmic reticulum Mitochondrion (/maitə'kondriən/,[1] plural mitochondria) is a double membrane-bound organelle found in most eukaryotic organisms. Mitochondria generate most of the cell's supply of adenosine triphosphate (ATP), used as a source of chemical energy.[2] Mitochondria were first discovered by Kolliker (1880 CE) in the voluntary muscles of the cell, first coined by Philip Siekevitz in a 1957 article of the same name.[3] Some cells in some multicellular organisms lack mitochondria (for example, mature mammalian red blood cells). A number of unicellular organisms, such as microsporidia, parabasalids, and diplomonads, have reduced or transformed their mitochondria,[5] and one multicellular organism, Henneguya salminicola, is known to have retained mitochondrial genome.[5][6][7] Mitochondria are commonly between 0.75 and 3 µm² in area[8] but they vary considerably in size and structure. Unless specifically stained, they are not visible. In addition to supplying cellular energy, mitochondria are involved in other tasks, such as signaling, cellular differentiation, and cell growth.[9] Mitochondria biogenesis is in turn temporally coordinated with these cellular processes.[10][11] Mitochondria have been implicated in several human diseases and conditions, such as mitochondrial disorders, [12] cardiac dysfunction, [13] heart failure [14] and autism. [15] The mitochondria in a cell can have more than 2000. [17] [18] The mitochondrion is composed of compartments that carry out specialized functions. These compartments or regions include the outer membrane, intermembrane space, inner membrane, intermembrane space, inner membrane, cristae and matrix. Although most of a cell's DNA is contained in the cell nucleus, the mitochondrion has its own genome ("mitogenome") that is substantially similar to bacterial genomes.[19] Mitochondrial proteins (proteins transcribed from mitochondria, [20] whereas in rats, 940 proteins have been reported. [21] The mitochondrial proteome is thought to be dynamically regulated. [22] Structure Simplified structure of a mitochondrion. Mitochondrion contains outer and proteins.[17] The two membranes have different shapes.[23] A mitochondrion contains outer and inner membranes have a number of different shapes.[23] A mitochondrion contains outer and proteins.[17] The two membranes have a number of different shapes.[23] A mitochondrion contains outer and proteins.[23] A mitochondrion contains outer and p mitochondrion: The outer mitochondrial membrane, The intermembrane space (the space between the outer and inner membrane), The inner membrane), and The matrix (space within the inner membrane), which is a fluid. Mitochondria have folding to increase surface area, which in turn increases ATP(Adenosine Tri Phosphate) production. Mitochondria stripped of their outer membrane are called mitoplasts. Outer membrane are called mitoplasts. Outer membrane (about 1:1 by weight). It contains large numbers of integral membrane proteins called porins. A major trafficking protein is the pore-forming voltage-dependent anion channel (VDAC). The VDAC is the primary transporter of nucleotides, ions and metabolites between the cytosol and the intermembrane space. [24][25] It is formed as a beta barrel that spans the outer membrane, similar to that in the gram-negative bacterial membrane.[26] Larger proteins can enter the mitochondrion if a signaling sequence at their N-terminus binds to a large multisubunit protein called translocase in the outer membrane. [27] Mitochondrial pro-proteins are imported through specialised translocation complexes. The outer membrane also contains enzymes include monoamine oxidase, rotenone-insensitive NADH-cytochrome c-reductase, kynurenine hydroxylase and fatty acid Co-A ligase. Disruption of the outer membrane permits proteins in the intermembrane space to leak into the cytosol, leading to cell death.[28] The mitochondrial outer membrane, in a structure called MAM (mitochondrial-associated ER-membrane). This is important in the ER-mitochondria calcium signaling and is involved in the transfer of lipids between the ER and mitochondria. [29] Outside the outer membrane space The mitochondrial intermembrane space is the space between the enter membrane. It is also known as perimitochondrial space. Because the outer membrane is freely permeable to small molecules, such as ions and sugars, in the intermembrane space is the same as in the cytosol.[17] However, large proteins must have a specific signaling sequence to be transported across the outer membrane, so the protein composition of this space is different from the protein composition of the cytosol. One protein that is localized to the intermembrane space in this way is cytochrome c.[28] Inner membrane Main article: Inner mitochondrial membrane contains proteins with three types of functions:[17] Those that perform the electron transport chain redox reactions ATP synthase, which generates ATP in the matrix Specific transport proteins that regulate metabolite passage into and out of the mitochondrial matrix. It contains more than 151 different polypeptides, and has a very high protein-to-phospholipid ratio (more than 3:1 by weight, which is about 1 protein for 15 phospholipids). The inner membrane is home to around 1/5 of the total protein in a mitochondrion.[30] Additionally, the inner membrane is rich in an unusual phospholipid, cardiolipin. This phospholipid was originally discovered in cow hearts in 1942, and is usually characteristic of mitochondrial and bacterial plasma membranes.[31] Cardiolipin contains four fatty acids rather than two, and may help to make the inner membrane impermeable.[17] Unlike the outer membrane, the inner membrane does not contain porins, and is highly impermeable to all molecules. Almost all ions and molecules require special membrane transporters to enter or exit the matrix. Proteins are ferried into the matrix via the translocase of the inner membrane (TIM) complex or via OXA1L.[27] In addition, there is a membrane potential across the inner membrane fusion is mediated by the action of the electron transport chain. Inner membrane fusion is mediated by the inner membrane (TIM) complex or via OXA1L.[27] In addition, there is a membrane fusion is mediated by the inner membrane fusion is mediated by the action of the electron transport chain. liver mitochondrion to demonstrate the likely 3D structure and relationship to the inner membrane Main article: Cristae The inner mitochondrial membrane is compartmentalized into numerous folds called cristae, which expand the surface area of the inner mitochondrial membrane is compartmentalized into numerous folds called cristae. the area of the inner membrane is about five times as large as the outer membrane. This ratio is variable and mitochondria from cells that have a greater demand for ATP, such as muscle cells, contain even more cristae. Mitochondria within the same cell can have substantially different crista-density, with the ones that are required to produce more energy having much more crista-membrane surface.[33] These folds are studded with small round bodies known as F1 particles or oxysomes.[34] Matrix The matrix is the space enclosed by the inner membrane. It contains about 2/3 of the total proteins in a mitochondrion.[17] The matrix is important in the production of ATP with the aid of the ATP synthase contained in the inner membrane. The matrix contains a highly concentrated mixture of hundreds of enzymes, the major functions include oxidation of pyruvate and fatty acids, and the citric acid cycle.[17] The DNA molecules are packaged into nucleoids by proteins, one of which is TFAM.[35] Function The most prominent roles of mitochondria are to produce the energy currency of the cell, ATP (i.e., phosphorylation of ADP), through respiration and to regulate cellular metabolism.[18] The central set of reactions involved in ATP production are collectively known as the citric acid cycle, or the Krebs cycle. However, the mitochondria is the production of ATP, as reflected by the large number of proteins in the inner membrane for this task. This is done by oxidizing the major products of glucose: pyruvate, and NADH, which are produced in the cytosol.[18] This type of cellular respiration, is dependent on the presence of oxygen, which provides most of the energy released.[36] When oxygen is limited, the glycolytic products will be metabolized by anaerobic fermentation, a process that is independent of the mitochondria.[18] The production of ATP from glucose and oxygen has an approximately 13-times higher yield during aerobic respiration compared to fermentation.[37] Plant mitochondria can also produce a limited amount of ATP either by breaking the sugar produced during photosynthesis or without oxygen by using the alternate substrate nitrite.[38] ADP returns via the same route. Pyruvate and the citric acid cycle Pyruvate and the citric acid cycle Pyruvate and the citric acid cycle Pyruvate molecules produced by glycolysis are actively transported across the inner mitochondrial membrane, and into the matrix where they can either be oxidized and combined with coenzyme A to form CO2, acetyl-CoA, and NADH,[18] or they can be carboxylated (by pyruvate carboxylated (by pyruvate carboxylated) to form oxaloacetate. increasing the cycle's capacity to metabolize acetyl-CoA when the tissue's energy needs (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle,
all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activity.[40] In the citric acid cycle, all the intermediates (e.g., in muscle) are suddenly increased by activi these intermediates to the mitochondrion therefore means that the additional amount is retained within the cycle, increasing all the other intermediates as one is converted into the other. Hence, the addition of any one of them to the cycle has an anaplerotic effect, and its removal has a cataplerotic effect. These anaplerotic reactions will, during the course of the cycle, increase or decrease the amount of oxaloacetate availability of ATP to the cell.[40] Acetyl-CoA, on the other hand, derived from pyruvate oxidation, or from the availability of ATP to the cell.[40] Acetyl-CoA, on the other hand, derived from pyruvate oxidation, or from the availability of ATP to the cell.[40] Acetyl-CoA, on the other hand, derived from pyruvate oxidation, or from the availability of ATP to the cell.[40] Acetyl-CoA, on the other hand, derived from pyruvate oxidation, or from the cell.[40] Acetyl-CoA, on the other hand, derived from pyruvate oxidation, or from the cell.[40] Acetyl-CoA, on the other hand, derived from pyruvate oxidation, or from the cell.[40] Acetyl-CoA, on the other hand, derived from pyruvate oxidation, or from the cell.[40] Acetyl-CoA, on the other hand, derived from pyruvate oxidation, or from the cell.[40] Acetyl-CoA, on the other hand, derived from pyruvate oxidation, or from the cell.[40] Acetyl-CoA, on the other hand, derived from pyruvate oxidation, or from the cell.[40] Acetyl-CoA, on the cell.[beta-oxidation of fatty acids, is the only fuel to enter the citric acid cycle. With each turn of the cycle one molecule of acetyl-CoA is consumed for every released captured in the form of ATP.[40] In the liver, the carboxylation of cytosolic pyruvate into intra-mitochondrial oxaloacetate is an early step in the gluconeogenic pathway, which converts lactate and de-aminated alanine into glucose,[18][40] under the influence of high levels of glucagon and/or epinephrine in the blood.[40] Here, the addition of oxaloacetate to the mitochondrion does not have a net anaplerotic effect, as another citric acid cycle intermediate (malate) is immediately converted into glucose, in a process that is almost the reverse of glycolysis.[40] The enzymes of the citric acid cycle are located in the mitochondrial matrix, with the exception of succinate dehydrogenase, which is bound to the inner mitochondrial membrane as part of Complex II.[41] The citric acid cycle oxidizes the acetyl-CoA to carbon dioxide, and, in the process, produces reduced cofactors (three molecules of NADH and one molecule of FADH2) that are a source of electrons for the electron transport chain, and a molecule of GTP (that is readily converted to an ATP).[18] NADH and FADH2: the electron transport chain in the mitochondrial intermembrane space The electron transport chain and Oxidative phosphorylation Electron transport chain and FADH2 are transferred to oxygen (O2), an energy-rich molecule, [36] and hydrogen (protons) in several steps via the electron transport chain. NADH and FADH2 molecules are produced in the cytoplasm by glycolysis. Reducing equivalents from the cytoplasm can be imported via the malate-aspartate shuttle system of antiporter proteins or feed into the electron transport chain using a glycerol phosphate shuttle.[18] Protein complexes in the inner membrane (NADH dehydrogenase (ubiquinone), cytochrome c oxidase) perform the transfer, and the incremental release of energy is used to pump protons (H+) into the intermembrane space. This process is efficient, but a small percentage of electrons may prematurely reduce oxygen, forming reactive oxygen, forming reactive oxygen, forming reactive oxygen species such as superoxide.[18] This can cause oxidative stress in the mitochondria and may contribute to the decline in mitochondrial function associated with the aging process.[42] As the proton concentration increases in the intermembrane space, a strong electrochemical gradient is established across the inner membrane. The protons can return to the matrix through the ATP synthase complex, and their potential energy is used to synthesize ATP from ADP and inorganic phosphate (Pi).[18] This process is called chemiosmosis, and was first described by Peter Mitchell,[43][44] who was awarded to Paul D. Boyer and John E. Walker for their clarification of the working mechanism of ATP synthase.[45] Heat production Under certain conditions, protons can re-enter the mitochondrial matrix without contributing to ATP synthesis. This process is known as proton leak or mitochondrial uncoupling and is due to the facilitated diffusion of protons into the matrix. The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The process results in the unharnessed potential energy of the proton electrochemical gradient being released as heat.[18] The proc channel called thermogenin, or UCP1.[46] Thermogenin is primarily found in brown adipose tissue, or brown fat, and is responsible for non-shivering thermogenesis. Brown adipose tissue is found in mammals, and is at its highest levels in early life and in hibernating animals. In humans, brown adipose tissue is present at birth and decreases with age [46] Storage of calcium ions Transmission electron micrograph of a chondrocyte, stained for calcium, showing its nucleus (N) and mitochondria (M). The concentrations of free calcium in the cell can regulate an array of reactions and is important for signal transduction in the cell. Mitochondria can transiently store calcium, a contributing process for the cell's homeostasis of calcium.[47] [48] Their ability to rapidly take in calcium for later release makes them good "cytosolic buffers" for calcium.[52] and there is a significant storage site of calcium.[53] The endoplasmic reticulum (ER) is the most significant storage site of calcium.[53] The storage site of calcium.[53] The endoplasmic reticulum (ER) is the most significant storage site of calcium.[53] The storage site of calcium.[54] The storage site calcium is taken up into the matrix by the mitochondrial membrane [54] It is primarily driven by the mitochondrial membrane potential.[48] Release of this calcium-induced-calcium-release" pathways.[54] This can initiate calcium spikes or calcium waves with large changes in the membrane potential. These can activate a series of second messenger system proteins that can coordinate processes such as neurotransmitter release in nerve cells. [55] Ca2+ influx to the mitochondrial matrix has recently been implicated as a mechanism to regulate respiratory bioenergetics by allowing the electrochemical potential
across the membrane to transiently "pulse" from $\Delta\Psi$ -dominated to pH-dominated to energy metabolism. Mitochondrial matrix calcium levels can reach the tens of micromolar levels, which is necessary for the activation of isocitrate dehydrogenase, one of the Krebs cycle.[57] Cellular proliferation regulation The relationship between cellular proliferation and mitochondria has been investigated. Tumor cells require ample ATP to synthesize bioactive compounds such as lipids, proteins, and nucleotides for rapid proliferation.[59] Interference with OxPhos cause cell cycle arrest suggesting that mitochondria play a role in cell proliferation.[59] Mitochondrial ATP production is also vital for cell division and differentiation, and cellular architecture.[61][62][63] ATP levels differ at various stages of the cell cycle suggesting that there is a relationship between the abundance of ATP and the cell's ability to enter a new cell cycle.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial derived ATP.[64] The variation in ATP levels at different stages of the cell cycle support the hypothesis that mitochondrial deriv Although the specific mechanisms between mitochondria and the cell cycle regulation is not well understood, studies have shown that low energy capability before committing to another round of cell division.[9] Additional functions Mitochondria play a central role in many other metabolic tasks, such as: Signaling through mitochondrial reactive oxygen species[65] Regulation of the membrane potential[18] Apoptosis-programmed cell death[66] Calcium signaling (including calcium-evoked apoptosis)[67] Regulation of cellular metabolism[9] Certain heme synthesis reactions[68] (see also: porphyrin) Steroid synthesis.[49] Hormonal signaling [69] Mitochondria are sensitive and responsive to hormones, in part by the action of mitochondrial estrogen receptors (mtERs). These receptors (mtERs). These receptors have been found in various tissues and cell types, including brain [70] and heart [71] Immune signaling [72] Neuronal mitochondria also contribute to cellular quality control by reporting neuronal status towards microglia through specialised somatic-junctions.[73] Some mitochondrial functions are performed only in specific types of cells. For example, mitochondria in liver cells contain enzymes that allow them to detoxify ammonia, a waste product of protein metabolism. A mutation in the genes regulating any of these functions can result in mitochondrial diseases. Organization and distribution Typical mitochondria (and related structures) are found in all eukaryotes (except two-the Oxymonad Monocercomonoides and Henneguya salminicola).[5][6][7][74] Although commonly depicted as bean-like structures they form a highly dynamic network in the majority of cells where they constantly undergo fission and fusion. The population of all the mitochondria vary in number and location according to cell type. A single mitochondrion is often found in unicellular organisms, while human liver cells have about 1000-2000 mitochondria per cell, making up 1/5 of the cell volume.[17] The mitochondrial content of otherwise similar cells can vary substantially in size and membrane potential,[76] with differences arising from sources including uneven partitioning at cell divisions, leading to extrinsic differences in ATP levels and downstream cellular processes.[77] The mitochondria can be found nestled between myofibrils of muscle or wrapped around the sperm flagellum.[17] Often, they form a complex 3D branching network inside the cell with the cytoskeleton. The association with the cytoskeleton determines mitochondrial shape, which can affect the function as well:[78] different structures of the mitochondrial network may afford the population a variety of physical, chemical, and signalling advantages or disadvantages.[79] Mitochondria in cells are always distributed along microtubules and the distribution of these organelles is also correlated with the endoplasmic reticulum.[80] Recent evidence suggests that vimentin, one of the components of the cytoskeleton, is also critical to the associated ER membrane (MAM) The mitochondria-associated ER membrane (MAM) Main article: Mitochondria-associated ER membrane (MAM) is another structural element that is increasingly recognized for its critical role in cellular physiology and homeostasis. Once considered a technical snag in cell fractionation techniques, the alleged ER vesicle contaminants that invariably appeared in the mitochondrial fraction have been re-identified as membranous structures derived from the MAM—the interface between mitochondria and the ER.[82] Physical coupling between these two organelles had previously been observed in electron micrographs and has more recently been probed with fluorescence microscopy.[82] Such studies estimate that at the MAM, which may comprise up to 20% of the mitochondrial outer membrane, the ER and mitochondria are separated by a mere 10-25 nm and held together by protein tethering complexes.[82][29][83] Purified MAM from subcellular fractionation is enriched in enzymes involved in phospholipid exchange, in addition to channels associated with Ca2+ signaling.[82][83] These hints of a prominent role for the MAM in the regulation of cellular lipid stores and signal transduction have been borne out, with significant implications for mitochondrial associated cellular phenomena, as discussed below. Not only has the MAM provided insight into the mechanistic basis underlying such physiological processes as intrinsic apoptosis and the propagation of calcium signaling, but it also favors a more refined view of the mitochondria. Though often seen as static, isolated 'powerhouses' hijacked for cellular metabolism through an ancient endosymbiotic event, the evolution of the MAM underscores the extent to which mitochondria have been integrated into overall cellular physical and functional coupling to the endomembrane system. Phospholipid transfer The MAM is enriched in enzymes involved in lipid biosynthesis, such as phosphatidylserine synthase on the ER face and phosphatidylserine decarboxylase on the mitochondrial face.[84][85] Because mitochondria are not only of phospholipids for membrane integrity.[86][87] But mitochondria are not only a destination for the phospholipids they finish synthesis of; rather, this organelle also plays a role in inter-organelle trafficking of the intermediates and products of phospholipid biosynthetic pathways, ceramide and cholesterol metabolism, and glycosphingolipid anabolism. [85][87] Such trafficking capacity depends on the MAM, which has been shown to facilitate transfer of lipid intermediates between organelles.[84] In contrast to the standard vesicular mechanism of lipid transfer, evidence indicates that the physical proximity of the ER and mitochondrial membranes at the MAM allows for lipid flipping between opposed bilayers.[87] Despite this unusual and seemingly energetically unfavorable mechanism, such transport does not require ATP.[87] Instead, in yeast, it has been shown to be dependent on a multiprotein tethering structure directly mediates lipid transfer or is required to keep the membranes in sufficiently close proximity to lower the energy barrier for lipid flipping.[87][88] The MAM may also be part of the secretory pathway, in addition to its role in intracellular lipid trafficking. In particular, the MAM may also be part of the secretory pathway, in addition to its role in intracellular lipid trafficking. and secretion.[85][89] The MAM thus serves as a critical metabolic and trafficking hub in lipid metabolism. Calcium signaling A critical role for the mitochondria was widely accepted, in part because the low affinity of Ca2+ channels localized to the outer mitochondrial membrane seemed to contradict this organelle's purported responsiveness to changes in intracellular Ca2+ flux.[82][52] But the presence of the MAM resolves this apparent contradiction: the close physical association between the two organelles results in Ca2+ microdomains at contact points that facilitate efficient Ca2+ transmission from the ER to the
mitochondria.[82] Transmission occurs in response to so-called "Ca2+ puffs" generated by spontaneous clustering and activation of IP3R, a canonical ER membrane Ca2+ channel.[82][29] The fate of these puffs—in particular, whether they remain restricted to isolated locales or integrated into Ca2+ waves for propagation throughout the cell—is determined in large part by MAM dynamics. Although reuptake of Ca2+ by the ER (concomitant with its release) modulates the intensity of the puffs, thus insulating mitochondria to a certain degree from high Ca2+ exposure, the MAM often serves as a firewall that essentially buffers Ca2+ puffs by acting as a sink into which free ions released into the cytosol can be funneled.[82][90][91] This Ca2+ tunneling occurs through the low-affinity Ca2+ receptor VDAC1, which recently has been shown to be physically tethered to the IP3R clusters on the ER membrane and enriched at the MAM.[82][29][92] The ability of mitochondria to serve as a Ca2+ sink is a result of the electrochemical gradient generated during oxidative phosphorylation, which makes tunneling of the cation an exergonic process.[92] Normal, mild calcium influx from cytosol into the mitochondrial matrix causes transient depolarization that is corrected by pumping out protons. But transmission of Ca2+ is not unidirectional; rather, it is a two-way street.[52] The properties of the Ca2+ pump SERCA and the channel IP3R present on the ER membrane facilitate feedback regulation coordinated by MAM function. In particular, the clearance of Ca2+ by the MAM allows for spatio-temporal patterning of Ca2+ signaling because Ca2+ alters IP3R activity in a biphasic manner.[82] SERCA is likewise affected by mitochondrial feedback: uptake of Ca2+ by the MAM stimulates ATP production, thus providing energy that enables SERCA to reload the ER with Ca2+ for continued Ca2+ efflux at the MAM.[90][92] Thus, the MAM is not a passive buffer for Ca2+ puffs; rather it helps modulate further Ca2+ signaling through feedback loops that affect ER dynamics. Regulating through feedback loops that affect ER dynamics. ER release of Ca2+ at the MAM is especially critical because only a certain window of Ca2+ uptake sustains the mitochondria, and consequently the cell, at homeostasis. Sufficient intraorganelle Ca2+ signaling is required to stimulate metabolism by activating dehydrogenase enzymes critical to flux through the citric acid cycle.[93][94] However, once Ca2+ signaling in the mitochondria passes a certain threshold, it stimulates the intrinsic pathway of apoptosis in part by collapsing the role of pro- and anti-apoptotic factors support this model; for example, the anti-apoptotic factor Bcl-2 has been shown to interact with IP3Rs to reduce Ca2+ filling of the ER, leading to reduced efflux at the MAM and preventing collapse of the mitochondrial membrane potential post-apoptotic stimuli.[82] Given the need for such fine regulation of Ca2+ signaling, it is perhaps unsurprising that dysregulated mitochondrial Ca2+ has been implicated in several neurodegenerative diseases, while the catalogue of tumor suppressors includes a few that are enriched at the MAM.[92] Molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of the molecular basis for tethering Recent advances in the identification of tethering Recent advances i structural functions. In yeast, ERMES, a multiprotein complex of interacting ER- and mitochondrial-resident membrane proteins, is required for lipid transfer at the MAM and exemplifies this principle. One of its components, for example, is also a constituent of the protein complex required for insertion of transmembrane beta-barrel proteins into the lipid bilayer.[87] However, a homologue of the ERMES complex has not yet been identified in mammalian cells. Other proteins implicated in scaffolding likewise have functions independent of structural tethering at the MAM; for example, ER-resident and mitochondrial-resident and mitochondrial organelle contact sites, although mitofusins were first identified for their role in fission and fusion events between individual mitochondria. [82] Glucose-related protein 75 (grp75) is another dual-function protein. In addition to the matrix pool of grp75, a portion serves as a chaperone that physically links the mitochondrial and ER Ca2+ channels VDAC and IP3R for efficient Ca2+ transmission at the MAM.[82][29] Another potential tether is Sigma-1R, a non-opioid receptor whose stabilization of ER-resident IP3R may preserve communication at the MAM is a critical signaling, metabolic, and trafficking hub in the cell that allows for the integration of ER and mitochondrial physiology. Coupling between these organelles is not simply structural but functional view. of this organelle as a static, isolated unit appropriated for its metabolic capacity by the cell.[97] Instead, this mitochondrial-ER interface emphasizes the integration of the mitochondria, the product of an endosymbiotic event, into diverse cellular processes. Recently it has also been shown, that mitochondria and MAM-s in neurons are anchored to specialised intercellular communication sites (so called somatic-junctions). Microglial processes monitor and protect neuronal functions at these sites, and MAM-s are supposed to have an important role in this type of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution Main article: Endosymbiotic theory There are two hypotheses about the origin of cellular quality-control.[73] Origin and evolution (figure are two hypotheses) about the origin of cellular quality-control.[73] Origin and evolution (figure are two hypotheses) about the origin of cellular quality-control.[73] Origin are two hypotheses about the origin of cellular quality-control.[73] Origin are two hypotheses about the origin of cellular quality-control.[73] Origin mitochondria: endosymbiotic and autogenous. The endosymbiotic hypothesis suggests that mitochondria were originally prokaryotic cells; they became endosymbionts living inside the eukaryote. [98] In the autogenous hypothesis, mitochondria were born by splitting off a portion of DNA from the nucleus of the eukaryotic cell at the time of divergence with the prokaryotes; this DNA portion would have been enclosed by membranes, which could not be crossed by proteins. Since mitochondria have many features in common with bacteria, the endosymbiotic hypothesis is more widely accepted.[98][99] A mitochondrion contains DNA, which is organized as several copies of a single, usually circular chromosome contains genes for redox proteins, such as those of the respiratory chain. The mitochondrial chromosome contains of the respiratory chain. ribosomes, and the 22 tRNAs necessary for the translation of mRNAs into protein. The circular structure is also found in prokaryotes. The proto-mitochondrion was formed at the same time or after the nucleus, remains controversial.[102] For example, it has been suggested that the SAR11 clade of bacteria shares a relatively recent common ancestor with the mitochondria,[103] while phylogenomic analyses indicate that mitochondria evolved from a proteobacteria lineage that is closely related to or a
member of alphaproteobacteria.[104][105] Schematic ribosomal RNA phylogeny of Alphaproteobacteria Magnetococcidae Magnetococcus marinus Caulobacteriaee, Hyphomicrobiales, etc. Holosporales Rickettsidae Pelagibacteraceae Pelagibacteraceae Pelagibacteraceae Subgroup Ib, II, IIIa, IIIb, IV and V Rickettsiales Proto-mitochondria Anaplasmataceae Ehrlichia Anaplasma Wolbachia Neorickettsia Midichloriaceae Midichloria Rickettsiaceae Rickettsia Orientia The cladogram of Rickettsidae has been inferred by Ferla et al. [106] from the comparison of 16S + 23Sribosomal RNA sequences. The ribosomes coded for by the mitochondrial DNA are similar to those from bacteria in size and structure.[107] They closely resemble the bacterial 70S ribosome and not the 80S cytoplasmic ribosomes, which are coded for by nuclear DNA. The endosymbiotic relationship of mitochondria with their host cells was popularized by Lynn Margulis.[108] The endosymbiotic hypothesis suggests that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cells that mitochondria descended from bacteria to conduct respiration in host cell considerable evolutionary advantage. This symbiotic relationship probably developed 1.7 to 2 billion years ago.[109][110] A few groups of unicellular eukaryotes have only vestigial mitochondria or derived structures: the microsporidians, metamonads, and archamoebae.[111] These groups appear as the most primitive eukaryotes on phylogenetic trees constructed using rRNA information, which once suggested that they appeared before the origin of mitochondria. However, this is now known to be an artifact of long-branch attraction—they are derived groups and retain genes or organelles derived groups and retain genes or organelles derived from mitochondria. and related organelles as found in some loricifera (e. g. Spinoloricus)[112][113] and myxozoa (e. g. Henneguya zschokkei) are together classified as MROs, mitochondrial functions seem to be carried out by cytoplasmic proteins now.[116] Genome The circular 16,569 bp human mitochondrial genome encoding 37 genes, i.e., 28 on the H-strand and 9 on the L-strand. Main article: Mitochondrial DNA Mitochondrial contain their own genome. The human mitochondrial genome is a circular DNA molecule of about 16 kilobases.[117] It encodes 37 genes: 13 for subunits of respiratory complexes I, III, IV and V, 22 for mitochondrial tRNA (for the 20 standard amino acids, plus an extra gene for leucine and serine), and 2 for rRNA.[117] One mitochondrial tRNA (for the 20 standard amino acids, plus an extra gene for leucine and serine), and 2 for rRNA.[117] One mitochondrial tRNA (for the 20 standard amino acids, plus an extra gene for leucine and serine), and 2 for rRNA.[117] One mitochondrial tRNA (for the 20 standard amino acids, plus an extra gene for leucine and serine), and 2 for rRNA.[117] One mitochondrial tRNA (for the 20 standard amino acids, plus an extra gene for leucine and serine), and 2 for rRNA.[118] As in prokaryotes, there is a very high proportion of coding DNA and an absence of repeats. genes are transcribed as multigenic transcripts, which are cleaved and polyadenylated to yield mature mRNAs. Most proteins are imported into the mitochondrial function are encoded by the nucleus and the mitochondrial genome differs between species. Most mitochondrial genomes; [119] however, introns have been observed in some eukaryotic mitochondrial DNA, [121] such as that of yeast[122] and protists, [123] including Dictyostelium discoideum.[124] Between protein-coding regions, tRNAs are present. Mitochondrial tRNAs have been found in the nuclear tRNAs but lookalikes of mitochondrial tRNAs have been found in the nuclear chromosome that is approximately 16 kb long and has 37 genes. The genes, while highly conserved, may vary in location. Curiously, this pattern is also found in other sucking lice, but not in chewing lice. Recombination has been shown to occur between the minichromosomes. Alternative genetic code in mitochondria[17] Organism Codon Standard Mitochondria[17] Organism Standard Mitochondria[17] Organism Standard Mitochondria[17] Organi Leucine Threonine All of the above AUA Isoleucine Methionine UGA Stop codon Tryptophan While slight variations on the standard genetic code had been predicted earlier, [127] none was discovered until 1979, when researchers studying human mitochondrial genes determined that they used an alternative code. [128] However, the mitochondria of many other eukaryotes, including most plants, use the standard code.[129] Many slight variants have been discovered since,[130] including various alternative mitochondrial codes.[131] Further, the AUA, AUC, and AUU codons are all allowable start codons. Some of these differences should be regarded as pseudo-changes in the genetic code due to the phenomenon of RNA editing, which is common in mitochondria. In higher plants, it was thought that CGG encoded for tryptophan and not arginine; however, the codon in the processed RNA was discovered to be the UGG codon, consistent with the standard genetic code has undergone parallel evolution within a phylum, with some organisms uniquely translating AGG to lysine.[133] Replication and inheritance Mitochondria division differs between eukaryotes. In many single-celled eukaryotes, their growth and division are linked to the cell cycle. For example, a single mitochondrion may divide synchronously with the nucleus. This division and segregation process must be tightly controlled so that each daughter cell receives at least one mitochondrion. In other eukaryotes (in mammals for example), mitochondria may replicate their DNA and divide mainly in response to the energy needs of the cell, rather than in phase with the cell cycle. When the energy needs of a cell are high, mitochondria are destroyed or become inactive. In such examples mitochondria are destroyed or become inactive. In such examples mitochondria are destroyed or become inactive. balance between mitochondrial fusion and fission, is an important factor in pathologies associated with several disease conditions.[135] The hypothesis of mitochondrial binary fission has relied on the visualization by fluorescence microscopy (TEM). (~200 nm) is insufficient to distinguish structural details, such as double mitochondrial membrane in mitochondrial division or even to distinguish individual mitochondrial division. Cryo-electron tomography was recently used to visualize mitochondrial division in frozen hydrated intact cells. It revealed that mitochondria divide by budding.[136] An individual's mitochondria divide by a sperm, the mitochondrial genes are inherited only from the mother, with rare exceptions.[137] In humans, when an egg cell is fertilized by a sperm, the mitochondrial genes are inherited only from the mother, with rare exceptions.[137] In humans, when an egg cell is fertilized by a sperm, the mitochondrial genes are inherited only from the mother, with rare exceptions.[137] In humans, when an egg cell is fertilized by a sperm, the mitochondrial genes are inherited only from the mother, with rare exceptions.[137] In humans, when an egg cell is fertilized by a sperm, the mitochondrial genes are inherited only from the mother of the mitochondrial genes are inherited on the mother of the mitochondrial genes are inherited on the mother of the mitochondrial genes are inherited on the mother of the mitochondrial genes are inherited on the mitochondrial gen egg only. The sperm's mitochondria enter the egg, but do not contribute genetic information to the embryo.[138] Instead, paternal mitochondria are marked with ubiquitin to select them for later destruction inside the embryo.[139] The egg cell contains relatively few mitochondria, but these mitochondria divide to populate the cells of the adult organism. This mode is seen in most organisms, including the majority of animals. However, mitochondria in some species can sometimes be inherited paternally. This is the norm among certain coniferous plants, although not in pine trees and yews.[140] For Mytilids, paternal inheritance only occurs within males of the species.[141][142][143] It has been
suggested that it occurs at a very low level in humans.[144] Uniparental inheritance leads to little opportunity for genetic recombination does take place maintaining genetic integrity rather than maintaining diversity. However, there are studies showing evidence of recombination in mitochondrial DNA. It is clear that the enzymes necessary for recombination.[146] The data are more controversial in humans, although indirect evidence of recombination are present in mammalian cells.[145] Further, evidence of recombination are present in mammalian cells.[145] Further, evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence of recombination.[146] The data are more controversial in humans, although indirect evidence o recombination exists.[147][148] Entities undergoing uniparental inheritance and with little to no recombinations until functionality is lost. Animal populations of mitochondria avoid this buildup through a developmental process known as the mtDNA bottleneck. The bottleneck exploits stochastic processes in the cell to increase in the cell-to-cell variability in mutant load as an organism develops: a single egg cell with some proportion of mutant mtDNA thus produces an embryo where different cells have different mutant loads. Cell-level selection may then act to remove those cells with more mutant mtDNA, leading to a stabilisation or reduction in mutant load between generations. The mechanism underlying the bottleneck is debated, [149][150][151] with a recent mathematical and experimental metastudy providing evidence for a combination of random turnover of mtDNA molecules within the cell.[152] DNA repair Mitochondria can repair oxidative DNA damage by mechanisms analogous to those occurring in the cell nucleus. The proteins employed in mtDNA repair pathways in mammalian mitochondria include base excision repair, double strand break repair, direct reversal and mismatch repair. [153][154] Also DNA damages may be bypassed, rather than repaired, by translesion synthesis. Of the several DNA repair process in mitochondria, the base excision repair pathway has been most comprehensively studied. [154] Base excision repair is carried out by a sequence of enzymatic catalyzed steps that include recognition and excision of a damaged DNA base, removal of the resulting abasic site, end processing, gap filling and ligation. A common damage in mtDNA that is repaired by base excision repair is 8-oxoguanine produced by the oxidation of guanine.[155] Double-strand breaks can be repaired by homologous recombinational repair in both mammalian mtDNA[156] and plant mtDNA.[157] Double-strand breaks in mtDNA can also be repaired by microhomology-mediated end joining.[158] Although there is evidence for the repair processes of direct reversal and mismatch repair in mtDNA. [157] Double-strand breaks in mtDNA can also be repaired by microhomology-mediated end joining.[158] Although there is evidence for the repair processes of direct reversal and mismatch repair in mtDNA. mitochondrial DNA Some organisms have lost mitochondrial DNA altogether. In these cases, genes encoded by the mitochondria that lack any DNA, presumably because all their genes have been lost or transferred. [159] In Cryptosporidium, the mitochondria have an altered ATP generation system that renders the parasite resistant to many classical mitochondria inhibitors such as cyanide, azide, and atovaquone.[159] Mitochondria that lack their own DNA have been found in a marine parasitic dinoflagellate from the genus Amoebophyra. This microorganism, A. cerati, has functional mitochondria that lack their own DNA have been found in a marine parasitic dinoflagellate from the genus Amoebophyra. lack a genome.[160] In related species, the mitochondrial genome still has three genes, but in A. cerati only a single mitochondrial gene (cox1) — is found, and it has migrated to the genome of the nucleus.[161] Population genetic studies Main article: Human mitochondrial genetics The near-absence of genetic recombination in mitochondrial DNA makes it a useful source of information for studying population genetics and evolutionary biology.[162] Because all the mitochondrial DNA is inherited as a single unit, or haplotype, the relationships between mitochondrial DNA is inherited as a single unit. trees can be used to infer the evolutionary history of populations. The classic example of this is in human evolutionary genetics, where the molecular clock can be used to provide a recent date for mitochondrial Eve.[163][164] This is often interpreted as strong support for a recent modern human expansion out of Africa.[165] Another human example is the sequencing of mitochondrial DNA from Neanderthals and living humans has been interpreted as evidence for the lack of interbreeding between the mitochondrial DNA reflects only the history of the females in a population. This can be partially overcome by the use of paternal genetic sequences, such as the non-recombining region of the Y-chromosome.[165] Recent measurements of the molecular clock for mitochondrial DNA[167] reported a value of 1 mutation every 7884 years dating back to the most recent common ancestor of humans and apes, which is consistent with estimates of mutation rates of autosomal DNA (10-8 per base per generation).[168] Dysfunction in mitochondrial diseases Main article: Mitochondrial diseas metabolism. Mitochondrial disorders often present as neurological disorders, including autism.[15] They can also manifest as myopathy, diabetes, multiple endocrinopathy, and a variety of other systemic disorders.[169] Diseases caused by mutation in the mtDNA include Kearns-Sayre syndrome and Leber's hereditary optic neuropathy.[170] In the vast majority of cases, these diseases are transmitted by a female to her children, as the zygote derives its mitochondria and hence its mtDNA from the ovum. Diseases such as Kearns-Sayre syndrome, Pearson syndrome, Pearson syndrome, and progressive external ophthalmoplegia are thought to be due to large-scale mtDNA rearrangements, whereas other diseases such as MELAS syndrome, Leber's hereditary optic neuropathy, MERRF syndrome, and others are due to point mutations in mtDNA.[169] In other diseases, defects in nuclear genes lead to dysfunction of mitochondrial proteins. This is the case in Friedreich's ataxia, hereditary spastic paraplegia, and Wilson's disease.[171] These diseases are inherited in a dominance relationship, as applies to most other genetic diseases. A variety of disorders can be caused by nuclear mutations of oxidative phosphorylation enzymes, such as coenzyme Q10 deficiency and Barth syndrome. [169] Environmental influences may interact with hereditary predispositions and cause mitochondrial disease. For example, there may be a link between pesticide exposure and the later onset of Parkinson's disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving
mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Other pathologies with etiology involving mitochondrial dysfunction include schizophrenia, bipolar disease, [172][173] Othe chronic fatigue syndrome, retinitis pigmentosa, and diabetes mellitus.[176][177] Mitochondria-mediated oxidative stress plays a role in cardiomyopytes, resulting in increased fatty acid oxidation in these cells. This process increases the reducing equivalents available to the electron transport chain of the mitochondria, ultimately increasing reactive oxygen species (ROS) production. ROS increases uncoupling proteins (UCPs) and potentiate proton leakage through the adenine nucleotide translocator (ANT), the combination of which uncouples the mitochondria. Uncoupling then increases oxygen consumption by the mitochondria, compounding the increase proportionally because the mitochondria are uncoupled. Less ATP availability ultimately results in an energy deficit presenting as reduced cardiac efficiency and contractile dysfunction. To compound the problem, impaired sarcoplasmic reticulum calcium release and reduced mitochondrial calcium concentration increases dehydrogenase dehydrog activation and ATP synthesis. So in addition to lower ATP synthesis due to fatty acid oxidation, ATP synthesis is impaired by poor calcium signaling as well, causing cardiac problems for diabetics.[178] Relationships to aging There may be some leakage of the high-energy electrons in the respiratory chain to form reactive oxygen species. This was thought to result in significant oxidative stress in the mitochondrial DNA.[179] Hypothesized links between aging and oxidative stress are not new and were proposed in 1956,[180] which was later refined into the mitochondrial free radical theory of aging.[181] A vicious cycle was thought to occur, as oxidative stress leads to mitochondrial DNA mutations, which can lead to enzymatic abnormalities and further oxidative stress. A number of changes can occur to mitochondria during the aging process.[182] Tissues from elderly humans show a decrease in enzymatic activity of the proteins of the respiratory chain.[183] However, mutated mtDNA can only be found in about 0.2% of very old cells.[184] Large deletions in the mitochondrial genome have been hypothesized to lead to high levels of oxidative stress and neuronal death in Parkinson's disease.[185] Mitochondrial cover a pivotal role in the ovarian function, by providing ATP necessary for the development from germinal vesicle to mature oocyte, a decreased mitochondria function is then reflected both in quantitative (such as mtDNA copy number and mtDNA deletions), qualitative (such as mutations and strand breaks) and oxidative damages (such as dysfunctional mitochondria due to ROS), which are not only relevant in ovarian aging, but perturb oocyte-cumulus crosstalk in the ovary, are linked to genetic disorders (such as Fragile X) and can interfere with embryo selection.[188] History The first observations of intracellular structures that probably represented mitochondria were published in the 1840s.[189] Richard Altmann, in 1898, Carl Benda coined the term "mitochondria" from the Greek μίτος, mitos, "thread", and χονδρίον, chondrion, "granule".[191] [189][192] Leonor Michaelis discovered that Janus green can be used as a supravital stain for mitochondria in 1900. In 1904, Friedrich Meves, made the first recorded observation of mitochondria in plants in cells of the white waterlily, Nymphaea alba[189][193] and in 1908, along with Claudius Regaud, suggested that they contain proteins and lipids. Benjamin F. Kingsbury, in 1912, first related them with cell respiration, but almost exclusively based on morphological observations. [189] In 1913, particles from extracts of guinea-pig liver were linked to respiration by Otto Heinrich Warburg, which he called "grana". Warburg and Heinrich Otto Wieland, who had also postulated a similar particle mechanism, disagreed on the chemical nature of the respiration. It was not until 1925, when David Keilin discovered cytochromes, that the respiration using one oxygen atom can form two adenosine triphosphate (ATP) molecules, and in 1941, the concept of the phosphate bonds of ATP being a form of energy in cellular metabolism was developed by Fritz Albert Claude allowed mitochondria to be isolated from other cell fractions and biochemical analysis to be conducted on them alone. In 1946, he concluded that cytochrome oxidase and other enzymes responsible for the respiratory chain were isolated to the mitochondria. phosphorylation in eukaryotes. Over time, the fractionation method was further developed, improving the quality of the mitochondria.[189] The first high-resolution electron micrographs appeared in 1952, replacing the Janus Green stains as the preferred way to visualize mitochondria.[189] This led to a more detailed analysis of the structure of the mitochondria that folded up in ridges dividing up the inner chamber and that the size and shape of the mitochondria varied from cell to cell. The popular term "powerhouse of the cell" was coined by Philip Siekevitz in 1957.[3] In 1967, it was discovered that mitochondrial genes, with the genetic and physical map of yeast mitochondrial DNA completed in 1976.[189] See also Antimitochondrial antibodies Mitochondrial metabolic rates Mitochondrial permeability transition pore Mitophagy Nebenkern Oncocyte Oncocytoma Paternal mtDNA transmission Plastid Submitochondrial particle References ^ "Mitochondrion | Definition of Mitochondrian by Lexico". 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