Mitochondrial bioenergetics and neurodegeneration: a paso doble

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Mitochondria and neuronal activity: The brain is one of the highest energy demanding organs, consuming ~20% of the total ATP produced by the whole body. Importantly, neurons mainly rely on ATP synthesized by mitochondrial bioenergetics and neuronal activity is strictly dependent on specific mitochondrial localization at synapses, sites consuming a high amount of energy requested for both pre- and post-synaptic processes. Here, mitochondria produce ATP and buffer Ca²⁺ rises, two essential processes for neurotransmission and generation of membrane potential along the axon (Magistratti and Allaman, 2015).

Mitochondrial ATP synthesis is driven by two major energy pathways: (1) the tricarboxylic acid cycles (TCA, also known as Krebs cycle), taking place in the mitochondrial matrix and using substrates produced in the cytosol (i.e., throughout glycolysis); (2) the oxidative phosphorylation, fuelled by the respiratory electron transport chain (ETC) at the inner mitochondrial membrane (IMM). ETC activity generates the mitochondrial membrane potential, coupling the activity of the four complexes with that of the ATP synthase, thus allowing ATP production. Importantly, the proper mitochondrial utilization of substrates produced in the cytosol, together with a correct mitochondrial Ca²⁺ uptake, are key features essential to sustain the bioenergetics of these organelles. Indeed, the import of substrates into the mitochondrial matrix is crucial for the proceeding of the TCA cycle and, consequently, for the ETC activity; equally, mitochondrial Ca²⁺ influx plays a pivotal role in the regulation of mitochondrial metabolism, because many mitochondrial enzymes involved in ATP production and several metabolite transporters are regulated by Ca²⁺ (Rossi et al., 2019).

Alterations in mitochondrial Ca²⁺ handling, mitochondrial substrate import and organelle dynamics, as well as an increase in oxidative stress leading to mitochondrial damage, cause defects in energy production requested by several neuronal activities.

Furthermore, mitochondrial metabolism has been shown to be important for brain health. Especially under stress conditions, when neurons are highly activated and a large amount of energy is needed, impaired mitochondria, unable to supply cellular ATP demand, cause alterations in neuronal excitability eventually leading to Ca²⁺ overload and cell death. The accumulation of damaged mitochondria, and consequently of dysfunctional neurons, cause, over the long term, neurodegeneration. Indeed, mitochondrial alterations, and in particular defects in bioenergetic pathways, have been widely reported to be a key factor contributing to neurodegenerative diseases, such as amyloid lateral sclerosis, Parkinson’s disease and Alzheimer’s disease (AD).

The "mitochondrial cascade hypothesis" for AD: A deleterious neurodegenerative disease compromising several neuronal functions; however, a high percentage of cases is due to autosomal dominant mutations in genes encoding the amyloid precursor protein and two homologous transmembrane proteins, Presenilin 1 (PS1) and 2 (PS2), mainly localized at endothaplastic reticulum (ER), but also Golgi apparatus and endosomal membrane. In fact, together with their enzymatic activity, they constitute the catalytic core of the γ-secretase, the enzymatic complex that efficiently cleaves APP generating amyloid-β (Aβ) peptides. These latter products, in pathological conditions due to mutation-driven alterations of γ-secretase enzymatic activity, accumulate with different molecular weights, culminating in an overall cellular toxicity underlying the onset and progression of AD. On the other hand, however, PSs have several independent cellular functions; among them, they have been showed to regulate Ca²⁺ homeostasis. In particular, PS2 mutants, linked to familial form of AD (FAD), have been implicated in Ca²⁺ homeostasis alterations, reducing the ER Ca²⁺ content and concomitant cellular Ca²⁺ overload and cell death. The mitochondrial Ca²⁺ transfer (Zampese et al., 2011; Rossi et al., 2020).

So far, based on the most accepted theory for AD pathogenesis in the last 30 years, the “amyloid cascade hypothesis”, the majority of the proposed therapies for the disease aimed at reducing and slowing the progression of neurodegeneration mainly by targeting the generation/accumulation of toxic Aβ peptides. Unfortunately, all these treatments failed to slow the pathology and to prevent mental decline.

In the last decade, a new hypothesis for disease pathogenesis came to light, the “mitochondrial cascade hypothesis” (Swedlow et al., 2014). Indeed, several mitochondrial defects have been observed in AD cases, both sporadic and familial, i.e., alterations in mitochondrial morphology, dynamics and movement, oxidative stress, metabolism and mitophagy. Any of these dysfunctional processes could lead to synaptic deficits and cell death with critical consequences not only for single neurons but also for the more complex structure of the brain.

Focusing on mitochondrial metabolism and using different AD models (based on FAD PS1 or PS2 mutations, as well as sporadic AD models), several groups observed impairments in mitochondrial functionality resulting in a defective cell bioenergetics (Swedlow et al., 2014). Importantly, bioenergetic alterations appear at the early stage of the disease, even before Aβ plaque and neurofibrillary tangle accumulation, the two main hallmarks of this neurodegenerative disorder. However, in this scenario, it is still unclear how these alterations could explain the observed bioenergetic defects have been poorly investigated. In order to develop effective new therapeutic strategies, unravelling the cascade of events that drives AD pathology and, in particular, the events occurring during early phases of the disease, is extremely important.

Mitochondrial bioenergetics as key factor to sustain neuronal function: By investigating the mitochondrial dysfunction observed in AD, we recently reported that FAD-PS2 mutants affect the overall mitochondrial bioenergetics.

In details, using several AD models (cell lines expressing FAD-PS2 mutants, primary cortical neurons from FAD-PS2-N141I transgenic mice and FAD-PS2-N141I patient derived-fibroblasts), we observed a reduction in the total ATP produced by mitochondria, as well as in the oxygen consumption rate, an index of ETC activity (Rossi et al., 2020). This energetic impairment was due to a defective pyruvate oxidation by mitochondria caused by high Ca²⁺ overload: in particular, mitochondrial Ca²⁺ uptake, as a consequence of a lower ER Ca²⁺ content caused by FAD-PS2 mutants (Zampese et al., 2011), resulting in a dampened TCA cycle progression and ETC activity; 2) an impairment in mitochondrial pyruvate uptake, due to a reduced expression of functional mitochondrial pyruvate carriers (MPC) (Rossi et al., 2020).

Under physiological conditions, pyruvate bridges cytosolic (glycolysis) with mitochondrial metabolism; indeed, once produced in the cytosol through glycolysis, pyruvate crosses first the outer mitochondrial membrane (OMM), through voltage-dependent anion channels (VDACs) that, in turn, can be associated with hexokinase1 (HK1), a cytosolic enzyme that, once being the first enzyme of the TCA cycle, is dynamically associated with VDAC, likely regulating its channel permeability (Robey and Hay, 2006). Once in the intermembrane space, pyruvate can cross the IMM via MPC, entering matrix. Interestingly, we observed a reduced HK1-mitochondria association in several FAD cellular models, as well as in wild-type cells treated with Aβ oligomers, extending the validity of our results also to sporadic AD cases. Moreover, during our attempt to unravel the mechanism responsible for HK1 detachment from mitochondria, we detected high levels of phosphorylated GSK3β (the active form of the enzyme), a feature constantly reported in AD (Llorens-Martín et al., 2014). Of note, GSK3β has been already shown to phosphorylate VDAC, in this form unable to efficiently bind HK1 (Robey and Hay, 2006). In agreement, we observed a reduced mitochondrial pyruvate utilization in our AD models, as well as in wild-type cells treated with Aβ oligomers, the latter observed also in wild-type cells treated with Aβ oligomers, extending the validity of our results also to sporadic AD cases. Moreover, during our attempt to unravel the mechanism responsible for HK1 detachment from mitochondria, we detected high levels of phosphorylated GSK3β (the active form of the enzyme), a feature constantly reported in AD (Llorens-Martín et al., 2014). Of note, GSK3β has been already shown to phosphorylate VDAC, in this form unable to efficiently bind HK1 (Robey and Hay, 2006). In agreement, we observed a reduced mitochondrial pyruvate utilization in our AD models, as well as in wild-type cells treated with Aβ oligomers, the latter observed also in wild-type cells treated with Aβ oligomers, extending the validity of our results also to sporadic AD cases. Moreover, during our attempt to unravel the mechanism responsible for HK1 detachment from mitochondria, we detected high levels of phosphorylated GSK3β (the active form of the enzyme), a feature constantly reported in AD (Llorens-Martín et al., 2014). Of note, GSK3β has been already shown to phosphorylate VDAC, in this form unable to efficiently bind HK1 (Robey and Hay, 2006). In agreement, we observed a reduced mitochondrial pyruvate utilization in our AD models, as well as in wild-type cells treated with Aβ oligomers, the latter observed also in wild-type cells treated with Aβ oligomers, extending the validity of our results also to sporadic AD cases. Moreover, during our attempt to unravel the mechanism responsible for HK1 detachment from mitochondria, we detected high levels of phosphorylated GSK3β (the active form of the enzyme), a feature constantly reported in AD (Llorens-Martín et al., 2014). Of note, GSK3β has been already shown to phosphorylate VDAC, in this form unable to efficiently bind HK1 (Robey and Hay, 2006). In agreement, we observed a reduced mitochondrial pyruvate utilization in our AD models, as well as in wild-type cells treated with Aβ oligomers, the latter observed also in wild-type cells treated with Aβ oligomers, extending the validity of our results also to sporadic AD cases. Moreover, during our attempt to unravel the mechanism responsible for HK1 detachment from mitochondria, we detected high levels of phosphorylated GSK3β (the active form of the enzyme), a feature constantly reported in AD (Llorens-Martín et al., 2014).
different molecular mechanisms in the diverse neurodegenerative pathologies (Plotgeber et al., 2020; Rossi et al., 2020).

As far as AD is concerned, a possible scenario involving mitochondrial associated membranes can be envisaged. These membrane domains have been reported to be altered in AD and represent the place where several proteins actually work causing the mitochondrial defect. Indeed, PS2, VDAC as well as GSK3β are enriched at mitochondrial associated membranes (Szabadkai et al., 2006; Filadi et al., 2016; Bantug et al., 2018), where also Aβ can be produced and accumulated (Schreiner et al., 2015); moreover, both PSs and Aβ oligomers have been reported to interact with GSK3β, favoring its activity (Llorens-Martín et al., 2014). Therefore, we can speculate that, at mitochondrial associated membranes, a pool of hyper-activated GSK3β, induced by PSs or Aβ peptides, causes the phosphorylation of VDAC and the detachment of HK1 from mitochondria. Possibly, HK1-VDAC (localized at the OMM) forms a functional complex with MPC (at the IMM), necessary to stabilize and make the metabolite carrier functional. The HK1 detachment from VDAC will run the HK1-VDAC-MPC complex eventually destabilizing MPC heterodimers, thus reducing the capability of mitochondria to take up and utilize pyruvate, leading to bioenergetic crises (Figure 1).

Shedding light on the molecular mechanisms undergoing mitochondrial bioenergetic dysfunctions will open the possibility for the discovery and the development for new therapeutic approaches, aimed at preventing and slowing down the origin and the progression of the specific disease.

Finally, the described AD mitochondrial bioenergetic defect could be linked to a cellular metabolic rewiring, possibly resulting in systemic alterations in specific metabolic profiles. A detailed metabolic fingerprint characterization of AD patient-derived biofluid samples might offer the possibility to discover new disease biomarkers helping AD diagnosis at early stages, years before the appearance of the first cognitive symptoms.

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Figure 1  
Molecular mechanisms inducing defective mitochondrial bioenergetics in Alzheimer’s disease.

Under physiological conditions, mitochondrial ATP production is stimulated by both a correct ER to mitochondria Ca2+ transfer and mitochondrial import of substrates produced in the cytosol (e.g., pyruvate). In particular, upon ER Ca2+ release through IP3R, mitochondria can take up Ca2+ through VDAC (at the OMM) and MCU (at the IMM). In parallel, once pyruvate is produced in the cytosol by glycolysis, it is imported inside mitochondria crossing first the OMM through VDAC associated with HK1, and then the IMM thanks to MPC activity. The amount of both Ca2+ and pyruvate that can cross the mitochondrial matrix is a key factor for TCA cycle regulation and ETC activity, modulating energy production. In pathological conditions (Alzheimer’s disease), the level of ATP produced by mitochondria is reduced due to a dampened Ca2+ signal and lower pyruvate uptake within mitochondria. Indeed, in FAD-PS2 expressing cells, ER Ca2+), and consequently ER-mitochondria Ca2+ shuttling, are reduced, negatively regulating bioenergetics. Moreover, both FAD-PS2 mutants and Aβ oligomers, present at the organelle interface, induce GSK3β activation, leading to a higher phosphorylation of VDAC and detachment of HK1 from mitochondria. The mitochondrial detachment of HK1, destabilizing MPC functionality, impairs mitochondrial pyruvate uptake and affects mitochondrial activity and ATP production. Aβ: Amyloid-β; ER: endoplasmic reticulum; ETC: electron transport chain; FAD: familial Alzheimer’s disease; GSK3β: glycogen synthase kinase 3β; HK: hexokinase; IMM: inner mitochondrial membrane; IP3R: inositol trisphosphate receptor; MCU: mitochondrial Ca2+ uniporter; MPC: mitochondrial pyruvate carrier; OMM: outer mitochondrial membrane; PS2: presenilin 2; SERCA: sarco-endoplasmic reticulum calcium ATPase; TCA cycle: tricarboxylic acid cycle; VDAC: voltage-dependent anion channel.