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Special Issue: Mitochondrial metabolic alterations in cancer cells and related therape	eutic targets
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Autophagy and mitophagy in cancer metabolic remodelling

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Abstract

Metabolic reprogramming in tumours is now recognized as a hallmark of cancer, participating both in tumour growth and cancer progression. Cancer cells develop global metabolic adaptations allowing them to survive in the low oxygen and nutrient tumour microenvironment. Among these metabolic adaptations, cancer cells use glycolysis but also mitochondrial oxidations to produce ATP and building blocks needed for their high proliferation rate. Another particular adaptation of cancer cell metabolism is the use of autophagy and specific forms of autophagy like mitophagy to recycle intracellular components in condition of metabolic stress or during anticancer treatments. The plasticity of cancer cell metabolism is a major limitation of anticancer treatments and could participate to therapy resistances. The aim of this review is to report recent advances in the understanding of the relationship between tumour metabolism and autophagy/mitophagy in order to propose new therapeutic strategies.

Keywords:

Cancer metabolism, autophagy, mitophagy, ROS, mitochondria, ion channel

Abbreviations:

AMPK: AMP-activated protein kinase

• CAF: cancer associated fibroblast

• Drp1:dynamin-related protein 1

• EMT: epithelial-to-mesenchymal transition

ER: endoplasmic reticulum

• FA: fatty acid

FAO: fatty acid oxidation

• HIF: Hypoxia-inducible factor

• IMM: inner mitochondrial membrane

• IMS: intermembrane space

• IP3R: Inositol trisphosphate receptor calcium channel

• MAM: mitochondrial-associated ER membrane

• MCU: mitochondrial calcium uniporter

• OMM: outer mitochondrial membrane

• OXPHOS: oxidative phosphorylation

• PE: phosphatidylethanolamine

PS: phosphatidylserine

• ROS: reactive oxygen species

TCA: tricarboxylic acid

TRP: transient receptor potential channel

VDAC: voltage-dependent anion channel

Introduction

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In solid tumours, cancer cells are subjected to very strong and selective metabolic pressures because of limited oxygen and nutrient availability. It is now recognised that the tumour microenvironment has a critical effect on cancer cell selection, tumour growth and progression. Only the most metabolically adapted cancer cells will survive to this inhospitable microenvironment, and to the stress factors generated by anticancer treatments. Notably, the metabolic plasticity of cancer cells allows them to use various metabolic substrates. Furthermore, the recycling of intracellular components through autophagy participates to the production of metabolic precursors to sustain cell growth. These adaptations are critical for tumour growth, metastasis appearance and the acquisition of resistances to anticancer treatments. One major challenge for the development of new anticancer treatments is to limit the metabolic adaptations of cancer cells which could allow better therapeutic efficacy and avoid the acquisition of resistance mechanisms. Because mitochondria and autophagy participate to the metabolic adaptation of cancer cells, one potential strategy would be to target related pathways in order to limit the acquisition of resistance to anticancer treatments. This review summarizes recent advances in the understanding of the regulation of autophagy by mitochondria through the control of energy metabolism, reactive oxygen species production and mitochondrialassociated ER membranes. Reciprocally, the regulation of mitochondrial mass and functioning by mitophagy will be discussed. We will focus on mitochondrial calcium transporters as potential new therapeutic targets for autophagy/mitophagy in cancer treatment.

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1. Targeting mitochondrial metabolism and autophagy in cancer

1.1. Mitochondrial metabolism in tumours

Mitochondria are major organelles with primary roles in energy production, Ca²⁺ and redox homeostasis, and apoptosis. It has long been thought that cancer cells do not produce energy by mitochondrial oxidation but through a high glycolytic rate coupled with lactic acid production even in presence of oxygen namely the Warburg effect (or aerobic glycolysis) [1]. Despite the initial characterization of a major role of aerobic glycolysis in cancer cells, it is now recognized that mitochondrial oxidative phosphorylation (OXPHOS) is not impaired in all cells constituting tumours and participates to ATP production [2]. In fact cancer cell metabolism is more complex than initially described related to oxygen availability, with the use of a wide range of substrates including glutamine [3], lactate [4] or fatty acids [5] to fulfil metabolic demands. The global reprogramming of cancer cell metabolism not only supports the production of ATP in metabolic stress conditions but also leads to the production of building blocks (amino acids, fatty acids, nucleotides) needed for a

high proliferation rate [6]. These building blocks are produced by the tricarboxylic acid (TCA) cycle uncoupled to ATP production by OXPHOS (cataplerosis) providing oxaloacetate and α -ketoglutarate for the synthesis of amino acids and citrate as a shuttle for the export of acetyl-coA to the cytosol for lipid synthesis. Furthermore an important part of the biomass is derived from glutamine and other amino acids which are able to replenish TCA cycle intermediates (anaplerosis) for amino acid biosynthesis [7]. Metabolites from glycolysis and the pentose phosphate pathway are additional important precursors for the synthesis of nucleotides and amino acids needed for cancer cell proliferation [6].

Through its important contribution in the production of ATP and macromolecules, it is now well described that mitochondria sustain tumour growth and cancer progression. Indeed mitochondrial function has been associated with cancer cell proliferation, resistance to cell death and metastasis (see reviews [8-11]). Consequently, targeting mitochondria in cancer cells has been proposed to reduce tumour progression [12-14].

1.2. Autophagy

Autophagy is a cellular catabolic pathway leading to the degradation and recycling of proteins and organelles, following the fusion between an isolation vesicle, the autophagosome, and a lysosome providing hydrolytic enzymes. Macroautophagy (hereafter called autophagy) is a non-selective form of autophagy, whereas several forms of autophagy are selective for intracellular organelles like mitochondria and therefore called mitophagy (see section mitophagy). The molecular process of autophagy is complex and involves sequential steps of nucleation, elongation, and fusion through several proteins including the autophagy-related (Atg) proteins (for review [15-17]). Autophagy connects substrate availability in the environment with cellular metabolic requirements. Indeed, autophagy is activated by nutrient starvation, as well as under oxidative stress conditions, through highly regulated pathways linked with energy metabolism. These pathways mostly converge on mTORC1 and the energy-sensing AMP-activated protein kinase (AMPK) [18-21]. Autophagy has two major physiological roles: the breakdown of dysfunctional proteins or organelles as a quality control mechanism, and the recycling of macromolecules under nutrient stress conditions in order to sustain metabolic demands [22, 23].

It is now well admitted that autophagy can have two roles in cancer: protective at early stage of the tumour but promoting tumour growth at later stages [24, 25]. Knockout of autophagy genes in mice increases tumour multiplicity mainly by increasing oxidative stress, indicating that autophagy protects against cancer development [26, 27]. However, in established tumours, the activation of

autophagy by the extracellular conditions (hypoxia, low nutrients and growth factors, reactive oxygen species (ROS), and lactate) [28-30] and by oncogenes Ras and p53 [31] sustains the survival of cancer cells and is favourable to tumour growth [24, 28, 32, 33]. In addition, autophagy plays a prominent role in the tumour microenvironment by modulating the interactions between cancer cells and non-cancer cells from the tumour [34, 35]. Besides these apparently opposite roles in tumour initiation and tumour growth, autophagy has also been associated with cancer progression. Markers of autophagy are increased in metastases compared with primary tumours [36] and are associated with poor prognosis [37, 38]. The role of autophagy in metastasis formation is complex but it is now proposed that autophagy participates to all the different steps of the metastatic cascade. Indeed, recent evidence suggest that autophagy promotes cancer cell migration, invasiveness, epithelial-to-mesenchymal transition (EMT) and anoikis resistance [39]. Autophagy regulates focal adhesion disassembly through direct degradation of paxillin and thus promotes cancer cell migration and metastasis [40]. Interestingly, the autophagic process can promote the secretion of the pro-migratory cytokine interleukin-6 (IL-6), matrix metalloproteinase 2 and WNT5A participating both in cancer cell migration and extracellular matrix degradation [41]. This unconventional function of autophagy has been described to promote cancer progression through secretion of proteins stimulating invasiveness, angiogenesis and limiting immunosurveillance [42]. Furthermore, autophagy is activated during matrix detachment and promotes anoikis resistance, thus allowing cancer cell survival in vessels and during metastatic colonization [43, 44]. Although the molecular mechanism is not clearly understood and depends on cancer models and status, autophagy has been associated with EMT, a process that participates to both cancer metastasis and resistance to anticancer treatments [45]. Autophagy is also activated during anticancer treatments by radiation therapy and chemotherapy. Whether autophagy is associated with cell death during cancer treatment or with cell survival and resistance to anticancer treatments is still debated. However it is now demonstrated in different models that inhibition of autophagy can sensitize cancer cells to several anticancer treatments [46-52].

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To date, hydroxychloroquine (HCQ), a weak base, lysosomotropic agent, used as an anti-malarial drug, is the only autophagy inhibitor clinically available. HCQ has been tested in several clinical trials as a broad spectrum inhibitor of autophagy in association with chemotherapy or radiotherapy. In patients with several types of solid tumours, studies showed the safety of HCQ and its ability to target autophagy [53]. However, its use is limited by side effects independent of autophagy [54-56]. Furthermore, HCQ activity decreases with acidity, which is found in the extracellular compartment around tumours [57]. Therefore, a better understanding of the regulations of autophagy is needed to propose new strategies for targeting cancer, depending on tumour type, stage and metabolism.

1.3. Mitochondrial metabolism in regulation of autophagy

1.3.1.Energy metabolism

Besides the activation of autophagy by low nutrient availability in the tumour microenvironment, the metabolic reprogramming of tumour cells can also support autophagy activation (Figure 1). Autophagy is highly regulated by ATP production and AMPK pathway. Therefore, a reduction of ATP production leads to the accumulation of AMP, the activation of AMPK and autophagy. Indeed, mitochondrial dysfunction induced by the inhibition of respiratory chain and complex III knock-out activates AMPK and autophagy [58, 59] to promote cell survival [59]. Autophagy is transcriptionally regulated during starvation by the induction of transcription factor TFEB which activates the transcription of Atg genes [60]. The acute inhibition of mitochondrial OXPHOS induces the expression of TFEB and lysosomal biogenesis [61], which can also participate to the activation of autophagy by mitochondrial dysfunction in cancer.

Unlike the activation of autophagy by mitochondrial dysfunction, it has been demonstrated in yeast and in mammalian cells that mitochondrial activity is required for autophagy induction [62, 63]. In yeast, amino acid starvation required functional mitochondria to induce LC3 expression and the activation of autophagic flux [62]. Interestingly, it has been demonstrated that mitochondria regulates autophagy through the cAMP-dependent kinase PKA [62]. It is not known whether this requirement of mitochondrial activity for autophagy occurs in cancer cells and how mitochondrial metabolic reprogramming in cancer cells can activate autophagy through PKA regulation. However, the requirement of mitochondrial activity for autophagy has been demonstrated also in mammalian cells and involves mitochondrial phospholipid remodelling (see section Mitochondrial-Associated ER Membranes) [63].

Autophagy is highly regulated by the presence or absence of metabolic substrates in the microenvironment. Therefore, several signalling pathways controlled by substrate availability in the tumour microenvironment, including glutamine, lactate or fatty acids have been associated with autophagy. Glutamine and leucine metabolism is linked with amino acid sensing via the lysosomes and mTORC1. The production of α -ketoglutarate through glutaminolysis has been demonstrated to be a major component of the amino acid sensing and of autophagy regulation. Indeed α -ketoglutarate is necessary for the activity of the EGLNs/prolyl hydroxylases, leading to the activation of the small GTPase RRAGB and subsequent translocation and activation of mTORC1 to the lysosome and inhibition of autophagy [64-66]. In cancer cells, the long term activation of glutaminolysis in condition of amino acid restriction induces the activation of mTORC1, represses autophagy and

activates apoptosis [67]. However the role of glutamine metabolism in autophagy regulation is complex. Besides fuelling the TCA cycle with α -ketoglutarate, glutaminolysis produces ammonia which has long been considered as a by-product before the discovery of its role in autophagy [68]. Although the mechanism is not clearly understood, ammonia activates autophagy through AMPK and the unfolded-protein response system independently of mTOR [69]. Ammonia is found in tumours at high concentration in the interstitial fluid [68]. Because ammonia is diffusible, it is proposed that glutaminolysis-derived ammonia activates autophagy even in the hypoxic core of the tumour as an adaptation mechanism to protect against cell death in condition of metabolic stress [70]. Furthermore, ammonia is at the basis of a self-fuelling system between cancer-associated fibroblasts (CAF) and cancer cells. The glutamine produced by CAF is imported in epithelial cancer cells to fuel the TCA cycle after its conversion to glutamate and α -ketoglutarate, while the ammonia produced diffuses and activates autophagy in CAF [71].

Another particular adaptation of cancer cells which depends on autophagy is the metabolic symbiosis based on lactate exchanges between glycolytic, lactate-producing cells, and oxidative, lactate-consuming cells. These lactate exchanges have been described between cancer cells from different metabolic phenotypes [4] and between cancer cells and fibroblasts [72]. This cooperation requires the entry of lactate into the oxidative cells, a process facilitated by the lactate-proton symporter monocarboxylate transporter type 1 (MCT1), and its oxidation to pyruvate by lactate dehydrogenase B (LDHB). In oxidative cancer cells, lactate is used for OXPHOS [4] and for the production of lipids [73]. Interestingly the oxidation of lactate by LDHB also participates to lysosome function and activates autophagy in cancer cells [28]. The activation of autophagy by lactate utilisation promotes cancer cell survival and tumour growth whereas it has no effect on autophagy and the survival of non-cancer cells [28].

In cancer cells, fatty acid (FA) metabolism is central to cancer progression since FA synthesis provides building blocks and FA oxidation (FAO) is an important energy source [74]. The relationship between FA and autophagy is not clearly understood, and both activation and inhibition of FAO have been associated to autophagy. In prostate cancer cells, the inhibition of FAO using etomoxir (Carnitine PalmitoylTransferase I inhibitor) activates autophagy through the activation of AMPK and inhibition of mTOR [75]. On the opposite, in colon cancer cells, the activation of FAO activates autophagy through the activation of AMPK and promotes tumour growth [76]. In this model, surrounding adipocytes provide cancer cells with FA to fuel FAO and promote survival under low nutrient conditions [76]. Bone marrow adipocytes can also activate FAO and AMPK in acute leukaemia cells, leading to autophagy activation [77]. This relation of tumours with the surrounding adipose tissue is particularly important for cancer progression and may potentially limit cancer treatment.

Furthermore, the relation of lipid metabolism and autophagy is complex because reciprocally, autophagy can provide FA for FAO [78].

1.3.2.Reactive Oxygen Species

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Mitochondria is the major source of ROS. An elevated level of ROS is an important feature of cancer cells, and could be attributed to mitochondrial electron transport chain activity (mainly Complex I and Complex III). Increased ROS production by mitochondria in cancer cells is associated with metastasis through the activation of Src and the Focal adhesion kinase Pyk2 [12]. Although a massive ROS generation is mainly associated with cell damage and cell death, moderate ROS production is known to activate autophagy through multiple pathways. Autophagy is activated by ROS through the activation of the sensor Ataxia-telangiectasia mutated (ATM) leading to mTORC1 inhibition through the LKB1/AMPK/TSC2 pathway [79]. Oxidative stress can also induce autophagy through an NFkBdependent upregulation of p62 [80]. Furthermore, ROS production is involved in starvation-induced autophagy [81]. During nutrient starvation, the ROS produced regulates the activity of the HsAtg4 protease, which is important for phosphatidylethanolamine (PE) conjugation to LC3 [81]. Mitochondrial ROS can also regulate autophagy through oxidation of lysosomal membrane proteins and modulation of Ca²⁺ homeostasis [82, 83]. The activation of TRPML1, a lysosomal Ca²⁺-permeable transient Receptor Potential (TRP) channel, by ROS induces lysosomal Ca²⁺ release, followed by the activation of calcineurin signalling, TFEB nuclear translocation and activation of autophagy and lysosome biogenesis [82]. On the opposite, the activation of the lysosomal Ca²⁺ channel TRPM2 by ROS induces Ca²⁺ CaMKII signalling, leading to autophagy inhibition [83]. Among ROS species, it has been proposed that superoxide O2 • is the major regulator of autophagy since superoxide production induced by the dysfunction of mitochondrial complexes I and III activates autophagy [84].

Although the mechanisms are not clearly described, elevated ROS production caused by dysfunction of mitochondria can participate to the regulation of autophagy in tumours, and consequently to cancer progression. ROS are produced during extracellular matrix detachment, which is an important step for metastatic dissemination [85, 86]. It has been demonstrated that ROS production during matrix detachment promotes autophagy through the activation of PERK1 and promotes anoikis resistance [87]. Interestingly active PERK1 and LC3 are increased in human breast ductal carcinoma compared to normal breast suggesting an important role of this signalling pathway during cancer progression [87]. ROS are also produced following anticancer treatments such as chemo and radiotherapies [88]. Although ROS play an important part for the mechanism of action of these anticancer treatments, the activation of autophagy by ROS could participate to cancer cell survival and therapy resistance. This has been demonstrated in bladder cancer cells in which the oxidative stress induced

by capsaicin activates autophagy as a pro-survival mechanism promoting drug resistance [89]. In lung adenocarcinoma, ROS induced by low dose radiations promote autophagy and confer radio-resistance [90].

1.3.3.Mitochondrial-Associated ER Membranes (MAM)

The juxtaposition of membranes from the ER and mitochondria, including specific proteins, forms a subdomain called MAM (Figure 1). This interface plays an important role for ion and lipid exchanges between mitochondria and ER allowing the proper function of the two organelles [91]. Mitochondrial membranes and MAM have been suggested to participate to autophagosome formation as lipid source. The first evidence that mitochondrial membrane participates to autophagosome formation came from the identification of phospholipid transfers from mitochondria to autophagosome in starved cells [92]. The role of MAM in autophagosome formation seems to involve the conversion of phosphatidylserine (PS) from the ER to phosphatidylethanolamine (PE) by inner mitochondrial membrane (IMM) phosphatidylserine decarboxylase [63], allowing PE-LC3 conjugation, and autophagy [93]. It has recently been demonstrated that the activation of autophagy by mTOR inhibition induced an increase in MAM formation and the remodelling of the mitochondrial membrane phospholipids, with an increase in PS and PE [63]. Interestingly, the activity of complex I is required for MAM formation, phospholipid remodelling and autophagy [63].

On the other hand, some studies showed that the disruption of MAM activates autophagy. MAM are important sites for the transfer of Ca²⁺ from the ER to the mitochondria to regulate mitochondrial enzymes as respiratory complexes and TCA cycle enzymes. This Ca²⁺ flux occurs mainly through IP3 Receptor and TRPM8 in the ER membrane [94, 95] and through the Voltage-Dependent Anion Channel (VDAC), the Mitochondrial Calcium Uniporter (MCU) and the Transient Receptor Protein Melastatin-related 2 (TRPM2) in the mitochondrial membranes [96, 97] (See section "mitochondrial calcium transporters as a new target for autophagy/mitophagy modulation"). The interruption of Ca²⁺ flux between the ER and mitochondria decreases OXPHOS, induces metabolic stress and activates autophagy as a survival mechanism [94]. However, the activation of autophagy by MAM disruption in cancer cells does not seem sufficient, unlike in normal cells, to maintain the energetic level needed, thus leading to cancer cell death and decrease in tumour growth [98]. Furthermore, tightening ER-mitochondria contact sites can inhibit rapamycin-induced autophagy but not starvation-induced autophagy suggesting that MAM play different roles depending on autophagy stimuli [99].

Several oncoproteins and tumour suppressor proteins have been identified in MAM, which highlighted the complex relationships between these structures and cancer progression. Indeed,

MAM is now proposed to play an important role in cancer metabolism and growth [100]. However, the alterations of MAM formation or architecture in cancer are not clearly understood. Although still controversial, the recent association of MAM with autophagy regulation might be responsible for their important roles in cancer. Pharmacological intervention could be a strategy to disrupt MAM and inhibit both mitochondrial metabolism and autophagy [63]. A better understanding of the involvement of MAM in cancer progression and its involvement in the regulation of autophagy is needed to propose new targeted therapies.

Altogether these studies highlight the complex regulation of autophagy by mitochondrial metabolism in tumours. On the one hand autophagy is activated by metabolic changes linked with a decrease in ATP production but also by ammonia production, ROS and interruption of Ca²⁺ transfers in MAM. On the other hand recent evidences suggest that mitochondrial function participates to autophagy induction as a lipid source or through the activation of PKA. Since mitochondria and autophagy are important players of cancer progression and resistance to treatment, it is crucial to better understand their mutual regulations. Therefore more studies are needed to clarify the regulation of autophagy by mitochondria in different tumour types and during tumorigenesis. Furthermore, the tumour microenvironment is much more complex than what can be reproduced in in vitro cell culture models: it contains various cell types like cancer-associated fibroblasts, adipocytes, immune cells, as well as gradients for oxygen and metabolites. All of these features of the tumours microenvironment require being assessed in vivo. Interestingly the microenvironment of tumours can also play a role in autophagy regulation in cancer cells by providing lactate, glutamine or FA and by regulating tumour-stroma interaction [34, 35]. Therefore it is important to clarify the effects of metabolic drugs on autophagy in tumours and to consider their association with autophagy inhibitors.

2. Targeting mitophagy in cancer

2.1. Mitophagy regulation and function

Mitochondrial mass is highly dynamic and tightly regulated through fusion/fission, but also by mitobiogenesis and mitophagy. Mitophagy is a specific form of autophagy that selectively degrades mitochondria through PINK1/Parkin and BNIP3/NIX/FUNDC1 pathways. It is triggered by mitochondrial depolarization, hypoxia and metabolic stress. The PINK1/Parkin pathway has been originally identified in Parkinson's disease where mutations in corresponding genes impair mitochondrial clearance. The activation of mitophagy by membrane depolarization involves the mitochondrial kinase PINK1, the localisation of which depends on mitochondrial membrane potential

[101]. In normal conditions, the voltage-dependent translocation of PINK1 to the IMM induces its cleavage by the mitochondrial protease PARL. When IMM is depolarized, PINK1 accumulates in the outer mitochondrial membrane (OMM) where it phosphorylates the E3 ubiquitin ligase Parkin, leading to its recruitment at the OMM [102]. Several mitochondrial proteins, including VDAC1, Miro, Mfn-1 and Mfn-2, are ubiquitinylated by Parkin [103] and recognized by LC3-interacting proteins p62, NDP52, optineurin, TAX1BP1 or NBR-1 to recruit the autophagic machinery [104-108]. Mitophagy is also activated by hypoxia through the induction of adaptor proteins: BNIP3, NIX (or BNIP3L) and FUNDC1. These proteins are localized in the OMM and contain an LC3-interacting motif to promote the recruitment of the autophagic machinery [109]. The expression of BNIP3 and NIX is increased by hypoxia through Hypoxia-inducible factor (HIF-1) [110, 111] whereas FUNDC1 is dephosphorylated in hypoxia by Src kinase inactivation, increasing its affinity for LC3 compared to phosphorylated FUNDC1 [112]. In addition, AMPK activation by low nutrient availability can directly activate mitophagy through phosphorylation of Ulk1 [20].

Besides the activation of PINK1/Parkin and BNIP3/NIX/FUNDC1 pathways, mitophagy is highly linked to mitochondrial function, enabling to equilibrate mitochondrial degradation with mitochondrial activity requirement. Mitophagy is activated by OXPHOS activity to stimulate the renewal of mitochondria and maintain their efficiency [113]. In addition, mitophagy induces the translocation of Nrf2 and TFEB transcription factors to the nucleus, inducing the transcription of autophagy, lysosome and mitochondria-related genes to renew lysosomal and mitochondrial compartments [114]. Furthermore, the recognition of injured mitochondria for degradation through mitophagy is regulated by mitochondrial membrane composition. In normal condition, cardiolipins, specific mitochondrial phospholipids, are mostly located in the IMM. Cardiolipin externalization to the OMM leads to its interaction with LC3 and acts as an elimination signal for mitophagy [115]. The hexameric intermembrane space protein, NDPK-D, has been identified as the cardiolipin translocation system, in case of mitochondrial depolarisation, which is needed for the elimination of damaged mitochondria by mitophagy [116].

Mitophagy cooperates with mitochondrial dynamic and it is now admitted that mitochondrial fission precedes mitophagy. The mitophagy proteins Parkin and BNIP3 interact with the mitochondrial fission factor dynamin-related protein (Drp) 1 [117, 118]. This cooperation is further enhanced in hypoxia with the recruitment of FUNDC1 in MAM due to its interaction with the ER protein calnexin, leading to the recruitment of Drp1 to allow mitochondrial fission and mitophagy [119]. Furthermore, during mitophagy induction, PINK1 and Beclin1 relocalize to the MAM and promote autophagosome formation [120].

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2.2. Mitophagy in cancer

Because mitophagy can degrade dysfunctional mitochondria and limit ROS production, its function has been associated with tumour suppression. Indeed, Parkin or PINK1 deletion in mice leads to the spontaneous development of hepatocellular carcinoma [121] and increases Kras-driven pancreatic tumorigenesis [122]. In human, Parkin deletion has been identified in tumours including colorectal cancer [123], glioblastoma [124], melanoma [125], lung cancer [126] and breast cancer [127, 128]. Loss of Parkin increases proinflammatory signals, promotes genomic instability [126], increases cancer cell proliferation and resistance to apoptosis [121, 125]. Interestingly the accumulation of mitochondrial dysfunctions induced by Parkin deficiency decreases mitochondrial OXPHOS, increases ROS production and increases glycolysis, therefore possibly contributing to the Warburg effect, and consequently increases tumorigenesis [129]. Furthermore, Parkin has been identified as an E3 ubiquitin ligase for HIF-1 α to promote its proteasomal degradation. Therefore, the downregulation of Parkin in breast cancer cells stabilizes HIF- 1α and promotes metastasis [130]. The BNIP3 pathway has also been linked with a tumour suppression function of mitophagy. A decrease of BNIP3 is found in pancreatic cancers and associated with chemoresistance and poor prognosis [131, 132]. In mammary tumours, BNIP3 decreases with cancer progression, leading to an accumulation of mitochondria associated with an increase ROS production and HIF- 1α stabilization [133]. The authors demonstrated that the loss of BNIP3 promotes mammary tumour growth, progression to metastasis and can be used as a prognostic marker in human triple-negative breast cancer [133]. Lastly, FUNDC1-deficient mice showed an increase in tumour initiation, also suggesting a tumour suppressor role for FUNDC1 [134]. Altogether, these studies highlighted the role of mitophagy as a tumour suppressor and the potential benefit of its induction to limit the consequences of mitochondrial dysfunction in cancer.

Like non-selective autophagy, the role of mitophagy is complex and can depend on tumour type and stage. Although mitophagy has been associated with tumour suppression in early stages of the tumour development, it can promote tumour growth at advanced stages. Indeed, mitophagy can be induced when AMPK is activated by low nutrient conditions [20], a condition found in tumours. Hypoxia, a common feature of solid tumours, has been shown to activate mitophagy in cancer cells through BNIP3 and NIX induction [110]. Furthermore, the induction of mitophagy depends on mitochondrial metabolism, such as glutamine availability and use which can increase BNIP3 expression and mitophagy in melanoma cells [135]. While few studies investigated mitophagy in tumours, its activity seems dependent on tumour metabolism and microenvironment.

In several cancer types, the degradation of damaged mitochondria and the recycling of metabolic precursors by mitophagy can promote cell survival and protect from cell death [110] [136]. In Parkindeficient mice melanoma growth and metastasis are suppressed, suggesting a pro-tumour role of Parkin-dependent mitophagy [137]. However, Parkin is often downregulated in many tumour types. It has been recently demonstrated that besides this frequent loss of parkin, PINK1-dependent mitophagy can be functional through the induction of the E3 ubiquitin ligase ARIH1/HHAR [138]. Interestingly ARIH1 is overexpressed in breast and lung cancer cells while Parkin expression is low [138]. In addition, BNIP3 induction has been reported to promote cell migration through cytoskeleton remodelling [139], resistance to anoikis [140] and invasion [141], suggesting a role of BNIP3-dependent mitophagy in metastasis formation. The pro-survival role of mitophagy has also been associated with resistance to anti-cancer treatments, such as the ARIH1-PINK1 mitophagy which protects against cisplatin-induced cell death [138]. A role of mitophagy in resistance to anticancer treatment is also suggested in a study showing that doxorubicin induces the expression of NIX in cancer stem cells and promotes resistance to treatment through limitation of ROS production [142]. Interestingly, FUNDC1 silencing has been proposed to improve chemotherapy efficiency by increasing cisplatin-induced cell death [143].

Consistently with the dual role of mitophagy in cancer progression, the expression of mitophagy proteins has been found to be either downregulated or overexpressed in different cancer types. BNIP3 has been found downregulated in invasive ductal carcinoma and metastases [144] and in pancreatic cancers [131, 132] but upregulated in breast ductal carcinoma *in situ* [145] and in other human cancer tissues (ovarian, head and neck squamous cell carcinoma) where BNIP3 localized in perinecrotic regions [111]. It has been suggested that some of these mitophagy proteins can be used as prognosis markers in specific cancers. A high expression of FUNDC1 has been associated with poor prognosis in cervical cancer [143]. High BNIP3 expression can be used as a prognosis marker in specific cancers such as uveal melanoma where a high BNIP3 expression is associated with a poor prognosis [146]. However, there is a controversy concerning the role of BNIP3-dependent mitophagy in cancer that could be explained by an alternatively spliced BNIP3 expressed preferentially in cancer cells: whereas the full-length BNIP3 promotes cell death, the Bnip3Δex3 isoform promotes cell survival [147]. Interestingly, a switch towards a glycolytic metabolism increases the expression of the Bnip3Δex3 isoform [147].

Altogether, these studies highlighted the complex role of mitophagy in cancer progression, showing either pro-tumour or anti-tumour activities depending on tumour type, stage, or its metabolic activity. However, recent evidence suggest an important role of mitophagy in tumour growth, metastasis and therapy resistance. Since mitophagy is an important regulator of mitochondrial

number and function, its pharmacological modulation in tumours could be a promising anticancer strategy. However, the proposition of mitophagy inhibition or activation is limited by the little knowledge of its role and regulation in preclinical models and in human tumours. Therefore, a major challenge will be to identify the specific roles of the different mitophagy pathways in human cancers before being able to propose mitophagy modulators for anti-cancer therapy. The identification of mitophagy biomarkers will be helpful to design mitophagy modulators for tumours having a high requirement for mitophagy. It is important to clarify the role of mitophagy in tumours and to investigate the effect of its modulation in tumour-bearing mice models to reflect the behaviour of tumours detected in patients. It is also important to develop specific tools to modulate mitophagy *in vivo* and not using general autophagy inhibitors. This issue could be addressed using mitochondrial targeted molecules, for example using triphenylphosphonium derivatives structures [148], to deliver autophagy inhibitors. Interestingly using this strategy with mitochondria-targeted redox agents can activate mitophagy selectively in breast cancer cells compared to non-cancer cells [149].

3. Mitochondrial calcium transporters as new targets for autophagy / mitophagy modulation

The OXPHOS activity leads to a strong proton concentration in the intermembrane space (IMS) and is the main factor that determines the very negative voltage (Ψ m) of the IMM. Therefore the modulation of OXPHOS activity can influence the proton gradient and consequently the IMM potential. The electrochemical gradient in the IMS is favourable to cation influx (mainly K⁺ and Ca²⁺) into the mitochondrial matrix and regulates the activity of mitochondrial enzymes, ROS and ATP production. This cation fluxes is tightly regulated by the expression of ion channels in the IMM: BK_{Ca}, K_{ATP}, Kv1.3, MCU, SK-family members, TRP-family members, CLIC4 and others, while the main actor in the OMM that allows ion flux is VDAC [96, 97, 150, 151] (Figure 1). An interruption of cation fluxes decreases OXPHOS activity and on the opposite a high cation influx induces mitochondrial membrane depolarization [152, 153]. Since autophagy and mitophagy are linked with mitochondrial function, the modulation of mitochondrial ion channels could be an interesting strategy to modulate autophagy or mitophagy in tumours. Indeed, mitochondrial depolarization induces mitophagy through the PINK1/Parkin pathway [101, 102] and the disruption of mitochondrial potential by FCCP and CCCP activates autophagy and mitophagy through Nrf2 pathway and TFEB transcription factor [154]. Therefore the inhibition of cation flux could have a dual effect in reducing mitochondrial function but also mitophagy by preventing mitochondrial depolarization.

Among cations, Ca²⁺ exchanges have been associated with autophagy and mitophagy regulation. VDAC is the most abundant protein in the OMM, and is ubiquitously expressed in all eukaryotic cells. In its open state it becomes an aspecific pore, allowing the flux of many substrates and ions smaller than 5 kDa. In this condition, VDAC is highly Ca²⁺ permeable and allows Ca²⁺ flux to IMS, thus modulating Ca²⁺ availability to Ca²⁺ permeant-channels in the IMM. MCU is a Ca²⁺ channel present in the IMM, ubiquitously expressed and generally considered as the main Ca²⁺ transporter in the matrix. Two pools of calcium can be imported into the mitochondria: one from the cytosol and another one from the ER. The juxtaposition of ER and mitochondria in MAM facilitates the generation of a high Ca²⁺ concentration that could be efficiently transferred to mitochondrial compartments. This Ca²⁺ flux in MAM has important roles for the regulation of mitochondrial function since its interruption decreases OXPHOS and activates autophagy [94] [98]. On the opposite, the disruption of MAM has been associated with a decrease in mitochondrial PE production and therefore a reduction of autophagy [63]. Although the mechanisms linked with autophagy are not clearly understood, VDAC and MCU could be interesting targets to disrupt Ca2+ and lipid exchanges in MAM in cancer cells, decreasing mitochondrial function and inducing cell death. Furthermore, VDAC is involved in Parkin recruitment to defective mitochondria, triggering mitophagy [155]. The Ca²⁺ fluxes in MAM through MCU is also important for Parkin-dependent mitophagy [156]. Because of their double role in mitochondrial Ca²⁺ flux and Parkin recruitment, VDAC and MCU could be used to target mitophagy and autophagy regulation in tumours. VDAC is overexpressed in several tumour types and pre-clinical models, suggesting that it could be an interesting anticancer target [157, 158]. Although the mechanism has not been linked to autophagy, VDAC downregulation decreases mitochondrial membrane potential, cellular ATP content, cancer cell migration, proliferation and tumour growth in lung cancer xenografts [159]. MCU has also been found to be altered in tumours from different tissues [160]. In particular, in human breast [161, 162] and hepatocellular [163] carcinomas, the expression of MCU is associated with cancer progression and metastasis.

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The MCU regulator 1 (MCUR1) is a secondary subunit of MCU complex allowing ion flux into the matrix [164, 165]. MCUR1 downregulation decreases Ca²⁺ flux, OXPHOS, ATP production and activates AMPK-dependent autophagy [164, 165]. MCUR1 is upregulated in hepatocellular carcinoma and its expression is associated with cancer cell survival and tumour growth [166]. In this model, MCUR1 induces mitochondrial Ca²⁺ accumulation and ROS production, showing that MCUR1 association with MCU is necessary for a functional MCU complex and its Ca²⁺-associated entry into mitochondria is a pro-survival factor for cancer cells [166].

Several other ion channels have been identified in the IMM of different cell type and could compensate for MCU-dependent Ca²⁺ flux. Among them, two splice variants of TRPM2 are expressed

in neuroblastoma. The functional TRPM2-L and the dominant negative TRPM2-S are both localized in mitochondria [167]. In xenograft models of SH-SY5Y glioblastoma cell line, the expression of the dominant negative isoform decreases mitophagy and led to smaller tumour growth, showing that a functional mitochondrial TRPM2 is necessary for mitophagy and cancer growth [167]. In this model, TRPM2-S was associated with a reduction in HIF-1/2α and BNIP3 expression [167]. The role of mitochondrial TRMP2 in mitophagy has also been demonstrated in gastric cancer cell lines where the downregulation of TRPM2 decreases mitochondrial oxygen consumption and ATP production associated with a reduction in mitophagy and autophagy through a JNK-dependent and mTOR-independent pathway [168]. The reduction of mitophagy and autophagy by the lack of functional TRPM2 is also associated with enhanced efficacies of doxorubicin, tamoxifen and paclitaxel chemotherapies, showing the potential benefit of targeting mitochondrial TRPM2 for cancer therapies [167-169]. Interestingly, TRPM2 inhibition or silencing did not increase doxorubicin cytotoxicity in non-cancerous HMEC cell line [169].

Conclusion

Altogether, these studies highlighted the complex relation between mitochondria (ATP and ROS production, MAM and calcium transporters) and autophagy. Autophagy could result, as a metabolic adaptation, from chemotherapies targeting mitochondria. In this context, targeting both autophagy and mitochondria could limit chemoresistance mechanisms. However, recent discoveries suggest that mitochondria are also involved in autophagic activity, mainly by providing lipids for autophagosome formation. Because of these two effects on autophagy, mitochondria could be considered as a target for cancer therapy. Mitophagy seems to play an important role in cancer cells, but its effects on cancer cell growth could be different depending on carcinogenesis stage and cancer types. Therefore, mitophagy modulation could be beneficial for metastasis prevention and improve therapy efficacy. Among mitochondrial proteins, calcium transporters have a key role in the regulation of mitochondrial function. These mitochondrial calcium transporters have been recently associated with autophagy and mitophagy regulation in cancer cells. Consequently they also represent attractive anticancer targets to modulate mitochondrial dysfunction autophagy/mitophagy in tumours. Studies are still needed to better understand the regulations of autophagy and mitophagy by cancer metabolism, and develop strategies targeting both cancer metabolism and autophagy to avoid adaptation and resistance mechanisms.

470 <u>Conflict of interests</u>

471 Authors declare no conflict of interest.

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- 478 Finally, we wish to apologize to all researchers whose relevant works, owing to the limited length of
- 479 this article format, could not be cited in this review.

480 Figure legend

Figure 1: Regulation of autophagy and mitophagy by cancer cell metabolism. Cancer cells use a wide range of metabolic substrates including glucose (blue arrows), lactate, fatty acids (green arrows) and glutamine (orange arrows) to sustain the production of ATP and intermediate precursors for nucleotides, fatty acids (FA) and amino acids (aa) synthesis needed for proliferation. Autophagy and mitophagy are highly regulated by nutrients availability and reprogrammed metabolic pathways used by cancer cells. When ATP production is sufficient, the inactivation of AMPK pathway represses autophagy and mitophagy. The production of α -ketoglutarate (α -KG) through glutaminolysis is a major component of aa sensing and of autophagy repression under high substrate availability. However, ammonia, lactate and reactive oxygen species (ROS) production are associated with autophagy activation. Fatty acid oxidation (FAO) can either activate or repress autophagy. Mitochondria are also involved in autophagy regulation through the formation of Mitochondria-Associated endoplasmic reticulum (ER) Membrane (MAM) subdomains which are important for ion and lipid (particularly phosphatidylserine, PS) exchanges between mitochondria and ER. On the one hand, MAM formation and the remodelling of mitochondrial membrane phospholipids, with production of phosphatidylethanolamine (PE) and subsequent LC3-PE promotes autophagy. On the other hand, the entry of Ca2+ from the cytosol and from the ER in MAM allows the proper functioning of mitochondrial enzymes and therefore represses autophagy. Similarly, the specific recycling of mitochondria by mitophagy is repressed by the maintenance of Ca²⁺ flux in mitochondria and by sustained ATP production. However, mitochondrial calcium channels voltage-dependent anion channel (VDAC), transient receptor potential channel M2 (TRPM2) and mitochondrial calcium uniporter (MCU) are involved in mitophagy activation by the protein Parkin or by hypoxia. In normal conditions, cardiolipins, specific mitochondrial phospholipids, are mostly located in the inner mitochondrial membrane (IMM). Cardiolipin externalization to the outer mitochondrial membrane (OMM) leads to its interaction with LC3 and acts as an elimination signal for mitophagy. Yellow pointed arrows (---->) represent a stimulation of mitophagy or autophagy. Yellow blunt-end arrows represent a repression or inhibition (----I) of mitophagy or autophagy. AcCoA is for acetyl-coenzyme A. IMS is for inter membrane space, limited by the OMM and IMM. OXPHOS is for mitochondrial oxidative phosphorylation. TCA cycle is for tricarboxylic acid cycle.

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