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Drugging cancer metabolism: Expectations vs. reality

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Abstract

As compared to their normal counterparts, neoplastic cells exhibit a variety of metabolic changes that reflect not only genetic and epigenetic defects underlying malignant transformation, but also the nutritional and immunobiological conditions of the tumor microenvironment. Such alterations, including the so-called Warburg effect (an increase in glucose uptake largely feeding anabolic and antioxidant metabolism), have attracted considerable attention as potential targets for the development of novel anticancer therapeutics. However, very few drugs specifically conceived to target bioenergetic cancer metabolism are currently approved by regulatory agencies for use in humans. This reflects the elevated degree of heterogeneity and redundancy in the metabolic circuitries exploited by neoplastic cells from different tumors (even of the same type), as well as the resemblance of such metabolic pathways to those employed by highly proliferating normal cells. Here, we summarize the major metabolic alterations that accompany oncogenesis, the potential of targeting bioenergetic metabolism for cancer therapy, and the obstacles that still prevent the clinical translation of such a promising therapeutic paradigm.

1. Introduction

In 1924, the German physiologist and physician Otto Heinrich Warburg (1883–1970) was the first to describe the tendency of cancer cells to take up increased amounts of glucose, even in normoxic conditions (Koppenol et al., 2011; Warburg, 1924). However, the so-called Warburg effect was translated into a medical procedure in the 1980s, which is known as ¹⁸F-deoxyglucose positron emission tomography (¹⁸FDG-PET) (Ben-Haim and Ell, 2009). It was not until the 2000s that the bioenergetic metabolism of cancer cells began to attract widespread attention as a potential target for the development of novel therapeutic interventions (Casero et al., 2018; Galluzzi et al., 2013; Tennant et al., 2010; Vander Heiden, 2011; Zhu and Thompson, 2019). Such an intensive area of investigation has provided profound insights into the metabolic alterations that accompany malignant transformation,

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tumor progression and response to therapy (Casero et al., 2018; Galluzzi et al., 2013; Tennant et al., 2010; Vander Heiden, 2011; Zhu and Thompson, 2019). Nonetheless, very few anticancer agents currently approved by the US Food and Drug Administration (FDA) or equivalent regulatory agencies worldwide for use in humans, have been specifically conceived as modulators of bioenergetic cancer metabolism. Conversely, several conventional chemotherapeutics commonly used in the clinic, including (but not limited to) 5-fluorouracil, etoposide, doxorubicin and cisplatin, were developed based on (some degree of) selectivity for highly proliferating cells (and hence target nucleic acid metabolism or the mitotic apparatus) (Casero et al., 2018; Galluzzi et al., 2013; Tennant et al., 2010; Vander Heiden, 2011; Zhu and Thompson, 2019). At least in part, the lack of anticancer drugs targeting bioenergetic metabolism reflects some specificity issues as well as multiple misconceptions that have permeated the field over the past two decades and *de facto* hindered progress. Here, we discuss the potential of drugging bioenergetic alterations associated with malignancy, and analyze the obstacles that still prevent the full realization of such a promising therapeutic paradigm.

2. Targeting carbohydrate metabolism for cancer therapy

Despite carbohydrates being known to constitute a key source of nutrients and metabolic intermediates for cancer cells since the early 1920s, it has been only during the past 2 decades that the utilization of glucose has attracted attention as a potential target for the development of novel therapeutic regimens (Gatenby and Gillies, 2004; Hay, 2016; Vander Heiden, 2011). Glucose occupies a central role in cancer metabolism owing to its ability to feed core catabolic circuitries (*i.e.*, glycolysis potentially coupled to mitochondrial respiration) as well as several anabolic pathways, including the so-called pentose phosphate pathway (PPP) and serine synthesis (Chen and Russo, 2012; Ganapathy-Kanniappan, 2018; Li and Zhang, 2016). Altogether, these metabolic circuitries not only provide cancer cells with ATP for biochemical reactions, but also (1) building blocks to sustain cell growth and proliferation (Chen and Russo, 2012; Ganapathy-Kanniappan, 2018; Li and Zhang, 2016), (2) antioxidants to counteract the potential accumulation of cytotoxic reactive oxygen species (ROS) (Perl et al., 2011; Rodic and Vincent, 2018), and (3) at least in some settings, metabolites that are sufficient to drive oncogenesis and tumor progression (Collins et al., 2017; Yang et al., 2013).

Glucose is taken up by cells *via* dedicated glucose transporters (GLUT1–4), and first acted upon by hexokinase (HK), resulting in the generation of glucose-6-phosphate (G6P) (Hay, 2016). G6P constitutes a branching point for glucose metabolism, as it can be either isomerized into fructose-6-phosphate (F6P) to proceed towards catabolism, or fed into the PPP (Chen and Russo, 2012; Ganapathy-Kanniappan, 2018; Li and Zhang, 2016). Similarly, the glycolytic intermediate 3-phosphoglycerate can either feed glycolysis or initiate serine biosynthesis (discussed in detail below) (Hay, 2016). The ultimate step of glycolysis consists of conversion of phosphoenol-pyruvate into pyruvate by one member of the pyruvate kinase (PK) enzyme family, and pyruvate either feeds into the tricarboxylic acid (TCA) cycle or is converted to lactate by lactate dehydrogenase (LDH) for secretion (Hay, 2016). Considerable efforts have been dedicated to the investigation of each step of the glycolytic cascade in cancer cells.

Despite the presence of four GLUT genes in the human genome, GLUT1 and GLUT3 appear to be the most relevant transporters harnessed for glucose uptake by cancer cells (Ancey et al., 2018). Increased expression of GLUT transporters has been documented across multiple cancer types, generally correlating with advanced disease stage and poor outcome (Brown and Wahl, 1993; Galluzzi et al., 2017a; Grobholz et al., 1993; Jiwa et al., 2014; Koh et al., 2017; Kurahara et al., 2018; Li et al., 2016a; Zhang et al., 2019). GLUT proteins represent attractive therapeutic targets, and some research groups have investigated extensively, the possibility to develop GLUT inhibitors for the management of some human neoplasms. Most of these molecules have been shown to mediate good anticancer effects *in vitro and in vivo* (generally in xenograft tumor models established in immu-nodeficient mice) (Chan et al., 2011; Liu et al., 2012; Ojelabi et al., 2016; Siebeneicher et al., 2016). However, the majority of GLUT inhibitors are poorly isoform-specific, which poses a robust challenge for clinical development. HK is overexpressed by multiple malignancies, often correlating with severity of the disease and dismal clinical outcome (Chen et al., 2014; He et al., 2016; Huang et al., 2015; Min et al., 2013; Palmieri et al., 2009; Pudova et al., 2018; Suh et al., 2014a; Wu et al., 2017; Zhang et al., 2018). Reflecting its key role in glucose retention (glucose enters cancer cells *via* GLUTs driven by its gradient, while GLUTs are impermeant to G6P), both pharmacological and genetic interventions targeting HK in cancer cells mediate robust cytostatic and cytotoxic effects, *in vitro and in vivo* (Deng et al., 2018; Gong et al., 2014; Li et al., 2016b, 2017a,b; Thamrongwarangoon et al., 2017; Wang et al., 2016; Yoo et al., 2019; Zhang et al., 2014a; Zhou et al., 2018). In fact, several clinical trials have been initiated to investigate the therapeutic activity of the HK inhibitor lonidamine, with mixed results (Amadori et al., 1998; Berruti et al., 2002; De Lena et al., 2001; Gebbia et al., 1997; Oudard et al., 2003; Papaldo et al., 2003; Portalone et al., 1999). However, the clinical development of lonidamine has been discontinued, at least in part reflecting its poor pharmacological specificity (Belzacq et al., 2001; Fulda et al., 2010; Ravagnan et al., 1999). Human PK exists in two major forms, M1 and M2, the latter being preferentially expressed by cancer cells (Christofk et al., 2008; Mazurek et al., 2005). The central role of PKM2 in malignant transformation and tumor progression has been repeatedly established, rendering this glycolytic enzyme another attractive target for the development of novel therapeutics (He et al., 2015; Kwon et al., 2012; Lim et al., 2012; Liu et al., 2015; Tamada et al., 2012; Wang et al., 2015a; Yuan et al., 2014; Zhan et al., 2013; Zhou et al., 2012). Consistent with this notion, pharmacological agents and genetic interventions targeting PKM2 have been shown to mediate consistent antineoplastic effects in multiple tumor models (Goldberg and Sharp, 2012; He et al., 2014; Iqbal and Bamezai, 2012; Israelsen et al., 2013; Jiang et al., 2012; Li et al., 2014; Sun et al., 2015). However, pharmacological PKM2 inhibitors generally have pleiotropic effects that are poorly reconcilable with clinical applications (Galluzzi et al., 2017b,c; Jiang et al., 2012). Thus, PKM2 inhibitors have not yet been tested clinically. In summary, while the multiple steps and several layers of regulation in glycolysis generate various potential therapeutic targets, the same complexity poses a challenge to targeting these nodes for therapeutic purposes.

Reducing dietary glucose and carbohydrate intake has been proposed as an alternative strategy to limit carbohydrate metabolism in cancer cells (Kroemer et al., 2018). Increasing dietary intake of carbohydrates has contributed to elevate the rate of obesity and associated

chronic illnesses in the US and Europe (Hochberg, 2018; Ludwig et al., 2018). Conversely, diets with low carbohydrate content, including so-called ketogenic diets have recently gained popularity in the general population as a healthy lifestyle change (Hochberg, 2018; Ludwig et al., 2018). Tolerability studies in mice proved that ketogenic diets are safe and favor beneficial changes in systemic metabolism despite unfavorable hepatic alterations (Douris et al., 2015). Recently, such a diet was shown to enhance the antitumor effects of phosphoinositide-3-kinase inhibitors in rodent tumor models (Hopkins et al., 2018). Whether implementing ketogenic diets in the management of cancer patients is feasible and useful remains to be determined. Yet another sugar that has witnessed increased consumption over the last few decades is fructose, also paralleling rising obesity rates (Marriott et al., 2009; Park and Yetley, 1993). A recent study demonstrated that administration of high-fructose corn syrup to mice enhanced intestinal tumor growth (Goncalves et al., 2019). Although some clinical trials testing various dietary regimens in cancer patients are ongoing (Lévesque et al., 2019), further investigation into the role of dietary carbohydrates in the pathogenesis of cancer is needed, which could provide a rationale for establishing nutritional guidelines for patients.

3. Targeting amino acid utilization for cancer therapy

Besides serving as building blocks for proteins, amino acids can feed into both catabolic and anabolic metabolism, and can deliver signals that support oncogenesis (Choi and Coloff, 2019; Jewell et al., 2013). In recent years, serine and glycine have garnered considerable interest in the cancer metabolism field, largely owing to key roles in one-carbon metabolism, which is central for the synthesis of purines and other oncogenic mediators (Ducker and Rabinowitz, 2017; Locasale, 2013; Mattaini et al., 2016; Yang and Vousden, 2016). Serine is synthesized from 3-phosphoglycerate upon sequential transformation by phosphoglycerate dehydrogenase (PHGDH), phosphoserine aminotransferase 1 (PSAT1) and phosphoserine phosphatase (PSPH) (Locasale, 2013; Mattaini et al., 2016; Yang and Vousden, 2016). Of note, the reaction catalyzed by PHGDH is coupled to the conversion of NAD⁺ into NADH (a substrate for mitochondrial respiration), while PSAT1 simultaneously generates α -ketoglutarate (a TCA cycle intermediate) from glutamate (Locasale, 2013; Mattaini et al., 2016; Yang and Vousden, 2016). Thus, serine synthesis is coupled to bioenergetic mitochondrial metabolism. Serine can be further processed to form glycine, a conversion that can feed into a series of complex biochemical reactions culminating with formate generation, which are cumulatively known as one-carbon metabolism (Locasale, 2013; Mattaini et al., 2016; Yang and Vousden, 2016). Formate is mainly metabolized to generate precursors for purine synthesis, which is one of the main mechanisms through which serine and glycine support cancer cell proliferation (Locasale, 2013; Mattaini et al., 2016; Yang and Vousden, 2016).

Intensive efforts have been devoted to the development of strategies to block the synthesis of serine in neoplastic cells. Importantly, the levels of these amino acids are elevated in several cancers, as is the expression of their respective biosynthetic enzymes, lending further support to the therapeutic potential of targeting these pathways in cancer (DeNicola et al., 2015; Hirayama et al., 2009; Locasale et al., 2011; Possemato et al., 2011; Vie et al., 2008; Zhang et al., 2017). Early work demonstrating that PHGDH silencing impairs cancer cell

proliferation provided strong rationale for the development of PHGDH inhibitors (Locasale et al., 2011; Possemato et al., 2011). First generation PHGDH inhibitors developed by the Cantley and Sabatini groups were able to reduce serine production and limit cancer cell proliferation, both *in vitro* and *in vivo* (Mullarky et al., 2016; Pacold et al., 2016). Subsequently, an allosteric inhibitor of PHGDH was also developed, displaying robust anticancer effects in multiple tumor models (Wang et al., 2017). Although these agents have shown promise *in vitro* and *in vivo*, their development is still in its infancy and it is hard to predict whether these or next generation compounds will have clinical utility.

One-carbon metabolism can also be targeted at reactions downstream, including those mediated by methylenetetrahydrofolate dehydrogenase (NADP⁺ dependent) 2, methenyltetrahydrofolate cyclohydrolase (MTHFD2) and serine hydroxymethyltransferase 1 (SHMT1) or SHMT2. Thus, deletion of MTHFD2 in human colorectal carcinoma HCT-116 cells slowed tumor growth in xenograft models, an effect that could be further enhanced by SHMT1 deletion, while SHMT1 deletion alone had no effect on tumor growth (Ducker et al., 2016). Of note, the need to delete both enzymes for maximal efficacy reflected the reversal of cytosolic one-carbon flux when the mitochondrial folate pathway was disrupted (Ducker et al., 2016). These findings highlight the adaptive nature of cancer cell metabolism and the accompanying complexity of targeting these pathways for cancer treatment. Thus, it is possible that combinatorial strategies may be required for effectively targeting one-carbon metabolism (and perhaps other metabolic circuitries) for clinical applications (Gustafsson et al., 2017; Ju et al., 2018; Ma et al., 2017).

Additional amino acids have attracted attention from the research community over the past 2 decades, including glutamine and asparagine. Each of these amino acids play a distinct but interrelated role in cell metabolism, providing rational targets for anticancer therapy. Glutamine, a precursor for glutamate, is key for the generation of glutathione and serves as a substrate for the production of TCA cycle intermediates (in support of cell proliferation) (Wise and Thompson, 2010). Glutamine-targeting agents include inhibitors of glutaminase (GLS), the enzyme that converts glutamine to glutamate, as well as agents targeting glutamine transport (Li et al., 2019; Schulte et al., 2018; Song et al., 2018; Ye et al., 2018). In fact, the glutaminase inhibitor CB-839 is being evaluated in patients affected by various cancers (source: <http://www.clinicaltrials.gov>). The key role of asparagine in malignant transformation and tumor progression is well-recognized, as recombinant variants of asparaginase (ASPG), the enzyme that converts asparagine to aspartic acid, have been used extensively as part of therapeutic regimens for acute lymphoblastic leukemia (Barr et al., 1992; Ertel et al., 1979; Pieters et al., 2011; Sutow et al., 1971). With that being said, it seems that asparagine synthetase—the enzyme that catalyzes the reverse conversion of aspartic acid into asparagine—may also constitute a therapeutic target, especially in asparaginase resistant cancers (Gutierrez et al., 2006; Yu et al., 2016). Additional work is required to elucidate this possibility.

It should be noted that cancer cells obtain amino acids (and other nutrients) not only from the extracellular milieu or via endogenous biosynthetic pathways, but also through autophagy (Galluzzi et al., 2017a, 2018; Rybstein et al., 2018). Autophagy, an evolutionary conserved response that recycles disposable cytosolic material *via* lysosomal degradation

(Galluzzi et al., 2017a; Morselli et al., 2010), is often upregulated in established cancers, reflecting not only nutritional needs, but also the relatively harsh conditions of the tumor microenvironment (Galluzzi et al., 2015; Sica et al., 2015). Moreover, amino acid levels are tightly linked to autophagic responses, so that limiting amino acid availability generally promoted autophagy activation, resulting in enhanced resistance to therapy (Efeyan et al., 2013; Jewell et al., 2013; Martinez-Outschoorn et al., 2017). Targeting autophagy for cancer therapy is an active area of investigation with multiple obstacles, including not only the limited specificity of currently available autophagy inhibitors, but also the critical role of autophagy in non-transformed cells (Galluzzi et al., 2017b).

Many of the amino acids under investigation as therapeutic targets for cancer therapy are non-essential, meaning that they are available from dietary sources and can be synthesized endogenously. In fact, several studies have demonstrated the importance of exogenous amino acid sources for cancer cell proliferation, *in vitro and in vivo* (Gao et al., 2018; Labuschagne et al., 2014; Maddocks et al., 2013, 2017). Strategies to reduce exogenous amino acid availability include inhibitors of amino acids transporters, such as inhibitors of solute carrier family 1 member 5 (SLC1A5, best known as ASCT2), and dietary interventions. The former approach has shown some promise in pre-clinical settings (Ndaru et al., 2019; Schulte et al., 2018; Ye et al., 2018). However, since ASCT2 controls the uptake of multiple amino acids, specificity is an issue (Ndaru et al., 2019; Schulte et al., 2018; Ye et al., 2018). The latter approach may also be challenging, as it will prove difficult to specifically reduce the dietary intake of select amino acids. That said, it has been proposed that a low-protein diet might be advantageous for cancer patients (Kerr et al., 2017; Logan and Bourassa, 2018; Yin et al., 2018), a possibility that remains to be fully explored.

4. Targeting lipid metabolism for cancer therapy

Lipids, which have historically been considered as mere structural components of cell membranes, are now widely considered as key nutrients and signal transducers that play a major role in oncogenic pathways (Hannun and Obeid, 2018; Loew et al., 2019; Wang et al., 2018).

Fatty acids (FAs) can be either obtained exogenously (from dietary sources) or be endogenously synthesized. At odds with normal cells, which generally take up FAs from the microenvironment, embryonic and cancer cells favor FA biosynthesis (Chakravarthy et al., 2005; Chirala et al., 2003; Maningat et al., 2009; Pizer et al., 1997). The first, rate-limiting step in FA synthesis is catalyzed by fatty acid synthase (FASN), which converts TCA cycle-derived acetyl-CoA into palmitate *via* a NADPH-dependent reaction (Jones and Infante, 2015). FASN plays a well-recognized role in oncogenesis and tumor progression, as first suggested by the fact that FASN levels are increased in both the circulation and neoplastic lesions of patients with cancer (Alo et al., 2007; Cai et al., 2015; Long et al., 2014; Walter et al., 2009; Witkiewicz et al., 2008). These observations drove the development of FASN inhibitors for anticancer applications, some of which demonstrated good preclinical activity (often in the context of significant off-target effects) (Flavin et al., 2010; Menendez and Lupu, 2017; Schcolnik-Cabrera et al., 2018; Zadra et al., 2019; Zhou et al., 2003). These agents, which are generally believed to operate by disrupting membrane synthesis, are being

tested in multiple clinical trials, including a completed Phase I study (). To the best of our knowledge however, the results of this study have not yet been revealed. Interestingly, proton pump inhibitors are being repurposed for cancer therapy following the demonstration that they effectively inhibit FASN (Fako et al., 2015). Supporting the clinical utility of this approach, proton pump inhibitors combined with standard-of-care chemotherapy prolonged survival in cohorts of patients with breast cancer (Fako et al., 2015; Wang et al., 2015b), and clinical trials are ongoing to further test this therapeutic paradigm (source: <http://www.clinicaltrials.gov>).

Cancer cells also employ FAs as nutrients for ATP production *via* fatty acid oxidation (Corbet and Feron, 2017). This biochemical cascade begins with the esterification of FAs into FA esters by acyl-CoA synthetase long chain family member 1 (ACSL1), followed by the conversion of FA esters into acylcarnitine esters, a carnitine-dependent reaction catalyzed by carnitine palmitoyltransferase 1A (CPT1A) (Casals et al., 2016; Corbet and Feron, 2017; Saavedra-Garcia et al., 2018; Schooneman et al., 2013). Acylcarnitine esters can enter the mitochondrial matrix, where carnitine is removed by CPT2 to form acyl-CoA, and the latter feeds into the TCA cycle for energy production (Casals et al., 2016; Corbet and Feron, 2017; Saavedra-Garcia et al., 2018; Schooneman et al., 2013). The key reaction in FAO is catalyzed by CPT1A, drawing attention to this enzyme as a possible target for cancer therapy (Corbet and Feron, 2017). Thus, CPT1A inhibitors such as etomoxir and perhexiline have demonstrated preclinical activity in models of leukemia and glioblastoma, as well as breast and colorectal cancer (Estan et al., 2014; Foster et al., 1988; Hernlund et al., 2008; Pike et al., 2011; Ramu et al., 1984; Samudio et al., 2010; Thupari et al., 2001; Tirado-Velez et al., 2012; Vella et al., 2015). However, none of these agents have reached clinical development so far (source: <http://www.clinicaltrials.gov>).

Arachidonic acid (AA) is a type of FA which has attracted considerable attention for the development of anticancer agents, reflecting the major oncogenic functions of AA-derived lipids, including prostaglandins (PGs). Following the actions of phospholipases on membrane phospholipids, AA is transformed by cyclooxygenase 1 (COX-1) or COX-2 to form PGG₂, further followed by conversion to PGH₂ (Dubois et al., 1998; Simmons et al., 2004). PGH₂ can subsequently be converted to multiple bioactive PGs by selective PG synthases (Dubois et al., 1998; Simmons et al., 2004). In this context, PGE₂ production has attracted considerable attention as a potential target for therapeutic interventions. Indeed, prostaglandin E synthase (PTGES) is overexpressed in cancers of the lung, colon, breast, brain and penis, generally correlating with elevated COX-2 expression (Cook et al., 2016; Golijanin et al., 2004; Mehrotra et al., 2006; Yoshimatsu et al., 2001a,b). Similarly, the PGE₂-catabolizing enzyme 15-hydroxyprostaglandin dehydrogenase (HPGD, also known as 15-PGDH) is commonly downregulated in the same tumors, indicating a two-fold mechanism by which cancers maintain elevated PGE₂ levels (Backlund et al., 2005; Ding et al., 2005; Hughes et al., 2008; Wolf et al., 2006; Yan et al., 2004). Moreover, PGE₂ synthesis can be boosted by caspase 3 (CASP3) activation, providing a mechanism for dying cancer cells to support the growth of their chemo- or radioresistant neighbors (Galluzzi et al., 2012a,b; Huang et al., 2011).

Pharmacological approaches to reduce PG production have been used clinically for decades. In particular, non-steroidal anti-inflammatory drugs (NSAIDs) were originally formulated to reduce pain and inflammation, largely reflecting the non-selective inhibition of COX-1 and COX-2 (Dubois et al., 1998; Simmons et al., 2004). Although clinically useful for their intended purpose, these drugs cause gastric and enteric complications in animals and a subset of individuals (Bjarnason et al., 1993; Halter et al., 2001; Sigthorsson et al., 2002; Thieffin and Beaugerie, 2005; Wallace and Devchand, 2005; Whittle, 2004), calling for the development of next-generation NSAIDs selectively targeting COX-2 (Everts et al., 2000). Second-generation NSAIDs were associated with reduced gastrointestinal events, but their use was rapidly linked with adverse cardiovascular effects (Bombardier et al., 2000; Silverstein et al., 2000).

In addition to their anti-inflammatory properties, NSAIDs have strong chemopreventive effects. Work in rodents demonstrated the chemopreventive efficacy of the selective COX-2 inhibitor celecoxib on intestinal tumorigenesis (Ignatenko et al., 2008; Jacoby et al., 2000; Montrose et al., 2016). Moreover, NSAID users exhibited lower propensities to develop both sporadic and genetically predisposed adenomas (Bertagnolli et al., 2006; Steinbach et al., 2000). The utility of other coxibs and sulindac (yet another NSAID) for the chemoprevention of gastrointestinal tumors has also been demonstrated in prospective clinical trials (Baron et al., 2006; Giardiello et al., 2002). Conversely, the chemopreventive efficacy of aspirin—which also operates as a COX-1/COX-2 inhibitor—appears to exhibit a considerable degree of variability with tumor type (Bardia et al., 2007; Benamouzig et al., 2010; Burn et al., 2011; Cook et al., 2005; Liao et al., 2012).

In spite of their utility as chemopreventive agents, COX inhibitors are impractical to use in the general population due to gastrointestinal and cardiovascular toxicities, as outlined above. These adverse effects are on-target, meaning that they result from COX inhibition and a consequent drop in PG bioavailability. To circumvent this problem, efforts have been redirected to the development of specific inhibitors of PGE₂ synthesis. Work in rodents demonstrated that *Ptges* deletion reduced intestinal and mammary tumor growth (Howe et al., 2013; Nakanishi et al., 2008; Sasaki et al., 2012). However, although pharmacological inhibitors of PTGES have been developed, their utility in humans for cancer prevention or treatment has yet to be demonstrated (Brenneis et al., 2006).

Sphingolipids represent another major class of lipids with central roles in malignant transformation and tumor progression (Bartke and Hannun, 2009; Hannun and Obeid, 2018). Sphingomyelin, an abundant sphingolipid of cell membranes, can be converted by sphingomyelinase into ceramide, a lipid second messenger with multipronged cellular effects (Bieberich, 2008). In turn, ceramide can be converted to sphingosine-1-phosphate (S1P) through the sequential actions of ceramidase and sphingosine kinases (Hannun and Obeid, 2008). Ceramide, sphingosine and S1P have all been involved in oncogenesis or tumor progression, and the enzymes responsible for their synthesis are upregulated in multiple cancer types (Furuya et al., 2011; Hannun and Obeid, 2018; Ogretmen, 2018). For example, ceramidase is elevated in leukemia as well as prostate and colorectal cancer (Beckham et al., 2013; Cheng et al., 2013; Garcia-Barros et al., 2016; Seelan et al., 2000; Tan et al., 2016). Consistent with these observations, inhibition of ceramidases caused

cancer cell death and delayed tumor growth in xenograft models (Mahdy et al., 2009; Selzner et al., 2001; Vijayan et al., 2019). The apoptotic effects of ceramidase inhibition largely result from intracellular ceramide accumulation, ultimately driving mitochondrial membrane permeabilization and downstream CASP3 activation (Galluzzi et al., 2010; Susin et al., 1997; Tait and Green, 2010). Accordingly, several studies have shown that supplementing rodent diets with sphingomyelin reduces intestinal tumor development (Dillehay et al., 1994; Schmelz et al., 1996). These preclinical results suggest that inhibitors of ceramidase may constitute effective anticancer agents for clinical applications, a possibility that remains to be tested.

S1P is a highly bioactive mediator known for its roles in normal physiology and pathology. Upon binding to one of its cognate receptors, S1P regulates angiogenesis, vascular permeability and physiological lymphocyte trafficking (McVerry and Garcia, 2005; Montrose et al., 2013; Pappu et al., 2007; Rivera et al., 2008; Wang and Dudek, 2009). Consistent with the importance of this signaling pathway, an S1P receptor modulator (i.e., fingolimod) has been approved by the US FDA for the management of multiple sclerosis, and similar compounds are in clinical development for the treatment of ulcerative colitis (Brinkmann et al., 2010; Sandborn et al., 2016). The potential utility of targeting this pathway for cancer treatment has also been demonstrated. Genetic deletion of *Sphk1* (coding for sphingosine kinase 1) reduced tumor burden in a murine model of intestinal neoplasia (Furuya et al., 2017a; Kohno et al., 2006). Interestingly, macrophages have been suggested as an important source for sphingosine kinase activity in the microenvironment of colorectal carcinoma (Furuya et al., 2017b). Moreover, the ability of a SPHK1 inhibitor to suppress colitis-associated tumorigenesis has been attributed to disruption of specific immune cell populations (Chumanovich et al., 2010). Other cancer types in which SPHK1 might constitute a relevant target for the development of therapeutic agents include glioma as well as breast and prostate carcinoma (Geffken and Spiegel, 2018; Kapitonov et al., 2009; Pchejetski et al., 2011; Shimizu et al., 2018; Zhang et al., 2014b). The existence of FDA-approved modulators of S1P receptors may facilitate the development of anticancer regimens based on these molecules.

5. Obstacles to drugging bioenergetic metabolism for therapeutic purposes

Despite the enthusiasm raised by the possibility of drugging bioenergetic metabolism as a novel pharmacological approach against neoplasia, such a therapeutic paradigm remains largely unrealized for several reasons. First, the bioenergetic circuitries harnessed by neoplastic cells to thrive despite the harsh conditions that generally characterize the tumor microenvironment (e.g., the Warburg effect) exhibit considerable overlap with the bioenergetic pathways employed by non-malignant cells that engage in rapid proliferative responses physiologically, such as T lymphocytes expanding in response to an antigenic challenge or the wound healing response (Buck et al., 2015, 2017; Lisowska et al., 2018; Ma et al., 2017; Rodrigues et al., 2019; Slominski et al., 2018). Thus, the systemic administration of glycolysis inhibitors such as 2-deoxy-*D*-glucose at pharmacologically meaningful doses has the potential to generate off-target effects that may limit the ability of

the immune system to control disease or repair injuries. In line with this notion, early clinical trials testing 2-deoxy-D-glucose plus docetaxel or radiation therapy in patients with advanced solid tumors demonstrate that the drug is well tolerated but fails to provide clinical benefits (Raez et al., 2013; Singh et al., 2005). Second, accumulating preclinical and clinical data suggest that malignant cells acquire metabolic alterations that are highly heterogeneous. This heterogeneity can occur across (1) cancer types (Camelo and Le, 2018; Crippa et al., 2017; Goodwin et al., 2017; Nguyen and Le, 2018), (2) patients with the same type of neoplasm (Cappelletti et al., 2017; Kim et al., 2015; Quinones and Le, 2018), (3) lesions at different sites within the same individual (*e.g.*, primary tumor *vs.* metastatic) (Guha et al., 2018; Kidd and Grigsby, 2008; Lehuede et al., 2016; Pahk et al., 2018), and (4) in different areas of the very same lesion (Carmona-Fontaine et al., 2017; Feichtinger et al., 2011; Yoshida, 2015). The ultimate metabolic configuration of a transformed cell indeed depends on genetic and epigenetic features that are not necessarily shared with other tumors of the same type, such as the loss of the oncosuppressor tumor protein 53 (TP53) (Vander Linden and Corbet, 2019). Moreover, the precise microenvironment in which a malignant lesion evolves has a major impact on which metabolic circuitries can be harnessed for survival and proliferation (Suh et al., 2014b; Yoshida, 2015). Additionally, cancer cells evolve at a rapid pace under microenvironmental pressure (including metabolic and immunological cues), which drives a considerable degree of diversification, even within the same lesion (Suh et al., 2014b; Vitale et al., 2019; Yoshida, 2015). These observations imply that drugging a specific metabolic circuitry associated with malignancy may ultimately be efficient only on a fraction of cancer cells, *de facto* operating as selective pressure and favoring the rapid emergence of resistant cells. Third, the metabolic changes that enable the malignant phenotype are not a self-standing hallmark of cancer, as proposed by many investigators (Hanahan and Weinberg, 2011). Rather, bioenergetic metabolism is finely coupled to (and hence indiscernible from) all other functions of cancer cells, meaning that all phenotypical, biological and immunological manifestations of malignancy are linked to bioenergetic metabolism, either quite directly (*e.g.*, a high proliferation rate requires robust anabolism in support of novel biomass generation) or less so (*e.g.*, a high ATP content facilitates the perception of cell death as immunogenic) (Galluzzi et al., 2017d; Michaud et al., 2011). This implies that any biological, immunological or therapeutic challenge faced by malignant cells alters their metabolism, often in ways that remain to be elucidated.

Taken together, these observations suggest that the development of efficient strategies to drug bioenergetic metabolism for therapeutic purposes calls for the identification of metabolic alterations that are (1) as specific to cancer (over normal) cells as possible, and (2) as common amongst cancer cells as possible (at least within individual patients). Moreover, it will be critical to keep under attentive consideration the fact that any therapeutic agent administered to cancer patients alters the bioenergetic configurations of cancer cells, potentially exposing (or concealing) susceptibilities (Michels et al., 2013; Obrist et al., 2018).

6. Concluding remarks

In summary, the bioenergetic machinery of malignant cells stands out as a promising source of targets for the development of novel therapeutic agents. However, drugging a cellular

function as conserved and flexible as bioenergetic metabolism remains challenging. In this context, considerable efforts will have to be dedicated not only to solving the specificity issues discussed here above, but also to obtaining in-depth knowledge on the interactions between bioenergetic metabolism in cancer cells and (1) currently employed anticancer agents, and (2) nutritional cues. Accumulating preclinical and clinical data indicates indeed that nutrition has a major impact on multiple steps of the oncogenic process (Galluzzi et al., 2017c; Goncalves et al., 2019; Hopkins et al., 2018; Kroemer et al., 2018; L'evesque et al., 2019; Ngo et al., 2019), calling for an attentive re-evaluation of dietary recommendations given to cancer patients. In spite of persisting obstacles, it is tempting to surmise that (but only the future will tell whether) targeting cancer metabolism with pharmacological agents or nutritional interventions will soon become a clinical reality.

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