

Towards a metabolic therapy of cancer?

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Abstract. It is increasingly appreciated that cancer cells must be endowed with specific metabolic adaptations to support enhanced growth and to ensure survival under stressful conditions. On the other hand, many oncogenic mutations of protooncogenes and tumor suppressor genes directly cause metabolic derangements and, conversely, mutations of enzymes have been found to underlie several forms of cancer. Thus, cancer-specific metabolic alterations are now considered among the hallmarks of malignant tumors. Most commonly, cancer cells exhibit enhanced glycolysis under aerobic conditions (the Warburg effect) but alterations in the metabolism of amino acids, such as glutamine, serine and proline are increasingly described as important metabolic features of selected tumor types. In theory, all these deranged cancer-specific metabolic pathways may constitute novel therapeutic targets, although the only “metabolic” drug in clinical use is still represented by the enzyme L-asparaginase. However, the increasing amount of experimental evidence, as well as the number of trials in progress, suggests that metabolic drugs will soon complement standard anti-cancer chemotherapy and modern biological drugs. (www.actabiomedica.it)

Key words: cancer, metabolism, glycolysis inhibitors, glutamine analogues

Introduction

In 2001 Hanahah and Weinberg published their pivotal review on the hallmarks of cancer (1). That contribution contained a comprehensive recognition of the main advances in the understanding of the molecular aspects of cancer as well clear cut prospective indications for the future. The hallmarks identified were, needless to say, self-sufficiency in growth signals, insensitivity to growth-inhibitory signals, evasion of programmed cell death (apoptosis), limitless replicative potential, sustained angiogenesis, and tissue invasion and metastasis.

After ten years, the same Authors decided to write a new review on the same subjects (2). In this contribution, which is also becoming a must of cancer bibliography, Hanahah and Weinberg propose two new hallmarks of cancer. One is evasion from immune destruction, the other being reprogramming of energy metabolism.

The “old” hallmarks were also proposed as likely therapeutic targets and the provision was correct: for instance, antiangiogenic drugs have crossed the border between the bench and the bedside. Similarly, since also the “new” hallmarks are forecast as possible therapeutic targets, we should expect the introduction of metabolic drugs or metabolic therapy in clinical oncology (3).

This short review intends to briefly summarize the major advances in the cancer metabolism field as well as to recount the perspectives for a metabolic therapy of neoplastic diseases.

The Warburg effect and metabolic alterations in cancer

Why this renewed interest for cancer metabolism? Actually, the hypothesis that cancer is also a metabolic disease is all but new. At the beginning of

the 20th century an ingenious German biochemist, Otto Warburg, proposed that cancer is essentially a metabolic disease, which he attributed to a basic mitochondrial defect present in all the cancer cells. Consequently, cancer cells would rely entirely on glycolysis even in the presence of normal oxygen tension, producing large amounts of lactate (the so called “aerobic glycolysis” or “Warburg effect”). Warburg won the Nobel Prize for Biochemistry and Physiology in 1931 for the discovery of cytochrome C oxidase but, until his death in 1956, he remained intimately sure that his major contribution to science was indeed the discovery of metabolic alterations in cancer (see the enlightening historical perspective in (4)). Warburg’s ideas led to bitter contrasts with other big names, such as, for instance, Sir Hans Krebs, and it was ascertained that most, but not all, of the cancer cells exhibit the Warburg effect and that not all tumors present defective mitochondria.

In the following years, Warburg hypothesis on the metabolic origin of cancer was rapidly overcome by the tumultuous progresses in viral carcinogenesis and molecular oncology, leading to the still dominant concept of cancer as a genetic disease. Yet, Warburg’s estimation on glycolytic rates in cancer cells proved astonishingly correct, demonstrating that in several cancer types the consumption of glucose is of hundreds of folds higher than in normal counterparts. Although not all the tumors exhibit comparable dependence upon glycolysis (5), Warburg effect has provided the rationale for one of the most important devices in clinical oncology, the ¹⁸F-deoxyglucose Positron Emission Tomography (PET), able to spot malignant lesions on metabolic rather than morphological grounds (6).

Why many tumors preferentially use glycolysis instead of Krebs cycle and oxidative phosphorylation, if their mitochondria are normal? The usual answer to this question is that glycolytic cancer cells are not too dependent upon oxygen and, hence, clearly favoured compared to ischemic normal counterparts. However, one may argue that, if glycolytic tumors are less dependent upon oxygen, at the same time they should be much more dependent upon glucose.

Recent studies have focussed on anaplerosis, a classical concept of intermediate metabolism (7, 8).

Anaplerosis is the continuous fuelling of metabolic intermediates of glycolysis and Krebs cycle that prevents their depletion (and hence an energy shortage of the cell) notwithstanding the sustained flux of 3-, 4- and 5-C units diverted towards anabolic reactions, such as protein and fatty acid synthesis. Thus, glucose can behave as an anaplerotic substrate if its oxidative metabolism stops to pyruvate but it is simply an energetic fuel if it is completely oxidized to CO₂. For a cancer cell, large availability of anaplerotic substrates is a prerequisite to couple under safe conditions high proliferative activity (and, hence, high rates of anabolic reactions) with high energetic charge.

Moreover, several of the enzymes involved in glycolysis, such as hexokinase (9) are also important regulators of apoptosis. More in general, excess of cytosolic ATP production through glycolysis inhibits mitochondrial ATP synthase, induces a chemiosmotic backpressure and hyperpolarizes the mitochondrial membrane (10). This is the basis for the so-called “Crabtree effect”, the net decrease of oxygen consumption upon glucose addition to the medium (11). Sustained hyperpolarization fixes mitochondria in an anti-apoptotic state, a phenomenon observed in both cancer and normal cells (12, 13), which has important consequences on the susceptibility of cancer cells to radiotherapy and chemotherapy.

Additional putative advantages yielded by aerobic glycolysis are lactate shuffling, through which highly glycolytic cancer cells may feed neighbouring cells (14, 15), and prevention of oxidative damage due to activation of the pentose phosphate pathway. Recent results suggest that the activation of this pathway may derive from the accumulation of phosphoenol pyruvate due to the increased expression in cancer cells of PKM2, the low-activity isoform of pyruvate kinase (16, 17).

Enzymes and mutations in cancer cells

What are the relationships between the large host of known oncogenic mutations and cell metabolism? Given the premises, it is by no means surprising that many common oncogenic mutations affecting both protooncogenes and cancer suppressor genes also affect metabolism, ensuring to the cancer cell high avail-

ability and enhanced rates of utilization of anaplerotic substrates. For instance, p53 mutations accelerate glucose influx and glycolysis and, conversely, the wild type protein enhances mitochondrial oxidative metabolism (18, 19), lowers the expression of GLUT transporters (20) and suppresses the activity of Glucose-6-Phosphate Dehydrogenase, the key enzyme for the pentose shunt pathway (21). The metabolic effects of p53, which recent work would indicate as the main responsible for the antitumor activity of the protein (22), are mostly dependent on its target TIGAR (TP53-induced glycolysis and apoptosis regulator) and synthesis of cytochrome c oxidase 2 (SCO2) (23). Also the metabolism of glutamine, the other important anaplerotic substrate, is modulated by p53 (24,26) as well as by the product of the oncogene *MYC*, involved in a large number of human tumors (27), which also increases glycolytic flux (28). Although alterations in *MYC*, p53 and HIF-1 are considered the most common causes of metabolic alterations in cancer (29), the role of other pathways is also increasingly recognized. For instance, a diversion of glucose metabolism from energy-producing glycolysis to anabolic pathways is a powerful means through which *KRAS* mutations drive pancreatic tumorigenesis (30). Moreover, in virus-induced tumors metabolic alterations can be traced back to the expression of viral genome (31). Whenever a relevant oncogenic mutation has clear cut metabolic effects promoting the consumption of a particular substrate, the tumor cells would require large amounts of that substrate, an “insatiable appetite” (32) quite properly named “addiction” (27).

Recent data demonstrate that mutations of enzymes involved in intermediate metabolism, and not obviously linked to cell cycle regulation, apoptosis or DNA repair, can promote cancerogenesis behaving as tumor suppressors or oncogenic products. These mutations can be grouped in two main classes: i) germ line inactivating mutations of enzyme-coding genes (which should be thus considered tumor suppressor genes), leading to rare familial cancer syndromes and ii) somatic activating mutations of enzyme genes (which should be thus considered oncogenes), present in subsets of common sporadic cancers.

As for the first class of mutations, it was already known that metabolic effects of mutations in compo-

nents of regulatory pathways such as HIF and VHL, which underlie familial pheochromocytomas (33), have dramatic metabolic consequences. However, it was surprising understanding that inactivating mutations of TCA cycle enzymes, such fumarate hydratase (*FH*) and succinate dehydrogenase (*SDHB*, *SDHC*, and *SDHD*) may directly promote oncogenesis behaving as true oncosuppressor genes (34). *FH* mutations in the germinal line cause the rare familial syndrome Hereditary Leiomyomatosis Renal Cell Cancer (HLRCC) (35). Other hereditary cancer conditions caused with mutations of these enzymes are hereditary paraganglioma–pheochromocytoma syndrome (36), and hereditary paraganglioma (37). Consistent with the classic two-hit theory, patients present the inherited mutation in one allele, while the second allele is lost or inactivated in the tumors. Although a common mechanism underlying the oncogenic effect of these mutations consists in the perturbation of the HIF pathway, known to be activated in many forms of cancer, other metabolic alterations may be also involved. For instance, oncogenic *FH* mutations result in glycolytic drift, along with decreased AMPK and p53 activities, and enhanced anabolic pathways in the tumor cells (38).

The most well known example of the second type is given by mutations of the two genes for Isocitrate Dehydrogenase isozymes (*IDH1* and *IDH2*), which are present in a large portion of Grade II and III astrocytomas, oligodendrogliomas and “secondary” glioblastomas, that is glioblastomas deriving from low-grade glial tumors (39). Mutated *IDH1* and *IDH2* were then found also in subsets of acute myelogenous leukemia (40) and in chondrosarcoma (41). Normally, *IDH1* and *IDH2* reversibly convert isocitrate into α -ketoglutarate (aKG) both in mitochondria (*IDH-1*) and in cytosol (*IDH2*), as a step of amino acid and fatty acid synthesis, while *IDH3* is the enzyme responsible for the irreversible conversion of isocitrate to aKG in the second step of the Krebs cycle. The oncogenic, mutated variants of *IDH1* and *IDH2* acquire a new activity and, instead of producing aKG, use it as a substrate to synthesize large quantities of (*R*)-2-hydroxyglutarate (D-2HG), an uncommon metabolite in normal cells. The mechanisms underlying the oncogenic activity of D-2HG are still to be

defined, although the oncometabolite can interfere with aKG-dependent dioxygenases (34) thus altering both HIF-dependent pathways and methylation patterns (42). However, cells carrying these mutations have also profound changes in glutamine, fatty acid, and citrate synthesis pathways (43).

The list of enzymes the mutation of which associates with oncogenic transformation is likely expected to elongate. The last additions are glycine decarboxylase, originally found expressed in Tumor initiating Cells (TICs) of Non Small Cell Lung Cancer (NSCLC) but overexpressed in around 25% of the cancer cell lines tested (44), and prolyl oxidase (POX), which catalyzes the first step in the catabolism of proline. POX was originally thought a tumor suppressor (45) negatively regulated by MYC (46) but can behave as a pro-survival factor under hypoxic conditions (47). Great interest is also devoted to phosphoglycerate dehydrogenase (PHGDH), the first enzyme of the biosynthetic pathway for the non essential amino acids serine and glycine. *PHGDH* is amplified in almost half of the melanomas, in a smaller but significant portion of breast cancers and, overall, in more than 15% of the human cancers (48, 49). The metabolic role of PHGDH in cancer cells does not seem to be restricted to serine and glycine fuelling but may also provide an alternate source of aKG, thus fulfilling a classical anaplerotic function (49).

Therapeutic perspectives

Given that enhanced glycolysis is essential for the growth of many cancers, it is not surprising that most attempts have considered glycolysis control as an effective therapeutic target. Although restoration of metabolic anomalies is a tumor-specific result of p53 function reinstatement and may significantly contribute to the anti-tumor effects of the procedure (50), inhibitors of glycolysis provide a more direct mean to interfere with deranged cancer metabolism (51). The nonmetabolizable glucose analogues 2-deoxyglucose or 3-bromopyruvate have been used since many years to inhibit glycolysis and ATP production, leading to the suppression of cancer cell growth in vivo with relatively little damage to healthy organs (52, 53). The

anticancer effects of 3-bromopyruvate have been recently reviewed (54), showing that the drug had fairly more complex activities than the straightforward inhibition of glycolysis. If these additive effects likely potentiate the antitumor effects of the drug, they may also complicate its clinical use. The inhibition of enhanced glucose transport (55) as well as of LDH activity (56) also exerts pro-apoptotic effects in tumor cells. Moreover, also the inhibition of carriers that provide the efflux route for lactate, such as the p53-regulated *MCT1/SLC16A1* (57) or the *MCTA4/SLC16A3* transporters (58), have remarkably effects on selected types of cancer cells.

Additional targets are also possible. For instance, ATP exerts a powerful feed-back inhibition on glycolysis so that, quite paradoxically, lowering intracellular ATP levels may provide an additional stimulus for high glycolytic flux and enhanced growth of cancer cells (see the discussion of this interesting item in (59)). Therefore, it is not surprising that many cancer cells have a high expression of Uncoupling Protein 2 (UCP2) as a means to suppress ATP synthesis and enhancing glycolytic flux (60). Thus, the inhibition of UCP2 may yield an approach to reprogram metabolism in cancer and to suppress tumor cell growth (61).

Also the widely used antidiabetic drug metformin, a well known AMPK activator, has recently gained much attention for its putative antineoplastic effects (62). For instance, the combination 2-deoxyglucose and metformin has dramatic antiproliferative and pro-apoptotic effects in prostate cancer cells (63). Even more interestingly, antiproliferative effects of metformin would be specific for p53^{-/-} cells (64), a genetic condition often associated with apoptosis-resistant cancer phenotypes. Also jasmonates, a class of experimental antitumor agents derived from plant stress hormones, interfere with oxidative glucose metabolism and circumvent apoptosis resistance, driving the tumor cell towards a non-apoptotic death (65).

Dichloroacetate (DCA) has gained much attention as an “anti-tumor metabolite”. DCA inhibits pyruvate dehydrogenase kinase isozymes, with a greater affinity for the isozyme II (which is commonly activated in glycolytic cancer cells), thus activating pyruvate dehydrogenase, increasing delivery of pyruvate into the mitochondria and enhancing oxidative

phosphorylation. Since DCA has been used in the treatment of lactic acidosis, its pharmacokinetic data are known, indicating a good tissue distribution (66). It has been claimed to exert antitumor activities *in vitro* and in xenografts (67) and to trigger apoptosis in non-small cell lung cancer, breast cancer, glioblastoma, endometrial cancer, and prostate cancer (66, 68, 69), although its activity may be restricted to tumor cells with mitochondrial low function (70). DCA has also other effects, such as the inhibition of HIF1 α by both a PHD-(Prolyl hydroxylase-) dependent mechanism (through an increase of mitochondria-derived aKG) and a PHD-independent mechanism (through p53 activation and activation of GSK3 β) (71). However, until now, no clinical study has confirmed the antineoplastic activities of DCA. Given that the big media pressure on this issue and the experience with MELAS syndrome (mitochondrial myopathy, encephalopathy, lactic acidosis and stroke-like episodes) patients treated with DCA (Kaufmann et al, 2006), which has indicated that DCA can cause symptomatic peripheral neuropathy, large and rigorous trials would be needed. It should be stressed, however, that since DCA is a simple, not patented, chemical no funding for such trials has to be expected from industry.

Also “old” drugs or drugs used for other indications are being evaluated as possible anti-tumor agents due to their effects on glycolysis. For instance, the antifungal agent clotrimazole decreases hexokinase (HK) binding to the outer mitochondrial membrane (72) and detaches phosphofructokinase-1 (PFK-1) and aldolase from the cytoskeleton (73, 74), is known to hamper glioma growth *in vivo* (75), to trigger apoptosis in breast and lung cancer cells *in vitro* (76, 77), and to specifically inhibit glycolysis in breast cancer tissue (78).

The metabolism of glutamine has also been targeted for therapeutic approaches (79). Actually, three glutamine analogues, acivicin, 6-diazo-5-oxo-L-norleucine (L-DON) and azaserine, were demonstrated many years ago to have a significant cytotoxic activity *in vitro* but attempts to translate these effects *in vivo* were hampered by significant multi-organ toxicity (80). One of the first effective antileukemic drugs to be introduced, the enzyme L-asparaginase (81, 82),

works as a metabolic drug, depleting extracellular asparagine with particularly severe consequences for those tumor cells that express low levels of Asparagine Synthetase (83) such as ALL blasts (84) and NK lymphomas (85). However, most of the commercially available forms of L-asparaginase have also a glutaminolytic activity and, hence, cause glutamine, as well as, asparagine depletion (86). The renewed interest for glutamine role in cancer cells is leading to the reconsideration of L-asparaginase in non haematological tumors with some encouraging results *in vitro* (87). Since glutaminase is requested for glutamine metabolism in tumor cells, glutaminase is also a potential therapeutic target, with promising results *in vitro* and in xenografts (88).

Besides exhibiting direct anticancer activities, metabolic interference with anaplerotic fuelling may sensitize tumor cells to chemotherapy, radiotherapy or biological agents that promote apoptosis and, conversely, metabolic effects of oncogenic mutations strongly contribute to resistant phenotypes. For instance, the antiapoptotic activities of AKT, which underlie several drug resistant tumor phenotypes, need adequate glucose availability, so that glucose shortage abolishes pro-life effects of the kinase (89). 2DG powerfully synergizes the antineoplastic effects of inhibitors of histone deacetylases on glioblastoma cells (90) and of doxorubicin, 5 FU, cyclophosphamide, and herceptin in breast cancer cells (91). Both 2DG and the fatty acid beta-oxidation inhibitor etomoxir synergize a panel of anticancer drugs (92). 2DG also sensitizes melanoma cells to TRAIL - (93) and TNF α -induced cell death (94), while 3-Bromopyruvate potentiates the anti-proliferative effects of low-dose platinum, even in resistant p53-deficient cells (95). Significant synergy with chemotherapeutic drugs is also exhibited by DCA (96) and phloretin, an inhibitor of GLUT transporters (97).

Finally, the possibility to modulate cancer growth with diet should be mentioned. Indeed, Ketogenic Diet (KD), a low-carbohydrate, high-fat regimen particularly rich in medium chain fatty acids currently in use in selected neurological disorders (98, 99), has the capability to reproduce the effects of glycolysis inhibitors, at least in term of reducing glucose availability and hence glycolytic flux in cancer cells. Most of

the evidence comes from work on brain tumors (100, 101). When treated with ketogenic diet, murine glioma models exhibit prolonged survival of the host, markedly decreased growth rates, reduced ROS production, and overall reversion of tumor-associated gene expression pattern (102). Anecdotal evidence in humans is consistent with those findings (103, 104) with the supplementary benefit of an improved quality of life (105). However, KD is substantially ineffective in the control of tumour growth in patients with tuberous sclerosis (106) and data from specific clinical trials are not yet available. The antitumor effects of KD, which are not restricted to gliomas (107), may involve the activation of PPAR by fatty acids, suggesting that components of KD may directly affect metabolic alterations in tumors (108).

Conclusions

Specificity for cancer cells, significant antitumor efficacy and failure to promote resistant phenotypes are the goals for any antitumor drug. No metabolic drug developed thus far fulfils these requirements. This is likely due to the relevance of the genetic context to determine which enzyme (pathway) is essential for a given cancer cell and to the remarkable ability of tumor cells to adapt to alterations in critical metabolic pathways. These caveats indicate that accurate selection of cancer phenotypes (and hence of patients in the future) will be needed to identify what enzyme(s) is (are) to be targeted in a given tumor (109).

The two most important reasons for the poor performance of antineoplastic drugs are the high adaptability of cancer cells and the molecular heterogeneity even within a single tumour. For this reason, it is highly unlikely that the metabolic approaches to cancer therapy cited above will ever yield a monotherapy, although intensive research work is trying to connect specific metabolic features to specific molecular alterations in a growing number of cancer types.

Rather, metabolic therapies will likely add to other therapeutic approaches. Indeed, metabolic alterations often constitute the cause of tumour resistance to radiotherapy and chemotherapy, so that normalization of tumor cell metabolism would probably also revert its re-

sistance to therapy. However, the extent to which metabolic alterations contribute to cancer phenotype, and even to cancerogenesis, is no more underestimated and drugs aimed to selectively address these alterations are expected to enter soon in clinical practice.

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