

Targeting Cancer Metabolism

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Abstract

The understanding that oncogenes can have profound effects on cellular metabolism and the discovery of mutations and alterations in several metabolism-related enzymes—*isocitrate dehydrogenase 1 (IDH1)*, *isocitrate dehydrogenase 2 (IDH2)*, *succinate dehydrogenase (SDH)*, *fumarate hydratase (FH)*, and *pyruvate kinase M2 (PKM2)*—has renewed interest in cancer metabolism and renewed hope of taking therapeutic advantage of cancer metabolism. Otto Warburg observed that aerobic glycolysis was a characteristic of cancer cells. More than 50 years later, we understand that aerobic glycolysis and uptake of glutamine and glycine allow cancer cells to produce energy (ATP) and the nucleotides, amino acids, and lipids required for proliferation. Expression of the *MYC* oncogene drives the increase in cellular biomass facilitating proliferation. PKM2 expression in cancer cells stimulates aerobic glycolysis. Among intermediary metabolism enzymes, mutations in SDH occur in gastrointestinal stromal tumors and result in a pseudo-hypoxic metabolic milieu. FH mutations lead to a characteristic renal cell carcinoma. *Isocitrate dehydrogenase (IDH1/2)* mutations have been found in leukemias, gliomas, prostate cancer, colon cancer, thyroid cancer, and sarcomas. These recently recognized oncogenic metabolic lesions may be selective targets for new anticancer therapeutics. *Clin Cancer Res*; 18(20); 5537–45. ©2012 AACR.

Introduction

Cancer requires specific metabolic programming for proliferation

Even in ancient times, cancer was recognized to be a problem of abnormal growth. The earliest anticancer drugs focused on attacking cancer through selective toxicity toward proliferating cells. Several of the earliest anticancer drugs are the purine and pyrimidine antimetabolites that directly target critical metabolic pathways required for proliferation (1). Taking advantage of the differential expression of specific enzymes by malignant cells led to the drug cyclophosphamide, which was designed to be activated selectively in tumor cells that overexpress phosphoramidase by a sequence of metabolic reactions (2). The Warburg effect, glycolysis under aerobic conditions, is one of the most highly validated observations in cancer research and continues to be of interest (3). The current wave of interest in cancer metabolism was stimulated by new knowledge about mutations in intermediary metabolism enzymes and by an understanding that "oncogenes" can have profound effects on cellular metabolic processes (4). This *CCR Focus* section highlights aspects of cancer metabolism and renewed hope of taking advantage of altered cancer metabolism therapeutically.

Cellular metabolic regulation is critically linked to availability of nutrients. Cellular proliferation requires active nutrient uptake; synthesis of DNA, RNA, proteins, and lipids; and energy (ATP). Thus, oncogenes that drive cells to proliferate also directly or indirectly drive metabolic changes (5, 6). Inhibitors of cellular proliferation that block or terminate DNA synthesis or that cross-link or fragment DNA characterize many classic anticancer agents. These drugs are directed toward normal cellular proliferation processes and therefore lack selectivity for neoplastic cells over proliferating normal cells. The same is true of classic inhibitors of intermediary metabolism, many of which were enzyme transition state analogues. Mutant enzymes in tumors provide the potential for discovery of selective, drug-like inhibitors of the mutant enzyme. The development of drug-like compounds that selectively block certain protein–protein interactions may allow targeting of amplified or overexpressed metabolism-controlling oncogenic proteins. The systematic characterization of the metabolic pathways active in cancer cells is an ongoing endeavor. Jain and colleagues (7) measured the consumption and release profiles of 219 small-molecule metabolites from cell culture media in the NCI-60 cancer cell line panel, integrated these data with gene expression, and found that glycine consumption and the mitochondrial glycine biosynthetic pathway correlated with cellular proliferation rate (7, 8).

Normal differentiated cells generate the energy mainly by mitochondrial oxidative phosphorylation, whereas normal proliferating cells and cancer cells favor aerobic glycolysis, a less efficient process for generating ATP but a process that allows production of nucleotides, amino acids, and lipids in addition to ATP, thus preparing the cell for division (Figs. 1, 2; refs. 9, 10). Cancer cells obtain energy and

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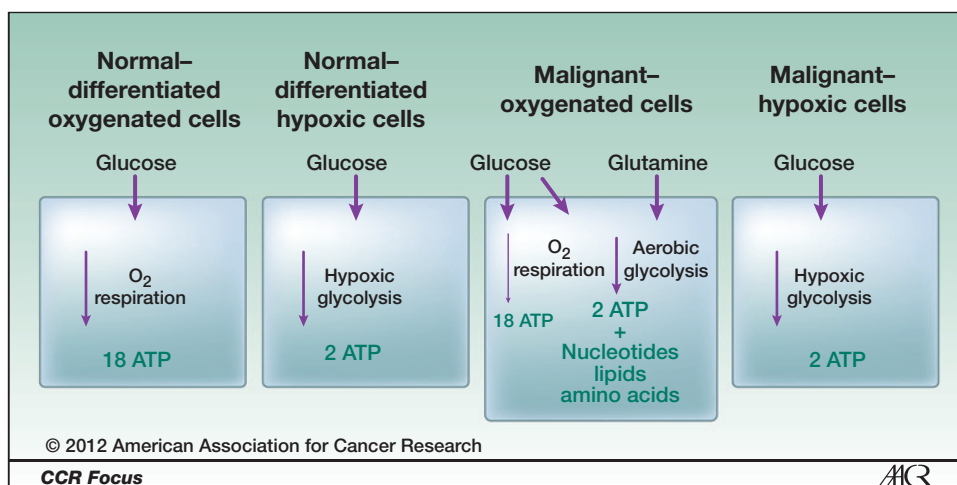


Figure 1. Schematic illustrating the sources of ATP energy used by normal and malignant cells under varied conditions of oxygenation.

carbon intermediates from glycolysis without accumulation of reactive oxygen species (ROS), which can damage DNA and other cellular components. Glucose glycolytic metabolism along with glutamine and glycine uptake provides the small carbon compounds, NADPH and ATP. Glucose glycolytic metabolism is dominant under hypoxic conditions (Figs. 1, 2; ref. 11). Understanding metabolism requires knowledge of metabolite profiles, concentrations, and fluxes and of enzyme kinetics and networking of intracellular metabolite fluxes. Cascante and colleagues identified metabolite fluxes through the oxidative and nonoxidative pentose phosphate pathway and routing of glucose to anaerobic glycolysis and the tricarboxylic acid (TCA) cycle (Fig. 2; ref.12). Stable isotope resolved metabolomics was applied to analysis of gene dysregulations by infusing uniformly labeled ^{13}C -glucose into patients followed by tumor resection. Nuclear magnetic resonance (NMR) and gas chromatography/mass spectroscopy (GCMS) were used for ^{13}C -based metabolomics analysis. Lactate, alanine, succinate, glutamate, aspartate, and citrate in tumors were ^{13}C -enriched, suggesting glycolysis and TCA cycle activity. Enhanced ^{13}C -aspartate production with 3 ^{13}C -labeled carbons and the buildup of ^{13}C -2,3-glutamate was consistent with the incorporation of glucose into aspartate or glutamate via glycolysis, pyruvate carboxylation, and the TCA cycle (Fig. 2). Pyruvate carboxylation may be important for replenishing TCA cycle intermediates, which can be diverted to lipid, protein, and nucleic acid biosynthesis (13). Several signaling pathways that incorporate nutrients into cellular components and some cancer-associated mutations facilitate nutrient metabolism to proliferation over ATP production (14).

Aerobic Glycolysis Supports ATP Production and Macromolecular Synthesis

Uncoupling glycolysis from oxidative phosphorylation in the TCA cycle fulfills requirements for energy production and biosynthesis of cellular components. In glycolysis, the 6-carbon sugar glucose is oxidized and split to make 2 molecules of pyruvate and 2 ATP molecules (Figs. 1, 2). The pyruvate is further metabolized to

acetyl-CoA, ethanol, or lactate. In normal oxygenated conditions, the pyruvate can be converted to acetyl-CoA and via the TCA cycle, and through oxidative phosphorylation to 18 ATP molecules (15).

Glutamine is an important tumor nutrient that contributes to nearly every metabolic function required of proliferating tumor cells (Fig. 2). Glutamine is involved in bioenergetics, defense against oxidative stress, and along with glucose metabolism in macromolecule precursor biosynthesis. The oncoprotein myc regulates glutamine uptake and degradation (16). Metabotropic glutamate receptors (gene, *GRM1*; protein, mGluR1) are G-protein-coupled protein receptors expressed in the normal central nervous system (CNS) and by some cancers including melanoma and triple-negative breast cancer. Metabotropic glutamate receptor 1 (mGluR1) inhibitors (riluzole or BAY36-7620) or mGluR1 knockdown can inhibit growth of melanoma and triple-negative breast cancer xenografts (17). mGluR1 has been implicated as an oncogene in melanomagenesis. Wangari-Talbot and colleagues developed a transgenic mouse expressing ectopic GRM1 in melanocytes, which was sufficient to induce melanoma (18). Combining the kinase inhibitor sorafenib or the mutant B-Raf inhibitor vemurafenib with riluzole had improved antitumor activity in GRM1-expressing melanoma cells harboring either wild-type or mutant B-RAF (19). Clinical trials with riluzole are under way in melanoma and other solid tumors (20, 21).

Myc and Hedgehog in Cancer Bioenergetics

The MYC oncogene is a driver in many human cancers stimulating cellular biomass accumulation (see review by Miller and colleagues in this issue; ref 22). The Myc transcription factor regulates genes involved in cell growth, including those regulating ribosome and mitochondrial biogenesis and intermediary metabolism; and glycolytic genes, enhancing glycolysis, glutamine uptake and metabolism, and lactate production. In normal cells, the MYC gene is regulated by intracellular and extracellular cues, such as nutrient and oxygen availability. When nutrients and/or oxygen are low, MYC is downregulated. In many cancers,

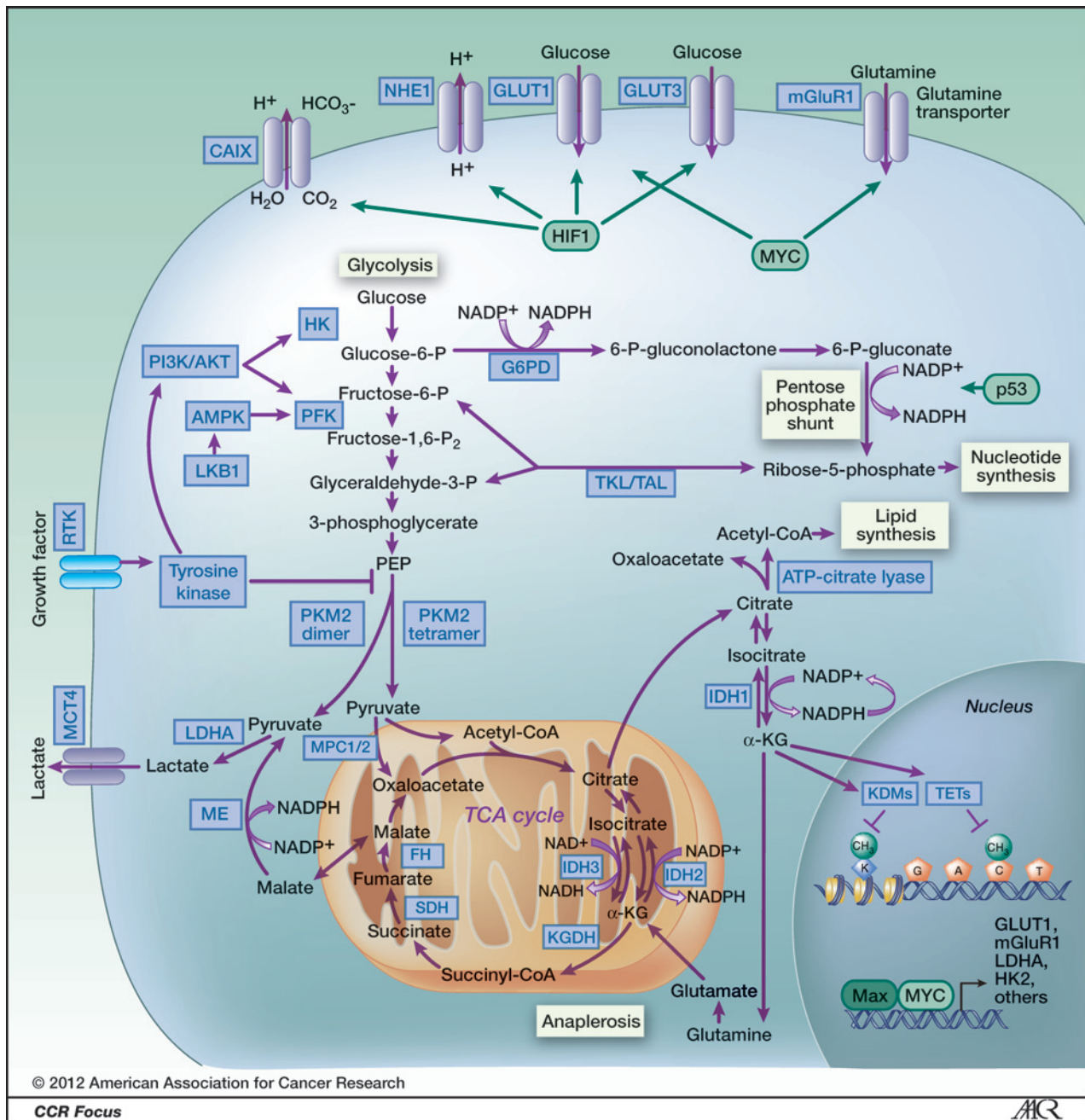


Figure 2. Schematic illustrating metabolic pathways prominent in malignant cells. Blue boxes indicate enzymes and transporters that may be useful therapeutic targets in cancer. Green ovals represent transcription factors that alter metabolic pathways. Glycolysis is the 10-step metabolic pathway that converts glucose into pyruvate. The free energy released in this process is used to form the high-energy compounds ATP and NADH. The pentose phosphate pathway is a process that generates NADPH and 5-carbon sugars as alternatives to glycolysis. Nucleotide synthesis provides molecules that make up the individual structural units of the nucleic acids RNA and DNA. In addition, nucleotides participate in cell signaling (cGMP and cAMP) and are cofactors of enzymatic reactions, and nucleoside triphosphates are sources of chemical energy. Fatty acid synthesis is the synthesis of fatty acids from acetyl-CoA and malonyl-CoA precursors via fatty acid synthases. Anaplerotic reactions are those that replenish and maintain intermediates of a metabolic pathway. CAIX, carbonic anhydrase IX; G6PD, glucose-6-phosphate dehydrogenase; GLUT1, glucose transporter 1; GLUT3, glucose transporter 3; HK, hexokinase; IDH3, isocitrate dehydrogenase 3; KDM, lysine histone demethylases; KGDH, 2-keto-glutarate dehydrogenase; LKB1, serine/threonine kinase 11 (STK11), liver kinase B1; MCT4, monocarboxylate transporter 4; ME, malic enzyme, malate dehydrogenase; NHE1, Na⁺/H⁺ exchanger; PEP, phosphoenolpyruvate; PFK, phosphofructokinase; PI3K/AKT, phosphatidylinositol-3-kinase/protein kinase b; RTK, receptor tyrosine kinase; TET, tet methylcytosine dioxygenases; TKL/TAL, transketolase/transaldolase.

MYC is activated or altered, resulting in dysregulated ribosome biogenesis and cell mass accumulation and thus addicting cancer cells to nutrients. In the absence of glucose or glutamine, cells with MYC overexpression die (23). Le and colleagues developed a MYC-inducible human Burkitt lymphoma P493 cell line and examined metabolic response under aerobic and hypoxic conditions, or glucose deprivation, using ^{13}C -based metabolomics. ^{13}C -glucose consumption and lactate production were increased by myc expression and hypoxia. ^{13}C -glutamine uptake and metabolism by the TCA cycle persisted under hypoxia, and contributed to citrate carbons. In the absence of glucose, glutamine-derived fumarate, malate, and citrate increased. Glutamine is essential for cell survival and proliferation in hypoxia and/or low glucose, which makes these cells susceptible to glutaminase inhibition (24). The relationship between oncogene signaling and glycolytic activity was explored using a Myc-driven liver cancer model to visualize glycolysis. Lactate dehydrogenase A (LDHA) abundance in tumors correlated with pyruvate conversion to lactate and decreased as tumors regressed (Fig. 2; refs. 25, 26). Targeting myc–max dimerization or myc-induced microRNA expression may also be effective therapeutically (27). Cancer cells require glucose and glutamine catabolism as well as other small molecules used for macromolecular synthesis to proliferate. Myc transcriptional regulation coordinates glutamine catabolism for protein and nucleotide biosynthesis. Myc-dependent glutaminolysis reprograms mitochondrial metabolism to glutamine catabolism to sustain TCA cycle activity. Mitochondrial glutamine metabolism decreases glucose carbon entering the TCA cycle and glucose mitochondrial-dependent synthesis of phospholipids. Thus, oncogenic MYC induces a transcriptional program that promotes glutaminolysis and cellular addiction to glutamine as a bioenergetic substrate (28).

Sonic hedgehog (Shh) signaling is aberrantly active in a spectrum of human malignancies. High lipid synthesis is a hallmark of Shh-driven medulloblastoma. Hedgehog signaling inactivates the Rb/E2F tumor-suppressor complex to promote lipogenesis. Shh-metabolic activity facilitates tumor progression in an E2F1- and FASN-dependent manner. The nutrient sensor PPAR- γ , a component of the Shh metabolic network, regulates glycolysis and is elevated in Shh-driven medulloblastoma. PPAR- γ inhibition and/or Rb inactivation inhibits cell proliferation and drives medulloblastoma cell death. Mitogenic Shh coupling to a nutrient sensor and metabolic transcriptional regulator defines the mechanism through which Shh drives cancer, controls the cell cycle, and regulates the glycolysis (29).

Addiction to Glucose and Glutamine

Targeting glucose metabolism may be a selective way to kill cancer cells. Several glycolytic enzymes are required to maintain a high glucose metabolism (30). Transcriptomic, proteomic, functional, and structural properties of cancer cell mitochondria indicate impaired biogenesis and organelle activity. Cancer has a bioenergetics signature described

by the ratio of oxidative phosphorylation and glycolysis that reflects metabolic activity and may correlate with response to chemotherapy (31). Some human carcinomas overexpress mitochondrial ATPase inhibitory factor 1 (IF1), which blocks the activity of mitochondrial H^+ -ATP synthase and facilitates metabolic adaptation to aerobic glycolysis. IF1 upregulation in colon cancer cells triggers mitochondrial hyperpolarization and promotes proliferation (32).

Cancer cells are resistant to mitochondrial apoptosis perhaps due to upregulation of glycolysis, accumulation of mitochondrial genome mutations, switch from respiration to glycolysis, or the metabolic reprogramming from mutant enzymes like fumarate hydratase (FH) and succinate dehydrogenase (SDH; ref. 33). In tumor cell mitochondria, oxidative metabolism of glucose- and glutamine-derived carbon produces citrate and acetyl-coenzyme A for lipid synthesis (Fig. 2). Tumor cells with defective mitochondria use glutamine-dependent reductive carboxylation via mitochondrial and cytosolic NADP/NADPH-dependent isocitrate dehydrogenase (IDH) as the major citrate forming pathway. Metabolism of glutamine-derived citrate provides both the acetyl coenzyme A for lipid synthesis and the 4-carbon intermediates needed to produce TCA cycle metabolites and related macromolecular precursors. The glutamine-dependent pathway is the dominant mode of metabolism in malignant cells with mutations in electron transport chain complex I or complex III, and in renal carcinoma cells with mutant FH. The glutamine-dependent pathway reverses many canonical TCA cycle reactions, supports tumor cell growth, and explains generation of TCA cycle intermediates by cells with impaired mitochondria (34).

Mitochondrial membrane permeabilization, a critical event in physiologic or stress-induced apoptosis, is controlled by the permeability transition pore complex. Oncoproteins from the Bcl-2 family and tumor-suppressor proteins from the Bax family interact with the permeability transition pore complex to inhibit or facilitate membrane permeabilization, respectively. Experimental agents, including lonidamine, arsenite, betulinic acid, CD437, and several amphipathic cationic α -helical peptides, act on mitochondrial membranes and/or on the permeability transition pore complex to induce apoptosis. Mitochondrial membrane stabilization by antiapoptotic Bcl-2-like proteins reduces the cytotoxicity of these agents (35, 36). In HCT116 colon cancer cells treated with oligomycin repression of nuclear-encoded mitochondrial protein synthesis occurs, but glycolytic protein synthesis is not affected. Translational control of mitochondrial proteins is controlled by AMP-activated protein kinase (AMPK), general control nonderepressible 2 (GCN2) kinase, and silencing of activating transcription factor 4. Thus, glycolysis and oxidative phosphorylation are controlled at different levels of gene expression, providing the cell a mechanistic strategy for metabolic adaptation under stressful conditions (37). Metformin inhibits gluconeogenesis gene transcription in the liver, increases glucose uptake in skeletal muscle, and decreases circulating insulin. Thereby, metformin reduces circulating

glucose, increases insulin sensitivity, reduces insulin resistance-associated hyperinsulinemia, and activates AMPK. Preclinical data showing potential metformin anticancer activity along with epidemiologic and retrospective data supporting metformin antineoplastic effects provided a rationale to evaluate metformin in clinical trials (38).

Using a synthetic lethal screen, Chan and colleagues identified compounds that exploit the loss of the von Hippel-Lindau tumor-suppressor gene in renal cell carcinoma. Renal cell carcinoma is dependent on aerobic glycolysis for ATP production, which is facilitated by induction of glucose transporter 1 (GLUT1; Fig. 2). Exposure to GLUT1 antagonists inhibits renal cell carcinoma cell proliferation by blocking glucose uptake (39). The spatial distribution of GLUT1 and monocarboxylate transporter (MCT) was examined in relation to vasculature and survival in non-small cell lung cancer fresh-frozen biopsies. Squamous cell carcinomas had the highest GLUT1 expression. In squamous cell carcinomas, GLUT1 and MCT expression increased with increasing distance from vasculature. In adenocarcinomas, high GLUT1 expression correlated with poor differentiation and high GLUT1 plus high MCT expression was associated with poor survival (40).

PKM2 and Glycolysis

Pyruvate kinase has 2 isoforms: M1 (PKM1) and M2 (PKM2). PKM2 expression in cancer cells stimulates aerobic glycolysis (Fig. 2; see review by Tamada and colleagues in this issue; ref 41). Several siRNAs targeting PKM2 decreased viability in multiple cancer cell lines. *In vivo*, siPKM2 delivery caused regression of established xenografts (42). Control of intracellular ROS is critical for cell survival. In human lung cancer cells, acute increases in intracellular ROS inhibited PKM2. PKM2 inhibition is required to direct glucose into the pentose phosphate pathway to generate reducing potential for ROS detoxification. Lung cancer cells transfected with an oxidation-resistant mutant PKM2 had increased sensitivity to oxidative stress. PKM2 may protect cancer cells from oxidative stress (43).

The mitochondrial pyruvate carrier (MPC) is a hetero-complex of mitochondrial pyruvate carrier 1 (MPC1) and mitochondrial pyruvate carrier 2 (MPC2) on the inner mitochondrial membrane, which carries pyruvate into mitochondria (44). The absence of MPC1 or MPC2 impairs pyruvate oxidation. Human genetic defects in 3 families with children suffering from lactic acidosis and hyperpyruvatemias mapped to the MPC1 locus (45). MCT inhibition is a potential metabolic therapeutic target in cancer. Cancer cells proliferate more rapidly in the presence of pyruvate supplementation, which stimulates mitochondrial oxygen consumption and increases reserve respiratory capacity. An MCT inhibitor decreased mitochondrial respiration and cell growth (46). PKM2 regulates the serine synthetic pathway. Tumor cells use serine-dependent regulation of PKM2 and GCN2 to modulate glycolytic intermediate flux in support of cell proliferation (47).

A proteomic screen for phosphotyrosine-binding proteins revealed that PKM2 binds directly to tyrosine-phos-

phorylated peptides resulting in release of fructose-1,6-bisphosphate and in PKM2 inhibition. PKM2 regulation by phosphotyrosine signaling diverts glucose metabolites from energy production to anabolic processes for cell growth (48). CD44 interacts with PKM2 and enhances the glycolytic phenotype of cancer cells that are either deficient in p53 or exposed to hypoxia. RNA interference (RNAi) CD44 ablation increases metabolic flux to mitochondrial respiration and inhibits glycolysis and the pentose phosphate pathway (49).

Mutant Succinate Dehydrogenase in Cancer

The frequent mutations of several metabolic enzymes in cancer support a driver role for altered metabolic enzymes in tumorigenesis (50). A mutation in a conserved SDH domain in 2 siblings with complex II deficiency presenting as Leigh syndrome, a rare neurometabolic disorder that affects the CNS, caused a mitochondrial respiratory chain deficiency (51). In cancer cells with mutant SDH, succinate can accumulate in mitochondria and cytosol and inhibit prolyl hydroxylase enzymes. Depending on the specific prolyl hydroxylase inhibited, cells become resistant to apoptotic signals and/or activate a pseudohypoxic response that enhances glycolysis via hypoxia-inducible factor (HIF; Fig. 2; ref.52). Carney-Stratakis syndrome, an inherited condition predisposing individuals to gastrointestinal stromal tumor and paraganglioma, is caused by SDH germline mutations, leading to electron transport chain complex II dysfunction. When patients with sporadic gastrointestinal stromal tumor were tested, 4 of 34 patients (12%) had germline mutations in SDH (53, 54). SDH germline mutations are responsible for sporadic paragangliomas (6%), sporadic pheochromocytomas (9%), and >80% of familial paraganglioma and pheochromocytoma (55). The loss of SDH leads to accumulation of succinate that acts as a competitor to α -ketoglutarate (α -KG) to inhibit TET catalyzed hydroxylation of 5-methylcytosine leading to DNA hypermethylation (56).

Mutant Fumarate Hydratase in Cancer

FH is an enzyme of the TCA cycle that catalyzes the hydration of fumarate into malate (Fig. 2). Hereditary leiomyomatosis renal cell carcinoma, an aggressive form of renal cell carcinoma characterized by *FH* germline mutation, is highly metastatic and often lethal. FH absence leads to fumarate accumulation, which impairs HIF degradation at normal oxygen tensions. Cell survival without a functional TCA cycle was explored using *Fh1*-deleted mouse kidney cells and a computer model of metabolism in these cells. A metabolic pathway beginning with glutamine uptake and ending with bilirubin excretion from *Fh1*-deleted cells involving the biosynthesis and degradation of heme enabled *Fh1*-deleted cells to use accumulated TCA cycle metabolites and permitted some mitochondrial NADH production. Targeting this pathway was lethal to *Fh1*-deleted cells, but not *Fh1* wild-type cells. Therefore, inhibition of heme oxygenation is synthetically lethal when combined with *Fh1*-deletion (57, 58). FH inactivation drives a

metabolic shift to aerobic glycolysis in FH-deficient kidney tumors resulting in decreased AMPK and p53 tumor suppressor and activation of the anabolic factors, acetyl-CoA carboxylase and ribosomal protein S6. Reduced AMPK leads to diminished iron transport. The consequent iron deficiency activates iron regulatory proteins and increases expression of HIF-1 α . HIF-1 α silencing or AMPK activation decreases invasion, suggesting that HIF-1 α and AMPK alterations contribute to FH-deficient cell growth (59). *FH* tumor-suppressor gene loss results in tumor development that can progress to aggressive, metastatic cancers. *Fh1* knockdown in mouse embryo fibroblasts results in increased c-met through HIF stabilization. Restoration of *Fh1* expression abrogated the mitogenic and transformed phenotype of *Fh1*-deleted cells (60). Von Hippel-Lindau (*VHL*) or *FH* gene mutations produce morphologically distinct renal cell carcinomas with altered HIF-1 α expression resulting in a pseudohypoxic state (61). The UOK 262 cell line, derived from a patient with an aggressive FH-deficient renal cell carcinoma, was characterized for gene expression, chromosome profiles, bioenergetics, mitochondrial ultrastructure, FH catabolic activity, invasiveness, and glucose requirements. UOK262 cells have compromised oxidative phosphorylation, are dependent on aerobic glycolysis and glucose, have high lactate efflux, and overexpress GLUT1 and LDHA (Fig. 2). UOK262 xenografts retain the characteristics of FH-deficient renal cell carcinoma (62). Inactivating FH mutations in UOK262 cells result in glucose-mediated ROS generation and ROS-dependent HIF-1 α stabilization (63). The germline FH missense mutation UOK268 cell line has a mutant FH protein that localizes to the mitochondria but has almost no catalytic activity resulting in compromised oxidative phosphorylation and increased glycolytic flux (64). *Fh1*-deficient mouse embryonic fibroblast lines have upregulated HIF-1 α and HIF target genes, dependence on glycolysis, and an elevated lactate efflux, associated with glycolytic enzyme upregulation. In a variety of FH-deficient tissues, there was increased PKM2 and LDHA (65).

IDH1 and IDH2 Mutants in Cancer

Frequent isocitrate dehydrogenase 1 (IDH1) and isocitrate dehydrogenase 2 (IDH2) heterozygous somatic mutations in acute myeloid leukemia (33%), glioblastoma (70% of low-grade gliomas and secondary glioblastomas), and chondrosarcomas (56%) have stimulated interest in targeting the mutant enzymes (see review by Yang and colleagues in this issue; ref 66). Mutant IDH1 and IDH2 activity changes in cell metabolic profile may be tied to cancer epigenetics (67–69). Glioblastoma genome-wide mutational analysis showed somatic IDH1 mutations occur frequently in tumors that evolved from lower-grade gliomas. Ichimura and colleagues (70) screened *IDH1* gene exon 4 for mutations in 596 primary intracranial tumors. Codon 132 mutation occurred in 54% of astrocytomas, 65% of oligodendroglial tumors, and in 6% of glioblastomas (3% of primary and 50% of secondary glioblastomas). *TP53* gene mutations and total 1p/19q deletions were mutually exclusive, and IDH1 mutation along with *TP53*

mutation or total 1p/19q loss was a frequent early change in oligodendroglial tumors, diffuse astrocytomas, anaplastic astrocytomas, and secondary glioblastomas (70, 71). In 445 CNS tumors and 494 non-CNS tumors, mutations that affect IDH1 amino acid 132 were found in more than 70% of astrocytomas and oligodendrogliomas and in glioblastomas developed from lower-grade lesions. Tumors without IDH1 mutations often had mutations affecting IDH2 amino acid R172. Patients with IDH1- or IDH2-mutant tumors had better outcomes than those with wild-type *IDH* genes (72, 73). When IDH1-mutant diffuse glioma infiltration patterns were determined by single tumor cell identification using an antimutant IDH1 R132H antibody, tumor cells appeared throughout the brain; thus, diffuse glioma is a whole-brain disease (74, 75).

The frequency of IDH R132 mutations in 1,200 mesenchymal tumors (220 cartilaginous tumors, 222 osteosarcomas, and 750 bone and soft tissue tumors) was determined. Cartilaginous tumors and chondroblastic osteosarcomas, wild-type for IDH1 R132, were analyzed for IDH2 (R172, R140) mutations. Heterozygous somatic IDH1/IDH2 mutations were detected in 56% of central and periosteal cartilaginous tumors (40% R132C; 60% R132H). The ratio of IDH1:IDH2 mutations was 10.6:1. IDH1 and IDH2 mutations are the first common genetic abnormalities identified in conventional central and periosteal cartilaginous tumors (76).

The mutant IDH enzymes produce 2-hydroxyglutarate (2HG) from α -KG (Fig. 2). 2HG-producing IDH mutants can prevent histone demethylation required for lineage-specific progenitor cells to differentiate. In glioma samples, IDH mutations associated with gene expression profiles enriched for genes expressed in neural progenitor cells and increased histone methylation. In adipocytes, mutant IDH transfection or exposure to cell-permeable 2HG repressed differentiation gene expression and increased repressive histone methylation marks. Stable 2HG-producing mutant IDH transfection in immortalized astrocytes produced progressive histone methylation (77). Glioblastomas and other cancers with the CpG-island methylator phenotype (CIMP) constitute a subset of tumors with extensive epigenomic aberrations. IDH1 mutation establishes CIMP by remodeling the methylome and transcriptome. Mutant IDH1 epigenomic alterations activate glioma-CIMP-positive proneural gene expression programs (78). Mutant IDH inhibitors in combination with the DNA methylation inhibitors, decitabine and azacitidine, may be useful therapeutically (79).

Human oligodendrogloma metabolites (>200) were profiled to examine mutant IDH1 and IDH2 effects. Amino acids, glutathione metabolites, choline derivatives, and TCA cycle intermediates were altered in mutant IDH1- and IDH2-expressing cells. Similar changes occurred after exposure to 2HG. *N*-acetyl-aspartyl-glutamate (NAAG), a brain dipeptide, was reduced 50-fold in IDH1-mutant cells and 8.3-fold in IDH2-mutant cells (80). 2HG is a competitive inhibitor of α -KG-dependent dioxygenases, including histone demethylases and TET family 5-methylcytosine (5mC)

hydroxylases (Fig. 2). IDH1 mutations are associated with increased histone methylation and decreased 5-OH-mC (81). In 460 pediatric AML samples, a small number of genes distinguished IDH-mutated patients and IDH wild-type patients, including a deregulated tryptophan metabolism pathway in IDH-mutated cases (82). Mutational and epigenetic patient profiling showed that IDH1/2-mutant leukemias had DNA hypermethylation. IDH1/2 mutations were mutually exclusive from α -KG-dependent enzyme TET2 mutations, and TET2 loss-of-function mutations were associated with similar epigenetic defects as IDH1/2 mutations. Mutant IDH1/2 expression or TET2 depletion impaired hematopoietic differentiation and increased progenitor cell marker expression (83). Metabolomic studies of IDH1/2-mutant cells indicate alterations in glutamine, fatty acid, and citrate synthesis pathways (84, 85).

Ollier disease and Maffucci syndrome are nonhereditary skeletal disorders characterized by multiple enchondromas (Ollier disease) combined with soft tissue spindle cell hemangiomas (Maffucci syndrome). Somatic heterozygous mutations in IDH1 (R132C and R132H) or IDH2 (R172S) occur in 87% of enchondromas (benign cartilage tumors) and in 70% of spindle cell hemangiomas (benign vascular lesions). In total, 35 of 43 (81%) Ollier disease and 10 of 13 (77%) patients with Maffucci syndrome carried IDH1 (98%) or IDH2 (2%) mutations. Immunohistochemistry for mutant IDH1 R132H protein suggested intraneoplastic and somatic mosaicism (86, 87).

Therapeutic Opportunities

Lessons from a century of metabolic research can be explained by a small set of biochemical principles. Glycolysis is a pathway that meets proliferating cellular demands (88). Metabolic modeling allows systematic, genome-scale study of human metabolism by using high-throughput omics data (see review by Jerby and Rupp in this issue; ref 89). The first genome scale network model of cancer metabolism, validated by correctly identifying genes essential for proliferation in cancer cell lines, predicted 52 drug targets of which 40% are targeted by approved or experimental anticancer drugs (90).

Metabolomics is the quantitative assessment of endogenous metabolites within a biologic system. Knowing a metabolome may allow early cancer detection and diagnosis or be a predictive and pharmacodynamic marker of drug effect. Metabolic and molecular imaging technologies, such as positron emission tomography (PET) and MRI, enable noninvasive metabolic marker detection (91). The HIF-1 pathway affects response to radiotherapy by HIF-1 protection of vasculature after irradiation and regulation of glycolysis and the pentose phosphate pathway, thus increasing

tumor antioxidant capacity (see review by Meijer and colleagues in this issue; ref. 92). [18F]-fluorodeoxyglucose-PET images can be used to quantitatively determine glucose metabolic rate and pharmacokinetic rate constants in tissue volumes, which is useful for radiotherapy pharmacokinetic analysis conducted to determine the rate constants of fluorodeoxyglucose metabolism on 41 patients (104 lesions). The highest glucose metabolic rate tumor regions had high cellular uptake and phosphorylation rate constants with relatively low blood volume. In regions with less metabolic activity, the blood volume fraction was higher and cellular uptake and phosphorylation rate constants lower. Thus, tumor glucose phosphorylation rate was not dependent on nutrient transport (93, 94).

Understanding the metabolic basis of cancer has the potential to provide the foundation for the development of novel approaches targeting tumor metabolism. Tumors characterized by aerobic glycolysis and/or glucose dependence could be more sensitive than other tumors to agents targeting the tumor vasculature and glucose transport. Tumors characterized by impaired TCA cycle function and/or respiration that is glutamine dependent could be sensitive to agents targeting glutamine metabolism (such as glutaminase). Tumors that have impaired mitochondrial/electron transport function could be sensitive to agents that target the reductive carboxylation and fatty acid synthesis pathways. Malignancies that are characterized by IDH1, IDH2, FH, or succinate dehydrogenase mutations could affect TET2 function, resulting in hypermethylation phenotypes (56, 83). Such malignancies could be responsive to hypomethylating agents.

The reemergence of interest in cancer metabolism stems from discoveries that a number of oncogenes and tumor suppressor genes control cell metabolism and that mutated intermediary metabolism enzymes can act as human tumor suppressors or oncogenes. Targeting cancer metabolism with drugs requires a therapeutic window in which tumor cells have a greater dependence on specific enzymes than normal tissues. Tumors with distinct oncogenic lesions are more likely to respond to drugs that target altered metabolic pathways (95).

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors' Contributions

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