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## Mitochondrial Metabolism as a Target for Cancer Therapy

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### Abstract

Recent evidence in humans and mice supports the notion that mitochondrial metabolism is active and necessary for tumor growth. Mitochondrial metabolism supports tumor anabolism by providing key metabolites for macromolecule synthesis and generating oncometabolites to maintain the cancer phenotype. Moreover, there are multiple clinical trials testing the efficacy of inhibiting mitochondrial metabolism as a new cancer therapeutic treatment. In this review, we discuss the rationale of using these anti-cancer agents in clinical trials and highlight how to effectively utilize them in different tumor contexts.

### Introduction

Historically, mitochondrial metabolism has been viewed as inconsequential to support the metabolic demands of rapidly proliferating cancer cells (Warburg, 1956). This view is founded upon the seminal observation, made in the 1920s by Otto Warburg, that tumor slices take up glucose and produce excess lactate regardless of oxygen availability (Koppenol et al., 2011). This has been referred to as aerobic glycolysis or the Warburg effect and has shaped the way generations of scientists think about the role of mitochondrial metabolism in cancer. Warburg postulated “injury to respiration” as a prerequisite for malignant transformation. Thus, glycolysis was ascribed to be the primary metabolic pathway necessary for tumor proliferation (Warburg, 1956). Ultimately, mitochondrial dysfunction and aerobic glycolysis have become widely accepted as hallmarks of cancer (Hanahan and Weinberg, 2011).

The long-standing belief that mitochondrial metabolism was dispensable for tumor growth has been challenged in recent decades by both human and mouse studies. In fact, the Warburg effect was shown to be dispensable for B16 melanoma tumor growth due to increased mitochondrial metabolism (Ždravlevi et al., 2018). Mitochondrial metabolism is required for oncogenic *Kras*-driven mouse models of lung adenocarcinoma (Guo et al., 2011; Weinberg et al., 2010). Positron emission tomography (PET) imaging using a radiotracer that measures mitochondrial membrane potential (MMP) in autochthonous

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mouse models of lung cancer demonstrates high MMP in lung adenocarcinoma (Momcilovic et al., 2019). Importantly, intraoperative infusions of [U-<sup>13</sup>C]glucose in human lung and brain tumors demonstrate high levels of glucose oxidation and tricarboxylic acid (TCA) cycle labeling, exceeding that of adjacent normal tissue (Hensley et al., 2016; Maher et al., 2012). Analysis of the Cancer Genome Atlas (TCGA) revealed that the mitochondrial DNA (mtDNA) content of cancerous tissues varies relative to their normal tissue counterparts. For example, lung adenocarcinomas display elevated mtDNA content relative to adjacent normal lung tissue (Reznik et al., 2016). Contrary to conventional wisdom, analysis of over 30 cancer types revealed that mitochondria with mtDNA mutations that are pathogenic are less likely to be maintained in cancer cells, suggesting that there is a positive selection for functional mitochondria to drive tumor growth (Ju et al., 2014). Furthermore, genetic defects leading to defective mitochondrial respiratory function produce a metabolic checkpoint that prevents malignant transformation (Joshi et al., 2015). These studies indicate that mitochondrial metabolism is an active essential process for tumor growth. More recent work suggests that this metabolic reprogramming is a dynamic process throughout tumorigenesis with metabolic flexibility serving the needs of the tumor at every stage, from tumor initiation to metastasis (Faubert et al., 2020). In this review, we highlight recent advances in our understanding of the essential role of mitochondrial metabolism and its potential as a target for cancer therapy.

## Mitochondrial Metabolism-Dependent Macromolecule Synthesis and Oncometabolite Production Support Tumor Growth

Tumor cells undergo metabolic reprogramming as a consequence of driver mutations, whereby metabolic flux through conventional metabolic pathways utilized by normal cells is increased or decreased in tumor cells relative to their premalignant tissue of origin (DeBerardinis and Chandel, 2016). Tumor cells robustly engage in both glycolysis, and its branching pathways, and TCA cycle metabolism in order to generate ATP, NADPH, and the building blocks necessary for macromolecule (nucleotides, lipids, and amino acids) synthesis, which are all essential for cell proliferation (Figure 1) (DeBerardinis and Chandel, 2020). Activation of major oncogenic drivers, such as *Myc* and *Kras*, and deregulation of signaling pathways, including the PI3K pathway, in part account for the elevated rate of glycolysis and TCA cycle flux seen in cancer cells. The elevated glycolytic rate allows for the generation of metabolic intermediates that can be shunted into multiple biosynthetic pathways required for cell proliferation, such as the pentose phosphate pathway (PPP) for ribose and cytosolic NADPH production, to sustain nucleotide synthesis and antioxidant activity, respectively, as well as one-carbon metabolism for mitochondrial NADPH production, nucleotide synthesis, and methylation reactions (DeBerardinis and Chandel, 2016; Vander Heiden and DeBerardinis, 2017). TCA cycle flux allows the generation of metabolites that funnel into nucleotide, lipid, amino acid, and heme synthesis (Zong et al., 2016). For example, oxaloacetate produced in the TCA cycle is exported from the mitochondrial matrix to the cytosol for nucleotide synthesis (Birsoy et al., 2015; Sullivan et al., 2015). Shunting of TCA cycle intermediates for biosynthetic purposes creates a need for replenishment of carbons to allow the TCA cycle to continue functioning, i.e., anaplerosis. There are multiple anaplerotic reactions utilized by cancer cells including the stepwise

oxidation of glutamine to generate the TCA cycle intermediate  $\alpha$ -ketoglutarate, branched-chain amino acid catabolism into succinyl-CoA, and pyruvate carboxylase generation of oxaloacetate (Cluntun et al., 2017). The TCA cycle also generates NADH and FADH<sub>2</sub> that need to be regenerated to NAD<sup>+</sup> and FAD by the mitochondrial electron transport chain (ETC) to allow the oxidative TCA cycle to function (Figure 2) (Chandel, 2015). Recent work demonstrates that oxidation of ubiquinol back to ubiquinone is the essential role of the ETC for tumor growth (Martinez-Reyes et al., 2020). Mitochondrial complex I and II donate electrons to ubiquinone generating ubiquinol. Mitochondrial complex III oxidizes ubiquinol back to ubiquinone, which allows complexes I and II to continue functioning and regenerate NAD<sup>+</sup> and FAD. Ubiquinone is also used as an electron acceptor by dihydroorotate dehydrogenase (DHODH), an enzyme required for *de novo* pyrimidine synthesis. Tumor cells with a diminished ability to regenerate mitochondrial ubiquinone have an impaired ability to form tumors *in vivo*. Moreover, mitochondrial complex III subunits are essential genes for cancer cell proliferation *in vitro* (Dempster et al., 2019; Meyers et al., 2017). Thus, tumor growth requires a functional ETC for oxidation of ubiquinol, which is necessary to maintain oxidative TCA cycle function and DHODH activity.

Besides the TCA cycle's essential role in supporting tumor cell anabolism, it can also generate oncometabolites in certain cancer contexts, defined as an accumulation of a metabolite that drives tumor growth. Although the large majority of cancers contain functional mitochondria, there exists a small subset that displays mutations in TCA cycle proteins that leads to an accumulation of oncometabolites (Nowicki and Gottlieb, 2015; Yong et al., 2020). In particular, loss-of-function mutations in the TCA cycle enzymes succinate dehydrogenase (SDH) and fumarate hydratase (FH) result in accumulation of succinate and fumarate, respectively (Linehan et al., 2019). Germline heterozygous genetic mutations in SDH complex subunits are observed in patients with hereditary paragangliomas and pheochromocytomas. The neoplastic transformation occurs when there is the loss of the remaining wild-type allele in the somatic cells, i.e., loss of heterozygosity (LOH), leading to the complete loss of enzymatic function. Similarly, LOH occurs in germline FH mutations in patients with hereditary leiomyomatosis and renal cell cancer (HLRCC). It remains unknown why these tissues can tolerate these mutations, as these genes are essential in most cancer cell lines (Dempster et al., 2019; Meyers et al., 2017). SDH- and FH-deficient tumors are dependent on glycolysis for the generation of ATP necessary for cellular proliferation and survival. It was presumed that these tumors would not be able to generate TCA cycle intermediates; however, FH tumors utilize glutamine-dependent "reductive carboxylation," a process whereby  $\alpha$ -ketoglutarate generated from glutamine takes a reverse path in the TCA cycle, to generate citrate for biosynthetic purposes (Metallo et al., 2011; Mullen et al., 2011; Wise et al., 2011), while SDH tumors have robust pyruvate carboxylase activity to generate oxaloacetate for nucleotide synthesis (Cardaci et al., 2015; Lussey-Lepoutre et al., 2015). Both FH- and SDH-deficient tumors are also dependent on part of the oxidative TCA cycle to generate the TCA cycle intermediates leading up to the deficiency (Cardaci et al., 2015; Sullivan et al., 2013). Importantly, tumors harboring SDH or FH mutations have an accumulation of succinate and/or fumarate, which inhibits  $\alpha$ -ketoglutarate-dependent dioxygenases, involved in histone and DNA methylation (Xiao et al., 2012), and the resulting epigenetic modifications are thought to contribute to malignant transformation

(Sciacovelli et al., 2016). Aside from direct genetic lesions that disrupt the oxidative TCA cycle, there are tumors with an intact TCA cycle that use reductive carboxylation and oncometabolites to sustain tumor growth. A salient example is that patients with clear cell renal cell carcinoma (ccRCC) given [U-<sup>13</sup>C]glucose infusions display enhanced glycolytic intermediate labeling, suppressed flux through pyruvate dehydrogenase, and reduced TCA cycle labeling (Courtney et al., 2018). Furthermore, glutamine-dependent reductive carboxylation is observed *in vivo* in subcutaneous xenografts of RCC cells in nude mice (Gameiro et al., 2013). This is due in part to the loss of the von-Hippel Lindau (VHL) tumor suppressor resulting in stabilization of hypoxia-inducible factors, activating a transcriptional program resulting in suppressed pyruvate oxidation (Gameiro et al., 2013). These tumors accumulate L-2-hydroxyglutarate (L-2HG), which like succinate and fumarate inhibits  $\alpha$ -ketoglutarate-dependent dioxygenases; increases methylation of histones, RNA, and DNA; and is necessary for tumor growth (Shim et al., 2014). Collectively, these observations indicate that although some tumors rely exclusively on glycolysis to meet their bioenergetic needs, they still rely on residual or reprogrammed aspects of mitochondrial metabolism to maintain pools of TCA cycle intermediates to meet the biosynthetic demands required for cell proliferation and generate oncometabolites that promote tumorigenesis.

## Targeting Mitochondrial ETC for Cancer Therapy

The cores of many solid tumors are poorly vascularized and, thus, contain nutrient-poor environments with limited glucose and oxygen availability (Jain et al., 2002). These tumor cores continue to use respiration (Le et al., 2014) since the ETC is able to function optimally even at oxygen levels as low as 0.5% (Rumsey et al., 1990). Therefore, poorly vascularized tumor cores have limited glucose availability but have enough oxygen to continue generating mitochondrial ATP for survival. Furthermore, as discussed above, decreasing ETC function prevents oxidative TCA cycle from functioning, thus diminishing macromolecule synthesis to support tumor growth. To date, the biguanide metformin as a putative mitochondrial ETC complex I inhibitor has been tried in multiple clinical trials as an anticancer agent in combination with standard of care therapies (Pollak, 2014).

Metformin is best known as a first-line therapy for patients with type 2 diabetes. Metformin's therapeutic effect in part is due to decreased hepatic gluconeogenesis resulting in improved insulin sensitivity. Initially, an epidemiological retrospective study reported an association between metformin use for controlling blood sugar and reduced cancer incidence (Evans et al., 2005). Patients who began taking metformin for blood sugar control after already developing cancer had an increased survival rate (Dowling et al., 2012). Additionally, multiple laboratory-based studies have also reported that metformin acts as an anticancer agent (Algire et al., 2011; Buzzai et al., 2007; Hirsch et al., 2009; Memmott et al., 2010; Tomimoto et al., 2008). It is important to note that dosing of metformin in mice is comparable to human studies (Chandel et al., 2016; Dowling et al., 2016). The efficacious dose of metformin (1,750 mg/day) in reducing tumor growth in humans is likely to be close to twice the anti-diabetic dosage (1,000 mg/day), but well below the maximum tolerated dose (MTD). There are a handful of clinical trials that have reported some efficacy of metformin in various cancers, while others have not observed robust anti-cancer efficacy. Recently, a phase II clinical trial found that combining metformin with standard EGFR-TKI

therapy in patients with advanced lung adenocarcinoma significantly improved both progression-free survival and overall survival (Arrieta et al., 2019). Furthermore, a stage II clinical trial in ovarian cancer demonstrated better-than-expected overall survival in the metformin-treated group (Brown et al., 2020). A multicenter phase III clinical trial at the University of Toronto will report their results in the coming year to establish the potential of metformin (1,750 mg/day) as a viable therapeutic strategy against breast cancer (Goodwin et al., 2015).

There are currently two different widely accepted mechanisms by which metformin may be exerting its antitumor effects that are not necessarily mutually exclusive (Birsoy et al., 2012). First, metformin decreases circulating insulin levels, a known mitogen for tumors. Insulin and insulin-like growth factors (IGFs) can stimulate the pro-tumorigenic PI3K signaling pathway (Pollak, 2012). However, this only applies to those tumors that are positive for insulin and/or insulin growth factor receptor. Since not all cancers are insulin responsive, metformin-mediated reduction of circulating insulin levels would be irrelevant to any potential anticancer effect. The second mechanism by which metformin exerts its anticancer effects is through inhibition of mitochondrial ETC complex I. Two seminal studies at the beginning of the century demonstrated that metformin inhibits mitochondrial complex I *in vitro* (El-Mir et al., 2000; Owen et al., 2000). Subsequent work in mice demonstrated that metformin inhibits mitochondrial complex I to exert its *in vivo* anti-tumorigenic effects (Wheaton et al., 2014). An integrative metabolomic analysis of metformin's mechanism of action in ovarian cancer using patient samples confirmed that the predominant anti-tumorigenic effect is driven by targeting tumor-cell-intrinsic mitochondrial metabolism (Liu et al., 2016). In breast cancer, metformin diminishes TCA cycle intermediate production through inhibition of complex I (Janzer et al., 2014). Integrated pharmacodynamic analysis identified two metabolic adaptation pathways to metformin in breast cancer patients: increased glucose flux and increased transcription of oxidative phosphorylation genes (Lord et al., 2018). Recent studies have shown other mechanisms of resistance including metabolic reprogramming due to activation of BACH1 or HIF-1 $\alpha$ , decreasing flux through one-carbon metabolism, and infiltration by tumor-associated macrophages (Khan et al., 2019; Kurelac et al., 2019; Lee et al., 2019; Yang et al., 2020). It will be important to assess the relevance of these resistance mechanisms in future metformin clinical trials as inhibitors of these different pathways may be used in combinatorial therapy.

At first glance, mitochondrial ETC inhibitors like metformin would be toxic. Metformin's high safety profile is in part due to its mechanism of cellular import. Metformin requires organic cation transporters (OCTs) to enter cells. OCTs are able to transport polyamines, thiamine, carnitine, dopamine, and acetylcholine (Nigam, 2018). Normal kidney, gut, and liver cells express OCTs (Emami Riedmaier et al., 2013). There is considerable heterogeneity within tumors regarding metformin sensitivity that, in part, could be due to OCT expression. Thus, we conducted a CRISPR-based functional genomic screen using a metabolic library to discover genes that confer metformin resistance in a human A549 lung adenocarcinoma cell line, which is sensitive to metformin (Figure S1). Loss of the OCT3 (SLC22A3) gene was the top gene hit that conferred resistance to metformin (Figure S2). Additionally, in both squamous cell carcinomas of the head and neck (HNSCC) and breast cancer, it has been shown that the anti-tumor effect of metformin requires the expression of

OCT3 (Cai et al., 2019; Madera et al., 2015). This may in part explain the variability in metformin's anti-tumor efficacy in clinical trials. Going forward, the identification of OCT protein-expressing tumors similar to Her2-positive tumors for Herceptin should be used to identify tumors that are good candidates for metformin therapy (Rusch et al., 2018). Recently, a group showed that homologous recombination-deficient tumors, such as those with BRCA mutations, are reliant upon mitochondrial metabolism to regenerate ATP for PARP-dependent repair mechanisms, leaving them susceptible to inhibitors such as metformin (Lahiguera et al., 2020). Understanding the interplay between cancer genetics and metabolism will allow for developing rational metabolism-targeted therapies. A robust mitochondrial membrane potential is required for uptake of the positively charged metformin at normal pH into the mitochondrial matrix, where it can inhibit complex I (Bridges et al., 2014; Wheaton et al., 2014). This leads to reversible accumulation within the mitochondrial matrix that contributes to metformin toxicity (Bridges et al., 2014). Recently, a PET radiotracer has been developed that can measure mitochondrial membrane potential and predict therapeutic response to mitochondrial complex I inhibitors such as metformin (Momcilovic et al., 2019). Beyond metformin, there have been other mitochondrial complex I inhibitors and other biguanides, such as phenformin (Birsoy et al., 2014; Shackelford et al., 2013), as well as other inhibitors of ETC complexes, that have shown efficacy in pre-clinical models (Molina et al., 2018; Naguib et al., 2018; Shi et al., 2019; Zhang et al., 2019). In addition to directly inhibiting the mitochondrial ETC, diminishing mitochondrial protein translation and stability has shown promise as another avenue to diminish ETC activity (Kuntz et al., 2017; Siegelin et al., 2011; Skrtic et al., 2011; Zhang et al., 2016).

## Targeting Nucleotide Metabolism Linked to Mitochondrial ETC Activity for Cancer Therapy

The mitochondrial ETC is intrinsically coupled to pyrimidine nucleotide generation by sustaining DHODH activity (Bajzikova et al., 2019). DHODH catalyzes the fourth enzymatic step, the ubiquinone-mediated oxidation of dihydroorotate to orotate, in *de novo* pyrimidine biosynthesis (Figure 3). It is found to be located on the outer surface of the inner mitochondrial membrane (Chen and Jones, 1976; Rawls et al., 2000). A recent study demonstrates the availability of ubiquinone to receive electrons from dihydroorotate, which is only compromised when mitochondrial complex III is inhibited, is a key factor for the maintenance of *de novo* pyrimidine synthesis (Martinez-Reyes et al., 2020). Thus, DHODH activity is dependent on mitochondrial complex III function but does not contribute to the ETC's role in oxidative phosphorylation or the TCA cycle. DHODH inhibition has demonstrated efficacy in a number of different pre-clinical mouse models of cancer, including highly aggressive small-cell lung cancer (SCLC), acute myeloid leukemia (AML), triple-negative breast cancer, and *Kras*-driven cancers (Brown et al., 2017; Hosseini et al., 2018; Koundinya et al., 2018; Li et al., 2019; Mathur et al., 2017; Sykes et al., 2016; Wang et al., 2019; White et al., 2011). Although the DHODH inhibitor leflunomide is FDA-approved as an anti-inflammatory drug for rheumatoid arthritis in adults, there are new-generation DHODH inhibitors that show greater potency (Christian et al., 2019; Ladds et al., 2018; Sykes, 2018; Sykes et al., 2016). It remains to be seen whether these new inhibitors will be efficacious as anti-cancer agents in humans.



## Targeting Mitochondrial TCA Cycle for Cancer Therapy

Due to the central role of the TCA cycle in producing the intermediate metabolites for growth, drugs that inhibit the TCA cycle would be predicted to be efficacious. CPI-613 is a first of its kind lipoate analog that can inhibit two major TCA cycle enzyme complexes that require lipoate for their activity,  $\alpha$ -ketoglutarate dehydrogenase ( $\alpha$ -KGDH) and pyruvate dehydrogenase (PDH) (Figure 4) (Stuart et al., 2014). Although the mechanism by which CPI-613 exerts its anti-cancer activity is not fully understood, it displayed a significant therapeutic index in promising phase I and II results in pancreatic cancer and AML (NCT01835041) (Alistar et al., 2016; Pardee et al., 2014). Currently, CPI-613 is undergoing phase III clinical trials in patients with relapsed/refractory AML or metastatic pancreatic adenocarcinoma (NCT03504410 and NCT03504423).

Glutamine is the major carbon source to replenish TCA cycle intermediates and sustain their use for biosynthesis of macromolecules (Altman et al., 2016). Recent work using [U-<sup>13</sup>C]glutamine infusion in a genetically engineered mouse model of pancreatic cancer demonstrated a large contribution of glutamine into the TCA cycle (Hui et al., 2017). Inhibition of mitochondrial glutaminase (GLS1), which converts glutamine into glutamate, demonstrates efficacy in mouse models of lung adenocarcinoma harboring loss of *Keap1*, renal cell carcinoma, and MYC-driven hepatocellular carcinoma and lymphoma (Le et al., 2012; Romero et al., 2017; Shroff et al., 2015; Xiang et al., 2015). Glutamate can either be converted into  $\alpha$ -ketoglutarate by glutamate dehydrogenase (GLUD) and aminotransferases or be utilized for glutathione synthesis. Human renal cell carcinomas display glutamine carbon incorporation into the TCA cycle (Courtney et al., 2018). Currently, the glutaminase inhibitor CB-839 (Telaglenastat), in combination with the mTOR inhibitor Everolimus or the multi-tyrosine kinase inhibitor Cabozantinib, is in phase II clinical trials for advanced or metastatic renal cell carcinoma (NCT03163667 and NCT03428217). There are also ongoing phase I/II clinical trials using CB-839 in hematological malignancies and solid tumors including NSCLC. Going forward, the use of [U-<sup>13</sup>C]glutamine infusion in patients to determine whether glutamine contributes carbon into the TCA cycle could identify patients for therapies targeting glutamine metabolism.

## Combining Mitochondrial Metabolism Inhibitors with Other Anti-Cancer Agents

A major advancement in the past two decades is the use of cancer genetics to identify patients that would be best served with a combination of anti-cancer therapies, i.e., personalized medicine. Currently, a major hurdle in using inhibitors targeting mitochondrial metabolism is identifying the right combination of other anti-cancer therapies with appropriate cancer genetics (Figure 5). An emerging theme is that cells that begin to emerge after treatment with chemotherapy, anti-angiogenic therapy, or targeted therapy, e.g., oncogenic Braf or Kras inhibition, are highly dependent on mitochondrial metabolism for survival and proliferation (Caro et al., 2012; Farge et al., 2017; Guièze et al., 2019; Henkenius et al., 2017; Kuntz et al., 2017; Lee et al., 2017; Navarro et al., 2016; Viale et al., 2014). These inhibitors diminish glycolysis and would potentially synergize with agents

targeting the mitochondrial ETC or TCA cycle. Mitochondrial respiration within cancer cells, along with low oxygen delivery due to improper tumor vasculature, contributes to intratumoral hypoxia. Thus, inhibiting mitochondrial metabolism would raise tumor oxygen levels, and could significantly improve the tumor cell killing after radiation. Indeed, the FDA-approved drug papaverine inhibits mitochondrial complex I, leading to increased oxygenation and enhanced radiation response in pre-clinical models of cancer (Benej et al., 2018). This pattern of reliance on oxidative phosphorylation is also seen in metastatic lesions. Brain metastases from human melanoma show enrichment for oxidative phosphorylation gene sets (Fischer et al., 2019). It currently remains unclear why there is an increased dependence upon mitochondrial metabolism in advanced disease, but this suggests a potentially shared, targetable metabolic vulnerability across cancers.

Mitochondrial metabolism inhibitors could also be combined with therapies that diminish glucose metabolism. The PI3K signaling pathway is a major activator of glucose metabolism. Thus, in certain settings the combination of PI3K inhibitors with mitochondrial metabolism inhibitors could be efficacious. Furthermore, certain cancer cells like early-stage lung adenocarcinoma display high levels of the sodium-dependent glucose transporter 2 (SGLT2) (Scafoglio et al., 2018). Targeting SGLT2 with FDA-approved inhibitors, the gliflozins, markedly reduced lung adenocarcinoma growth and prolonged survival in pre-clinical autochthonous mouse models and patient-derived xenografts (Scafoglio et al., 2018). To date, directly inhibiting enzymes in glycolysis has proved to be difficult. Lactate dehydrogenase (LDH) and hexokinase 2 (HK2) inhibition, two key enzymes within glycolysis, has shown efficacy in pre-clinical models (Fantin et al., 2006; Patra et al., 2013). Recent work demonstrated that LDH inhibition in glycolytic tumors leads to redirection of pyruvate to support mitochondrial metabolism, creating a vulnerability to combination therapy with a mitochondrial ETC inhibitor such as metformin (Oshima et al., 2020). HK2 loss in adult mice is well tolerated and, importantly, its inhibition does not affect T cell function (Mehta et al., 2018). Nevertheless, clinical inhibitors that distinguish between HK2 and the widespread isoform hexokinase 1 (HK1) are not currently available.

Multiple mitochondrial inhibitors could be combined since they have distinct targets. For example, metformin could be combined with TCA cycle inhibitor CPI-613 or DHODH inhibitors. In pre-clinical models of prostate cancer, metformin decreases glucose oxidation but increases glutamine-dependent anaplerosis through reductive carboxylation (Fendt et al., 2013; Griss et al., 2015). Interfering with glutamine metabolism may synergize with metformin to improve outcomes. A major limiting factor would be whether these combinations would have a favorable therapeutic index.

The recent successes of immune checkpoint blockade and adoptive cellular therapy (ACT) have revolutionized cancer treatment strategies and have become an established treatment modality moving forward. Similar to cancer, mitochondrial metabolism has been demonstrated to play a critical role in the survival and function of immune cells. As such, when using metabolically targeted therapies for cancer, it is important to consider the potential detrimental effects it may have upon the immune system, as it has been shown that activated immune cells utilize many of the same metabolic pathways attributed to cancer cells (Andrejeva and Rathmell, 2017).



T cells are a key immune effector cell population for a robust and effective anti-tumor immune response. When naive T cells recognize their cognate antigen in the context of co-stimulatory signaling, they increase flux through glycolysis and the TCA cycle to meet the biosynthetic and bioenergetic demands of growth and proliferation (Frauwirth et al., 2002; Ma et al., 2019; Menk et al., 2018). Inhibiting mitochondrial ETC diminishes effector T cell proliferation (Bailis et al., 2019; Sena et al., 2013; Tarasenko et al., 2017) as well as regulatory T cell (Treg) function (Chapman et al., 2018; Fu et al., 2019; Weinberg et al., 2019). Although effector T cells are essential for an anti-tumor response, durable long-lasting immunotherapeutic responses require the establishment of memory T cells. Memory CD8<sup>+</sup> T cells preferentially rely on TCA cycle metabolites for function (Geltink et al., 2018). Furthermore, the tumor microenvironment can limit nutrients that can diminish CD8 T cell-dependent tumor killing (Chang et al., 2015). Many studies have observed mitochondrial dysfunction in CD8 T cells within the tumor microenvironment (Scharping et al., 2016). Importantly, enhancing mitochondrial function within these CD8 T cells improved anti-tumor responses (Chamoto et al., 2017; Siska et al., 2017).

A key combinatorial regimen with immune checkpoint blockade is inhibiting glutamine metabolism. After activation, effector T cells can utilize glutamine anaplerosis, similar to cancer cells, due to upregulation of *Myc* in response to TCR stimulation (Wang et al., 2011). This leads to significant upregulation of SLC1A5, the glutamine transporter, leading to glutamine addiction (Nakaya et al., 2014). Genetic inhibition of GLS diminishes T cell activation and impairs TH17 differentiation *in vitro* and *in vivo*. However, transient pharmacologic GLS inhibition leads to increased Th1 and cytotoxic T lymphocyte (CTL) numbers with enhanced anti-tumor immune responses (Johnson et al., 2018). An exciting new study demonstrated that a prodrug for (JHU083) of the glutamine antagonist 6-diazo-5-oxo-L-norleucine (DON) becomes activated in the tumor microenvironment and enhances T cell mitochondrial metabolism to drive anti-tumor immune responses (Leone et al., 2019). Going forward, it will be interesting to see whether inhibiting glutamine metabolism will be efficacious in patients that have poor responses to immune checkpoint blockade. Furthermore, how other mitochondrial metabolism inhibitors, like CPI-613, perturb immune responses remains to be determined.

## Conclusion

The field of cancer metabolism is rooted in the observation that cancer cells exhibit the Warburg effect *in vitro*. This has misled many to believe that mitochondrial metabolism is either dispensable or only a minor metabolic pathway in tumor growth. Recent advances in our understanding and appreciation of mitochondrial metabolism as a key metabolic driver of cancer and the success of clinical trials targeting mitochondrial metabolism have brought mitochondria to the forefront of both cancer metabolism and immunometabolism fields. Over the next few years, phase III clinical trials of metformin and CPI-613 will be available, and those of us working in cancer metabolism eagerly await these results. The advances in PET imaging and metabolomics and their coupling to cancer genomics can help identify patients that would benefit from use of these inhibitors. We are beginning to understand that the metabolic needs and vulnerabilities of cancer change throughout tumorigenesis, from tumor initiation and growth to metastasis and therapy resistance. In the coming years,

elucidating these different vulnerabilities will allow for stage-specific metabolism-targeted therapies. The identification of rational combinations of mitochondrial inhibitors with standard of care treatment including chemotherapy, radiotherapy, and immunotherapy will hopefully bring new and efficacious anti-cancer treatments.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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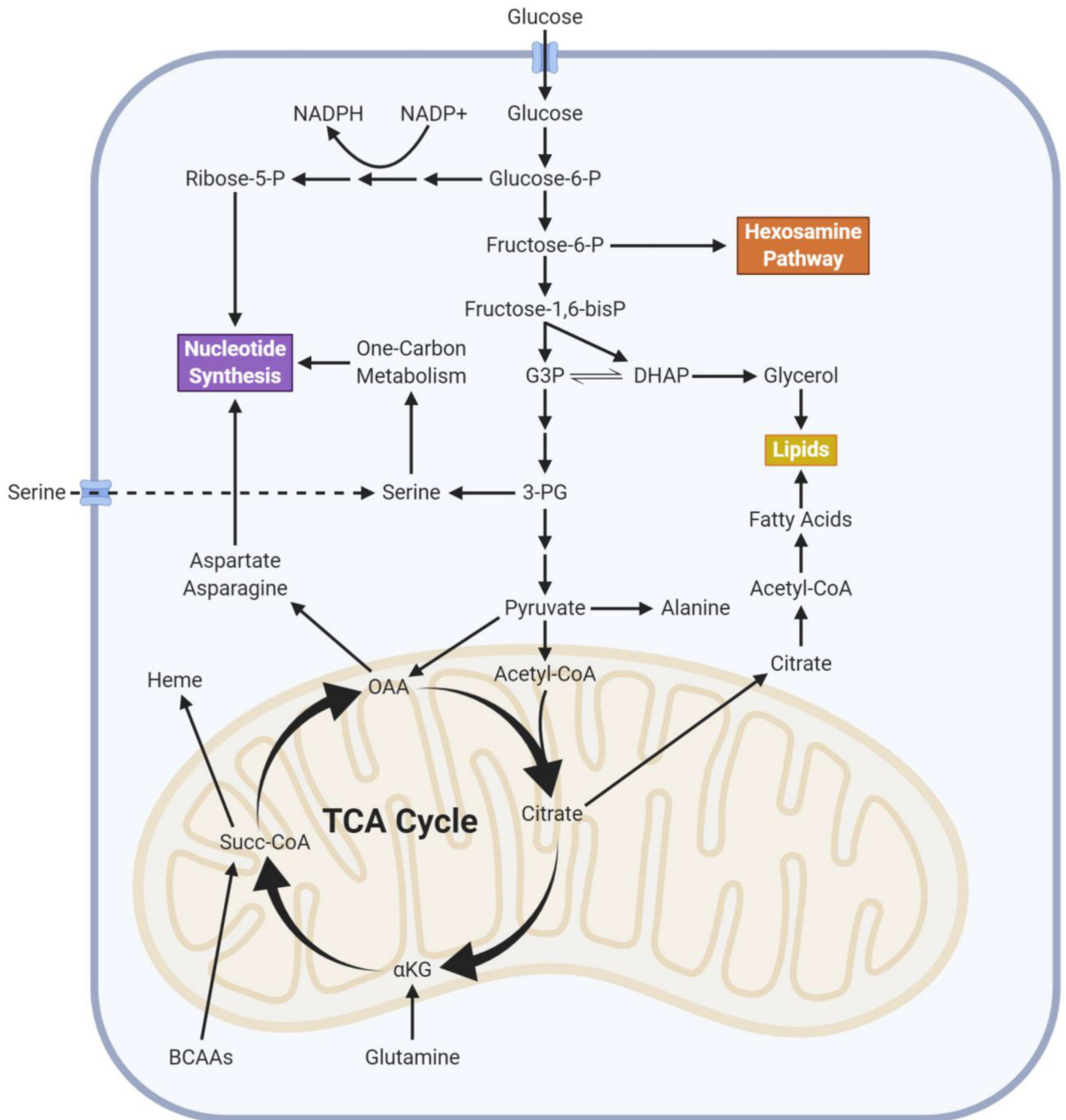


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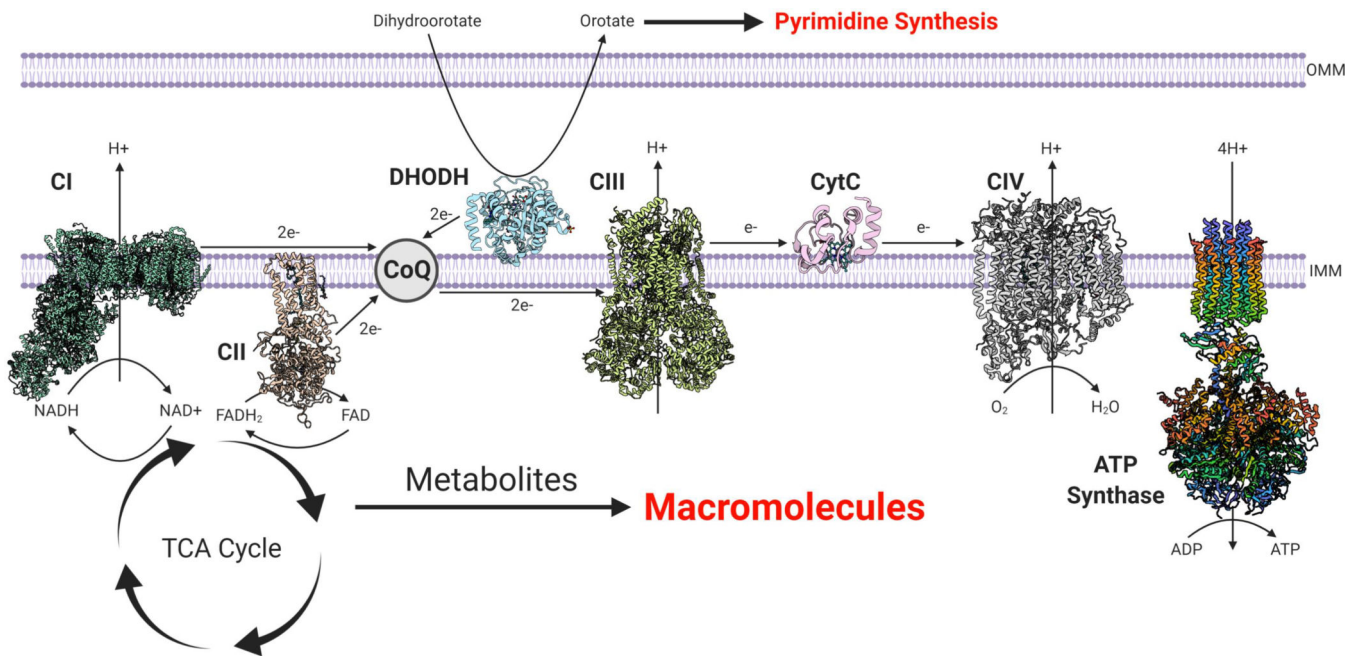
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**Figure 1. Metabolism Supports Macromolecule Synthesis for Growth**

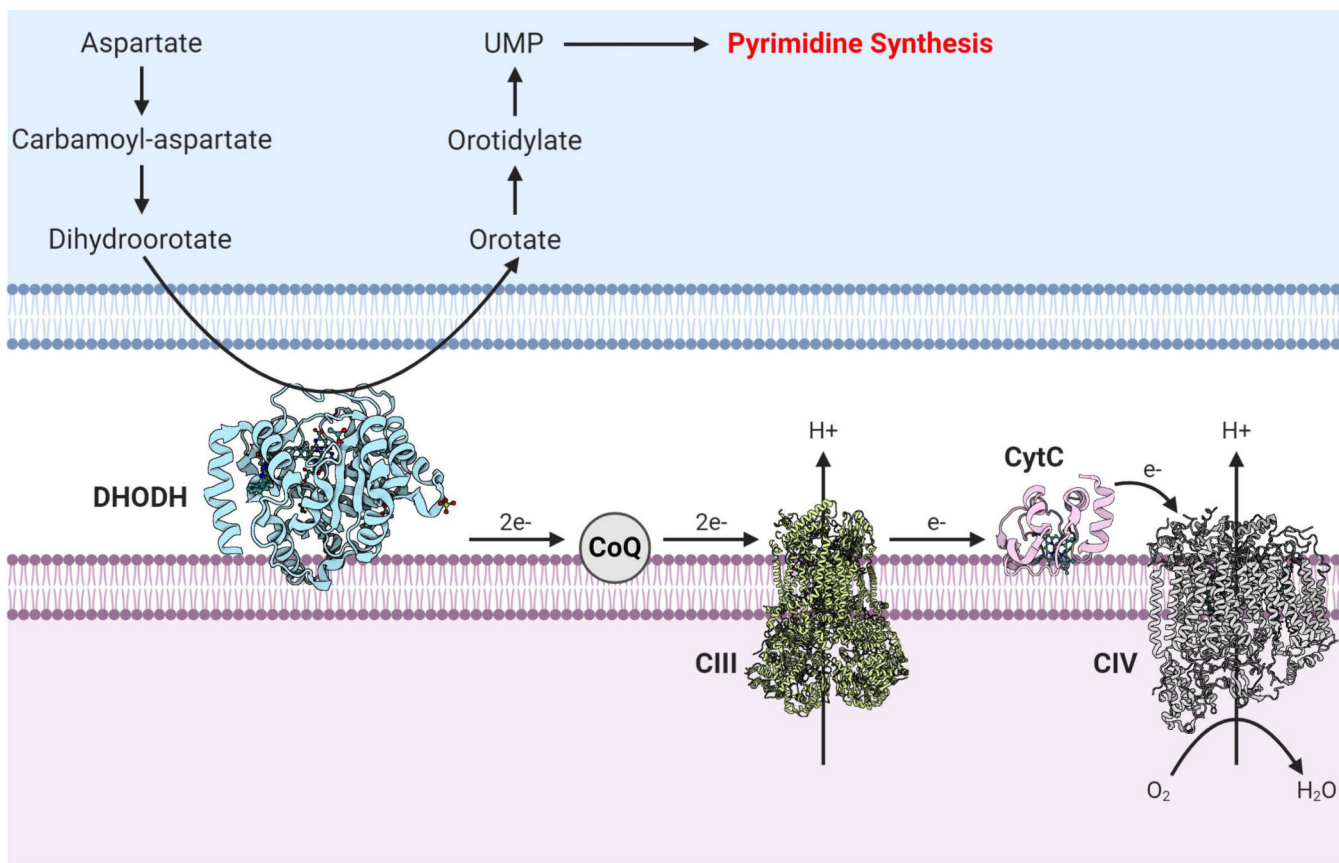
Cancer cells upregulate both glycolysis and TCA cycle metabolism in order to provide the substrates required for synthesis of macromolecules such as lipids and nucleotides that are required for cell proliferation. Multiple substrates feed into these biosynthetic pathways, thus providing cancer cells with metabolic flexibility to support tumor growth.





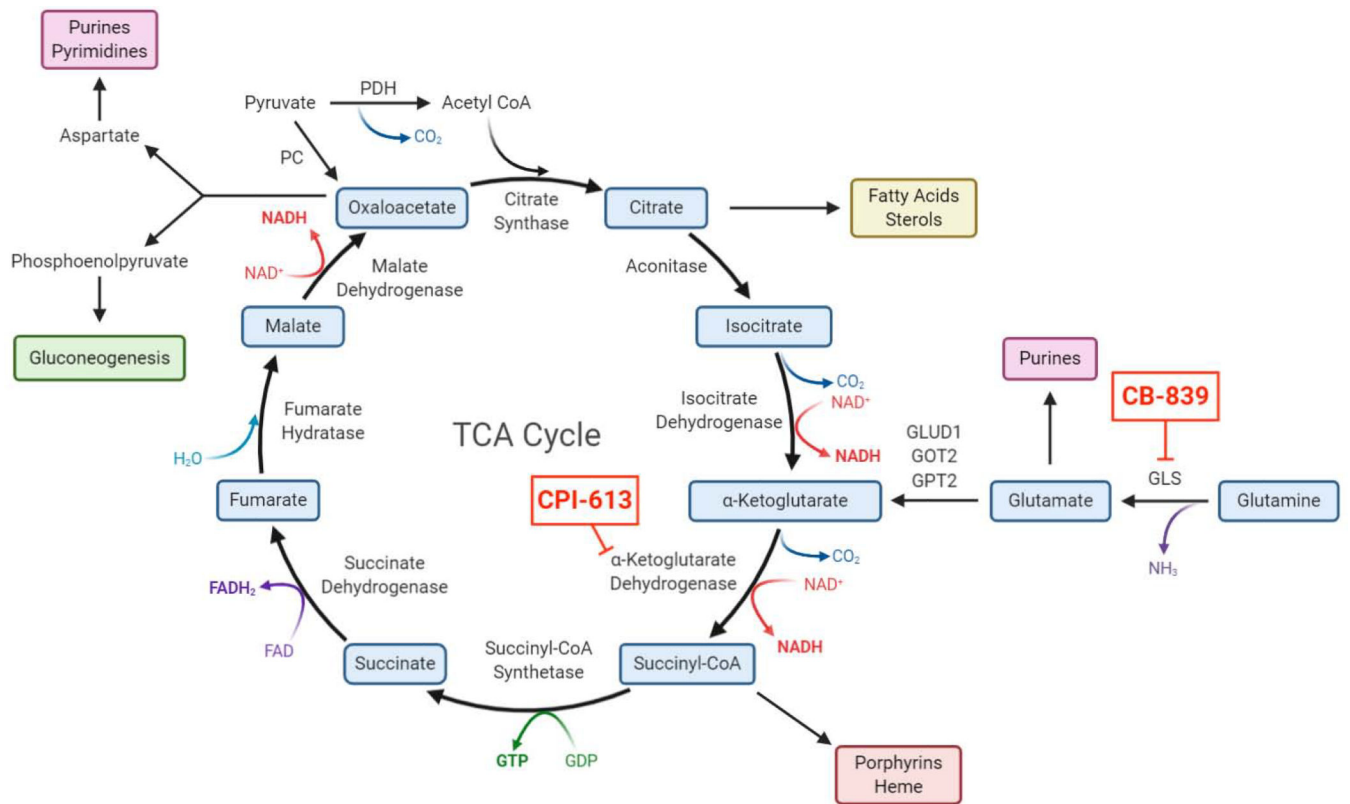
**Figure 2. Mitochondrial ETC Serves Bioenergetic and Biosynthetic Needs of Cancer Cells**  
 The five complexes of the ETC serve to produce the majority of ATP utilized by cancer cells as well as oxidize NADH and FADH<sub>2</sub> to NAD<sup>+</sup> and FAD, respectively. This allows for the TCA cycle to continue functioning, producing metabolites that support macromolecule synthesis. DHODH donates electrons to mitochondrial ubiquinone (CoQ) during the conversion of dihydroorotate to orotate, a key step in *de novo* pyrimidine synthesis. Atomic structures: mitochondrial complex I (PDB: 6RFR) (Parey et al., 2019), complex II (PDB: 1ZOY) (Sun et al., 2005), DHODH (PDB: 4LS1), complex III (PDB: 6Q9E) (Letts et al., 2019), cytochrome *c* (PDB: 2B4Z) (Mirkin et al., 2008), complex IV (PDB: 5Z62) (Zong et al., 2018), and ATP synthase (PDB: 5FL7) (Hahn et al., 2016).





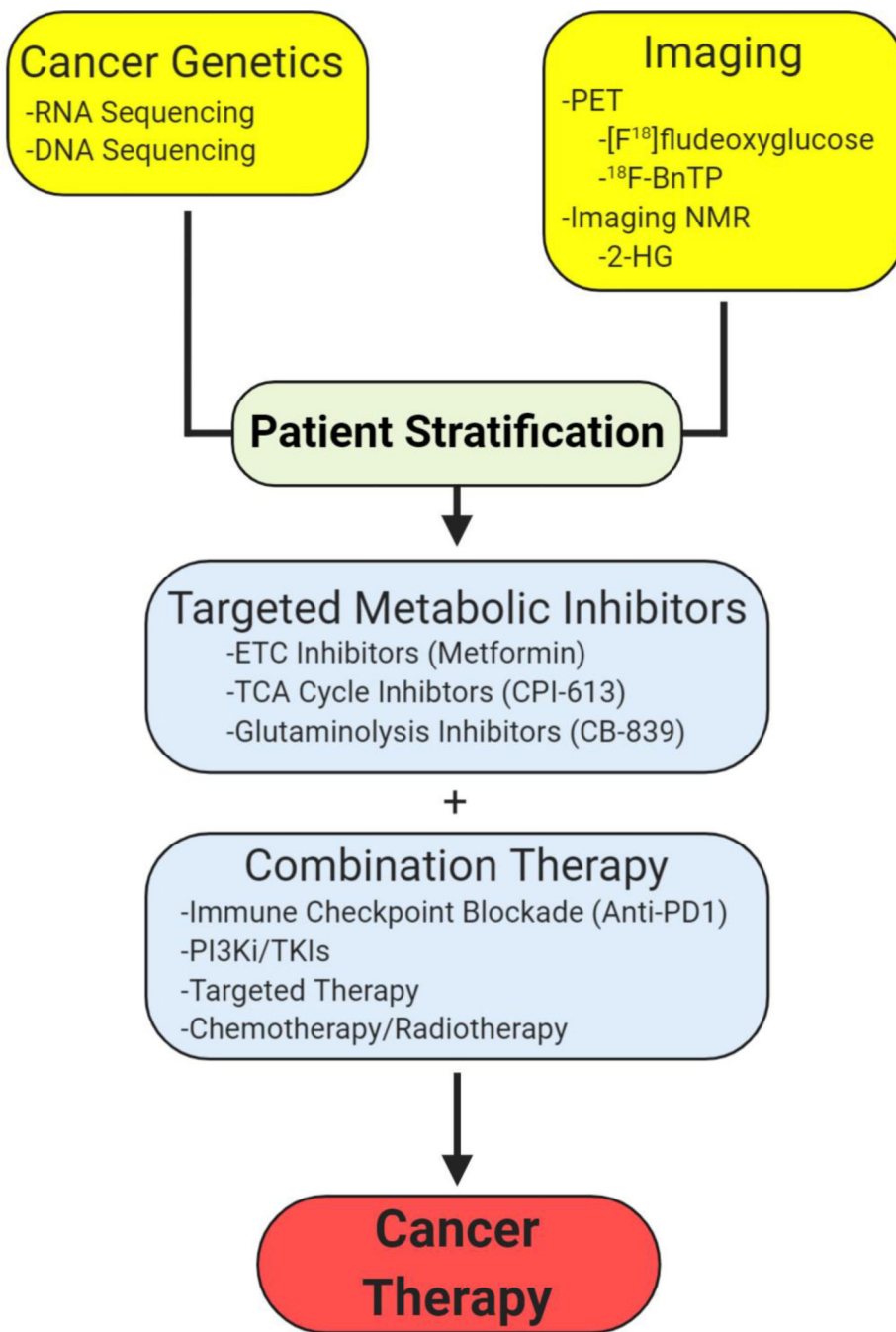
**Figure 3. DHODH Links the Mitochondrial ETC to Pyrimidine Synthesis**

DHODH, a mitochondrial enzyme tethered to the inner mitochondrial membrane, converts dihydroorotate to orotate in the intermembrane space. DHODH donates two electrons to mitochondrial ubiquinone (CoQ) within the ETC. There are currently FDA-approved DHODH inhibitors used for rheumatoid arthritis like leflunomide, as well as other newer DHODH inhibitors. DHODH inhibition has shown promise in preclinical studies of cancer. Atomic structures: DHODH (PDB: 4LS1), complex III (PDB: 6Q9E) (Letts et al., 2019), cytochrome *c* (PDB: 2B4Z) (Mirkin et al., 2008), and complex IV (PDB: 5Z62) (Zong et al., 2018).



**Figure 4. TCA Cycle Feeds Multiple Biosynthetic Pathways**

Mitochondrial TCA cycle intermediates are utilized as precursors for biosynthetic purposes. This depletion of carbons requires replenishment, i.e., anaplerosis, usually from glutaminolysis and/or pyruvate carboxylase. Multiple inhibitors targeting different steps within the cycle have shown promise in phase I and II clinical trials.



**Figure 5. Rational Design of Metabolic Cancer Therapy**

Combining Cancer genetics with metabolism-based imaging techniques will allow for patient stratification for targeted metabolic inhibitors. These metabolic inhibitors may be used in combination with chemotherapy, radiotherapy, or even immunotherapy to provide new avenues for cancer therapeutic strategies.