



CPT1A in cancer: Tumorigenic roles and therapeutic implications

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Abstract: Metabolic reprogramming frequently occurs in the majority of cancers, wherein fatty acid oxidation (FAO) is usually induced and serves as a compensatory mechanism to improve energy consumption. Carnitine palmitoyltransferase 1A (CPT1A) is the rate-limiting enzyme for FAO and is widely involved in tumor growth, metastasis, and chemo-/radio-resistance. This review summarizes the most recent advances in understanding the oncogenic roles and mechanisms of CPT1A in tumorigenesis, including in proliferation and tumor growth, invasion and metastasis, and the tumor microenvironment. Importantly, CPT1A has been shown to be a biomarker for diagnosis and prognosis prediction and proved to be a candidate therapeutic target, especially for the treatment of drug- and radiation-resistant tumors. In summary, CPT1A plays remarkable roles in promoting cancer progression and is a potential anticancer therapeutic target.

Introduction

Metabolic reprogramming is one of the critical features of cancer and maintains the rapid proliferation of cancer cells by affecting energy metabolism. In addition to the well-studied dysregulation of glucose metabolism (the Warburg effect), compelling studies have revealed the significant roles of changes in lipid metabolism during carcinogenesis (Santos and Schulze, 2012). Lipid metabolism consists of lipid synthesis and oxidation, and importantly, enhancement of fatty acid oxidation (FAO) promotes the metastasis, stemness, and treatment resistance of cancer cells (Wright *et al.*, 2017; He *et al.*, 2019; Jiang *et al.*, 2022). CPT1, a key enzyme of FAO, has three isoforms: Carnitine palmitoyltransferase 1A (CPT1A; liver isoform), CPT1B (muscle isoform), and CPT1C (brain isoform) (Bonnefont *et al.*, 2004). CPT1A controls the rate-limiting process in fatty acid β -oxidation, during which acyl-coenzyme A (acyl-CoA) esters are converted into acyl-carnitines. CPT1A is reported to be dysregulated in many types of cancers and regulates nearly all aspects of tumorigenesis (Lu *et al.*, 2021a; Peng *et al.*, 2021; Tang *et al.*, 2022b; Wang *et al.*, 2020b). Herein, we reviewed the most recent findings on the roles, mechanisms, diagnostic and prognostic relevance, and therapeutic applications of CPT1A in cancer.

The Biological Function of Carnitine Palmitoyltransferase 1A in Fatty Acid Oxidation

FAO is a vital metabolic pathway that produces nicotinamide adenine dinucleotide phosphate (NADPH) and adenosine triphosphate (ATP). Human cells have three types of FAO: α - (functions in peroxisomes), β - (functions in peroxisomes and mitochondria), and ω -oxidation (functions in the endoplasmic reticulum) (Talley and Mohiuddin, 2022). In mitochondria, diet-derived fatty acids are β -oxidized to produce energy, while β -oxidization in peroxisomes is usually carried out to generate H_2O_2 (Reddy and Hashimoto, 2001). Enhancement of mitochondrial β -oxidization confers stemness and chemoresistance to cancer cells; therefore, β -oxidization might be developed as a therapeutic target in the future (Li *et al.*, 2022; Liu *et al.*, 2023).

Cells take up fatty acids (FAs) by fatty acid transport molecules such as the CD36 molecule (CD36) (Glatz and Luiken, 2018) and FA-binding proteins (Lee *et al.*, 2018). Then, fatty acyl-CoA synthetases convert FAs to fatty acyl-CoA, and then fatty acyl-CoA participates in oxidation. CPT1 catalyzes the transformation of fatty acyl-CoA to fatty acyl-carnitine and transfers it across the outer mitochondrial membrane. Then, carnitine/acylcarnitine translocase shuttles fatty acyl-carnitine into the mitochondrial matrix, and CPT2, which is located on the matrix surface of the inner membrane, reconverts fatty acyl-carnitine to fatty acyl-CoA (Adeva-Andany *et al.*, 2017). Next, fatty acyl-CoA is sequentially catalyzed by acyl-CoA dehydrogenase, enoyl-CoA hydratase, hydroxyacyl-CoA dehydrogenase, and

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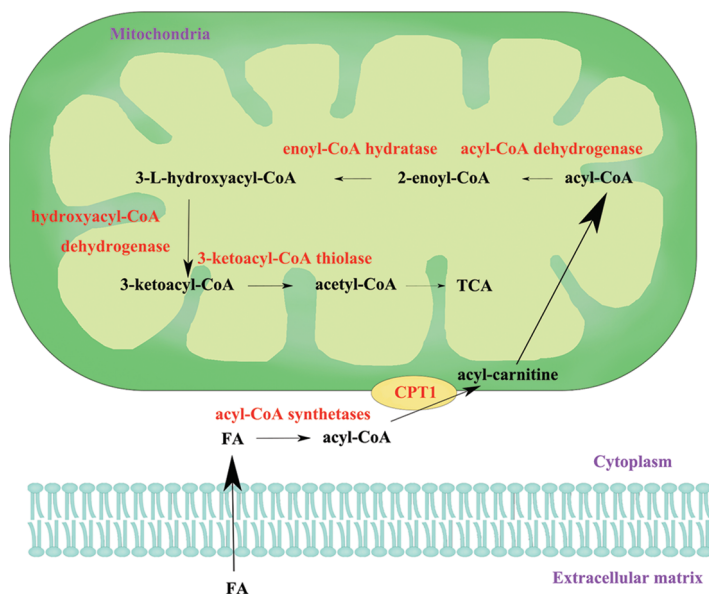


FIGURE 1. The process of fatty acid oxidation. FA, fatty acid; CPT1, carnitine palmitoyltransferase 1; TCA, tricarboxylic acid cycle.

3-ketoacyl-CoA thiolase. The final product, acetyl-CoA, is used to generate ATP via the tricarboxylic acid cycle (Fig. 1).

The CPT1A gene is located on 11q13.3 and is widely expressed in the brain, intestine, kidney, lung, ovary, pancreas, and spleen tissues (Jariwala *et al.*, 2021). Owing to its critical role in FAO, dysregulation of CPT1A is involved in the progression of many diseases, such as obesity, psoriasis, type 2 diabetes, and cancer (Rufer *et al.*, 2009; Schlaepfer *et al.*, 2014; Schlaepfer and Joshi, 2020). CPT1A was reported to be overexpressed in many types of cancers, such as acute myeloid leukemia (Mao *et al.*, 2021), high-grade glioma (Petővári *et al.*, 2020), breast cancer (Jariwala *et al.*, 2021) and ovarian cancer (Ghoneum *et al.*, 2020), and to play important oncogenic roles in tumorigenesis.

Roles and Mechanisms of CPT1A in Tumorigenesis

CPT1A participates in nearly all aspects of tumorigenesis. During the progression of nonatrophic gastritis to gastric cancer (GC), the expression level of CPT1A was consistently increased (Dhondrup *et al.*, 2022). A high-fat diet promotes the regeneration and tumorigenesis of intestinal tissues by activating the PPAR-CPT1A-FAO signaling pathway (Mana *et al.*, 2021). CPT1A supported the growth of castration-resistant prostate cancer by increasing histone acetylation in an androgen-dependent manner (Joshi *et al.*, 2019). In particular, blocking CPT1A with biodegradable polyethyleneimine-functionalized polyhydroxybutyrate nanoparticle (PHB-PEI NP)-delivered miR-124, whose binding and negative regulation of CPT1A hindered the tumorigenicity of prostate cancer cells (Conte *et al.*, 2020). Therefore, we reviewed the most recent findings on the roles and regulatory mechanisms of CPT1A in tumorigenesis.

Proliferation and tumor growth

CPT1A is overexpressed in many types of cancers, and its high expression promotes the proliferation and tumor growth of cancer cells. In luminal breast cancer (BC), CPT1A was amplified and overexpressed, and both *in vitro* and *in vivo*

experiments revealed that CPT1A potentiated the proliferation, colony formation, and mammosphere formation of luminal breast cancer cells by augmenting FAO (Jariwala *et al.*, 2021). In acute myeloid leukemia (AML), CPT1A was highly expressed, and knockdown of CPT1A suppressed cell proliferation; additionally, it exerted synergistic therapeutic effects with ABT199 (BCL2 inhibitor) and ST1326 (CPT1A-selective inhibitor) on AML cells (Mao *et al.*, 2021). In nasopharyngeal cancer cells and biopsy tissues, CPT1A was highly expressed, and CPT1A mechanically promoted tumor formation *in vivo* and proliferation and colony formation *in vitro* by enhancing FAO (Tang *et al.*, 2022a). In gastric cancer (GC) cells and tissues, CPT1A was significantly upregulated, and its high expression activated FAO by increasing the NADP⁺/NADPH ratio and improved cell proliferation in GC (Wang *et al.*, 2020b). CPT1A binds to and succinylates lactate dehydrogenase A (LDHA) at K222, suppresses lysosomal degradation of LDHA by blocking the interaction between LDHA and p62 and finally promotes GC cell proliferation and invasion (Li *et al.*, 2020). Silencing CPT1A induced anoikis and decreased the suspension-cultured viability of high-grade serous ovarian cancer (HGSOC) cells *in vitro*; CPT1A inhibitor etomoxir markedly suppressed tumor progression in a patient-derived xenograft model (Sawyer *et al.*, 2020). CPT1A was preferentially expressed in non-stem tumor cells compared with glioma stem cells (GSCs), and overexpression of CPT1A in GSCs promoted mitochondrial fusion and differentiation by phosphorylating dynamin-related protein 1 at Ser637 (Luo *et al.*, 2021). Knockdown of CPT1A in an animal model of glioblastoma suppressed tumor growth and increased survival (Sperry *et al.*, 2020). Depletion of CPT1A increased the cellular lipid concentration and inhibited the colony formation of pancreatic cancer cells and breast cancer cells (Guan *et al.*, 2019).

CPT1A is involved in the oncogene-induced proliferation and tumor growth of cancer cells (Fig. 2). In HepG2 liver cancer cells, nuclear receptor subfamily 6,

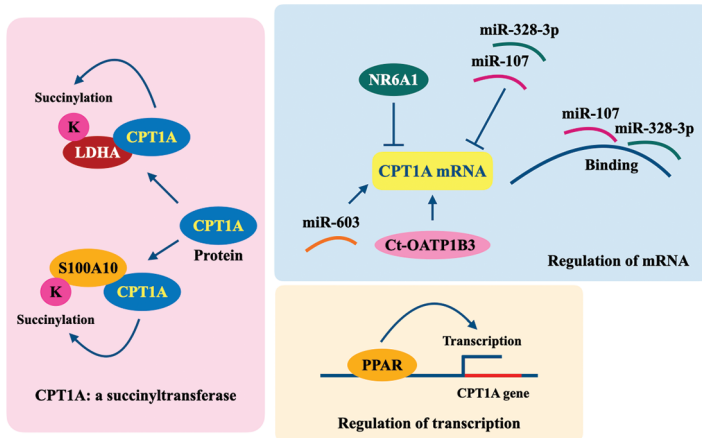


FIGURE 2. Regulation of CPT1A in cancer cells. K, lysine; CPT1A, carnitine palmitoyltransferase 1A; LDHA, lactate dehydrogenase A; S100A10, S100 calcium-binding protein A10; NR6A1, nuclear receptor subfamily 6, group A, member 1; Ct-OATP1B3, cancer-type organic anion transporting polypeptide 1B3; PPAR, peroxisome proliferator-activated receptor.

group A, member 1 decreased CPT1A expression and attenuated cell proliferation (Wang *et al.*, 2019b). In GSCs, silencing peroxisome proliferator-activated receptor- α (PPAR α) downregulated CPT1A and suppressed the proliferation and colony formation abilities of GSCs *in vitro* and tumorigenicity *in vivo* (Haynes *et al.*, 2019). In breast cancer, the long noncoding RNA nuclear paraspeckle assembly transcript 1 (NEAT1)/miR-107 axis directly targeted and regulated CPT1A and ultimately promoted the growth and metastasis of breast cancer (Xiong *et al.*, 2019). In hepatocellular carcinoma (HCC), miR-603 targeted and downregulated fatty acid-binding protein 1 (FABP1), increased downstream CPT1A expression and promoted the proliferation, migration, and invasion of cancer cells (Lin *et al.*, 2021b). In summary, these findings suggested that overexpression of CPT1A promotes tumor growth, probably in an FAO-dependent manner.

Invasion and metastasis

High expression of CPT1A is correlated with the metastasis status of several types of cancers and confers improved migration and invasion abilities to tumor cells. Overexpression of CPT1A has been observed in breast cancer cell lines, tissues, and serum, and its high expression is significantly associated with metastasis and poor prognosis of breast cancer patients (Han *et al.*, 2019; Jariwala *et al.*, 2021; Tan *et al.*, 2021). CPT1A is overexpressed in papillary thyroid cancer (PTC), and its increased expression is correlated with lymph node metastasis, TNM stage, and unfavorable outcome in PTC patients. CPT1A overexpression functionally promoted the migration of PTC cells (Lu *et al.*, 2021a). CPT1A was overexpressed in GC tissues, and its overexpression potentiated the invasion and epithelial-mesenchymal transition (EMT) of GC cells (Wang *et al.*, 2020b). As a succinyltransferase, CPT1A succinylated S100A10 at Lys47 and functionally promoted the invasion and migration of GC cells (Wang *et al.*, 2019a).

Many oncogenic factors promote tumor cell metastasis by regulating CPT1A (Fig. 2). Mitochondrial fission, which is often increased in many types of cancers, promotes cell proliferation and metastasis, partially by regulating the PPAR γ coactivator-1 α (PGC-1 α)/PPAR α /CPT1A axis

(Wu *et al.*, 2022). In HGSOC, overexpression of cancer-type organic anion transporting polypeptide 1B3 (Ct-OATP1B3) upregulated CPT1A via insulin-like growth factor 2 mRNA-binding protein 2-dependent mRNA stability and promoted FAO, ultimately enhancing cancer cell migration and invasion (Huang *et al.*, 2022). One study reported that miR-33b expression decreased in HGSOC tissues from metastatic omental cancer, owing to promoter hypermethylation, while miR-33b overexpression inhibited malignant phenotypes of ovarian cancer cells by suppressing fatty acid synthase-mediated *de novo* lipogenesis and CPT1A-mediated FAO and ultimately inhibited tumor metastasis (Wang *et al.*, 2021). CPT1A participates in the miR-603/FABP1-induced migration and invasion of liver cancer cells (Lin *et al.*, 2021b). The expression level of miR-328-3p is low in breast cancer, especially in metastatic breast cancer. MiR-328-3p directly regulates CPT1A and promotes breast cancer metastasis (Zeng *et al.*, 2021).

In summary, on the one hand, CPT1A can promote tumor cell proliferation by activating FAO or succinylating the target genes as a succinyltransferase; on the other hand, CPT1A itself is regulated via transcription and mRNA stability during tumorigenesis (Fig. 2).

Tumor microenvironment

In addition to tumor cells, reprogramming of FAO and dysregulation of CPT1A also frequently occur in cancer-associated fibroblasts, adipocytes, immune cells, and other cells, eventually leading to a cancer-promoting microenvironment and immune suppression (Fig. 3). Long-term nicotine exposure improves the metastatic potential of lung cancer cells, and mechanically promotes the secretion of exosomal miR-4466 by N2-neutrophils and then enhances the metastatic ability of primary cancer cells in a CPT1A-dependent manner (Tyagi *et al.*, 2022). Cancer-associated fibroblasts promote the migration and invasion of colon cancer cells by increasing CPT1A expression and enhancing FAO (Peng *et al.*, 2021). Exosomal CD44, secreted by lymphatic metastatic gastric tumor cells, promoted lymph node metastasis of primary cancer cells by augmenting CPT1A-mediated FAO (Wang *et al.*, 2022). In the tumor microenvironment, myeloid-derived suppressor cells express β 2 adrenergic receptor and sequentially increase FAO by

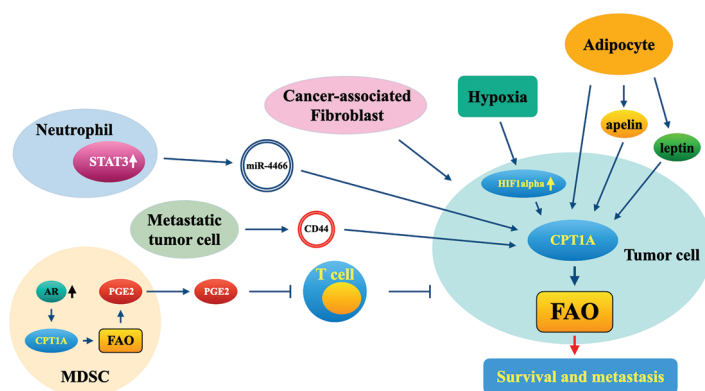


FIGURE 3. Functional roles of CPT1A in the tumor microenvironment. MDSC, myeloid-derived suppressor cell; FAO, fatty acid oxidation; AR, adrenergic receptor; CPT1A, carnitine palmitoyltransferase 1A; PGE2, prostaglandin E2; STAT3, signal transducer and activator of transcription 3; CD44, CD44 molecule.

upregulating CPT1A, then secrete the immunosuppressor PGE2 and attenuate antitumor immunity (Mohammadpour *et al.*, 2021). Importantly, the blockade of lipid oxidation using ranolazine inhibited tumor growth and led to antitumor immune activation, including increased infiltration of dendritic cells and CD8⁺ T cells in a CPT1A-dependent manner in a prostate cancer animal model (Guth *et al.*, 2020).

As one of the predominant components in the tumor microenvironment, adipocytes accelerate tumor growth and metastasis. Adipocytes can promote the invasion of colon tumor cells into surrounding adipose tissues. In one study, fatty acid or adipocyte treatment enhanced the invasion of colon cancer cells by activating the CPT1A-FAO- β -catenin signaling pathway (Xiong *et al.*, 2020). Adipocyte-secreted apelin potentiated the metastasis of apelin receptor-expressing ovarian cancer cells by enhancing lipid oxidation and energy production in a CPT1A-dependent manner (Dogra *et al.*, 2021). The adipocyte-secreted hormone leptin enhanced FAO in colorectal and breast cancer cells by upregulating CPT1A (Liu *et al.*, 2019). Coculture of prostate cancer (PCa) cells with periprostatic adipose tissue cells increased the expression of CPT1A in these cells (Altuna-Coy *et al.*, 2022).

Hypoxia plays a critical role in the progression of cancers and is also a major characteristic of the tumor microenvironment; thus, targeting hypoxia-regulated signaling pathways probably offers novel therapeutic strategies. In gastric adenocarcinoma, hypoxia leads to the induction of hypoxia-inducible factor (HIF)-1 α and reduces the expression of FAO-related genes, including CPT1A, and CPT1A expression was negatively correlated with the level of HIF-1 α in gastric adenocarcinoma tissues (Ezzeddini *et al.*, 2021). Rios-Colon *et al.* (2021) reported that in PCa cells, CPT1A promoted the cell proliferation of cancer cells under hypoxic conditions *in vitro*; CPT1A also accelerated tumor growth *in vivo* with more hypoxic regions. Moreover, CPT1A overexpression in PCa cells significantly promoted the pathways of lipid catabolism, ER stress, and serine synthesis and repressed the androgen response (Joshi *et al.*, 2020). Considering the crucial roles of CPT1A in the proliferation and migration of tumor cells and in processes related to the cancer-promoting microenvironment and immune suppression, targeting CPT1A will benefit tumor

therapy because of its antitumor effects on both tumor cells and microenvironment cells.

Diagnostic and Prognostic Relevance and Therapeutic Applications

CPT1A is often reported to be highly expressed in several types of cancers and is identified as a potential diagnostic and prognostic cancer biomarker (Table 1). High expression of CPT1A was associated with pathological stage and grade in patients with GC and was closely associated with poor survival in GC, AML, and HGSOC (Sawyer *et al.*, 2020; Wang *et al.*, 2020b; Mao *et al.*, 2021). The expression level of CPT1A is higher and was negatively correlated with tumor differentiation grades in canine mammary tumor tissues (Cacciola *et al.*, 2020). High expression levels of CPT1A were significantly associated with the TNM stage and histological grade. Of note, the level of CPT1A is higher in the serum of breast cancer patients than in healthy patients (Tan *et al.*, 2021). According to immunohistochemical analysis, the transcript and protein levels of CPT1A and pyruvate kinase muscle isozyme 2 decreased in cervical squamous cell carcinoma and also in HPV16-positive cervical intraepithelial neoplasia stages II–III tissues compared with HPV16-negative tissues (Abudula *et al.*, 2020).

In contrast to most cancers, CPT1A expression was decreased in renal carcinoma (RC), and high expression of CPT1A was associated with good overall survival in RC (Zhao *et al.*, 2019; Xu *et al.*, 2020b). Overexpression of CPT1A suppressed malignant phenotypes of RC cells (Xu *et al.*, 2020b). Another study also confirmed a decrease in CPT1A expression in clear cell renal carcinoma (ccRCC) and further revealed that overexpression of CPT1A attenuated lipid accumulation and tumor growth by regulating the PPAR α /CD36 signaling pathway (Yang *et al.*, 2022). STF-62247 increased the expression level of CPT1A in ccRCC and showed potential antitumor activities (Johnson *et al.*, 2022). HIF could also downregulate CPT1A expression and diminish FAO in ccRCC (Tan and Welford, 2020), and LRPPRC was found to be the downstream regulator of CPT1A in ccRCC cells (Lu *et al.*, 2021b).

TABLE 1

Correlations between the expression of carnitine palmitoyltransferase 1A (CPT1A) and clinicopathologic and prognostic features

No.	Cancer type	Up/Down	Detection methods, cohort size/Subtype	Sample source	Clinicopathologic features	Prognosis	References
1	GC	Up	RNA-seq: primary tumor ($n = 415$) vs. normal tissues ($n = 34$)	Tissues	Stage, histological grade, lymph node metastasis	OS, PPS, FP	Wang <i>et al.</i> (2020b)
		Up	IHC: tumor tissues ($n = 129$) vs. normal tissues ($n = 45$)	Tissues	Stage, histological grade, lymph node metastasis	—	
2	CMT	Up	IHC: tumor tissues ($n = 46$) vs. normal tissues ($n = 6$)	Tissues	Differentiation grade	—	Cacciola <i>et al.</i> (2020)
3	AML	—	qRT-PCR: tumor cells ($n = 325$) vs. normal cells ($n = 8$)	Cells	—	OS	Mao <i>et al.</i> (2021)
4	BC	Up	ELISA: tumor patients ($n = 430$) vs. healthy controls ($n = 400$) vs. benign disease patients ($n = 200$)	Serum	Lymph node status, tumor size, TNM stage, histological grade, HER2 status	—	Tan <i>et al.</i> (2021)
5	OC	—	Microarray: tumor tissues ($n = 319$)	Tissues	—	OS	Sawyer <i>et al.</i> (2020)
6	CSCC	Up	IHC: tumor tissues ($n = 34$) vs. CIN tissues ($n = 38$) vs. normal tissues ($n = 51$)	Tissues	—	—	Abudula <i>et al.</i> (2020)

Note: GC: gastric cancer; CMT: canine mammary tumor; AML: acute myeloid leukemia; BC: breast cancer; ELISA: enzyme-linked immunosorbent assay; OC: ovarian cancer; CSCC: cervical squamous cell cancer; IHC: immunohistochemistry; OS: overall survival; PPS: post progression survival; qRT-PCR: quantitative real-time-polymerase chain reaction; FP: free progression.

Many clinical drugs and candidate drugs exert antitumor effects by suppressing FAO and/or CPT1A in tumor cells or cells in the tumor microenvironment. In a mouse model of lung cancer, high-dose dexamethasone, often used in the treatment of immunotherapy-induced autoimmune diseases, inhibited tumor progression and reduced the expression levels of FAO-related genes, including CPT1A (Xu *et al.*, 2020a). An *in vivo* study showed that bezafibrate, an agonist of the PGC-1 α /PPAR complex, promoted the infiltration of CD8 $^+$ T cells into lung tumor tissues and upregulated FAO-related genes, including CPT1A, in tumor cells (Wan *et al.*, 2020). Anticancer roles of betulinic acid were reported in previous studies, and nanoliposomes loaded with betulinic acid attenuated the proliferation and glycolysis of CRC cells and decreased the CPT1A levels (Wang *et al.*, 2020a). *Withania somnifera* root extract could decrease total free FAs and the expression level of CPT1A in prostate cancer cells (Kim *et al.*, 2020). In diethylnitrosamine-induced HCC, both sterol O-acyltransferase 1 (SOAT1) and CPT1A were upregulated, and blocking these two exerted synergistic antitumor effects on HCC (Ren *et al.*, 2021). The combination of CPT1A knockdown and blocking of cyclin-dependent kinase 9 exerted synergistic anticancer effects in PCa cells (Itkonen *et al.*, 2019).

Resistance to chemotherapy is often a critical determinant of patient survival in several types of cancers, and blocking FAO/CPT1A shows promising therapeutic effects in chemoresistant tumors. Both *in vitro* and in patient-derived xenograft models, knockout and pharmacologic suppression of CPT1A sensitized HGSOC cells to platinum (Huang *et al.*, 2021). In epithelial ovarian cancer, NK2 homeobox2-8 epigenetically suppressed key FAO genes, including CPT1, and importantly, blocking FAO using perhexiline enhanced the therapeutic effects of

platinum (Zhu *et al.*, 2019). The expression of CPT1A is higher in oxaliplatin-resistant than in oxaliplatin-sensitive colon cancer cells, and oxaliplatin treatment induces CPT1A expression. Both *in vitro* and *in vivo* experiments suggested that silencing CPT1A by siRNAs or etomoxir could sensitize drug-resistant tumor cells to oxaliplatin (Lin *et al.*, 2021a). MAPK inhibitor treatment enhanced FAO in melanoma cells by regulating CPT1A, and elevated FAO allowed BRAF^{V600E} cells which frequently acquired resistance to MAPK-targeted therapy to survive after MAPK inhibitor treatment. Blocking FAO, MAPK, and glycolysis synergistically repressed cancer cell growth both *in vitro* and *in vivo* (Aloia *et al.*, 2019). CB-839 is an inhibitor of glutaminase, and in triple-negative breast cancer cells resistant to CB-839, the expression of CPT2 and activity of CPT1 were elevated. Blocking CPT1 and glutaminase synergistically inhibited the migration and proliferation of CB-839-resistant triple-negative breast cancer cells (Reis *et al.*, 2019).

Radioresistant cancer cells often enhance metabolism to provide more energy to allow tumor cells to survive under adverse conditions. High PGC-1 α expression was associated with poor survival in patients with nasopharyngeal carcinoma who received radiation therapy. CPT1A, which was transcriptionally activated by the PGC1 α /CCAAT enhancer binding protein beta complex and sequentially improves FAO and participates in the radiation resistance of nasopharyngeal tumor cells (Du *et al.*, 2019). The expression of CPT1A/CPT2 was higher in patients with recurrent breast cancer and correlated with unfavorable outcomes. Knockout of CPT1A/CPT2 repressed radiation-induced ERK phosphorylation and radioresistance in radioresistant breast cancer cells and radiation-derived breast cancer stem cells (Han *et al.*, 2019).

In summary, CPT1A is dysregulated in many types of cancers and has the potential as a diagnostic and prognostic biomarker. Importantly, genetic or pharmacologic inhibition of CPT1A sensitizes tumor cells of several types of cancers to chemotherapy and radiotherapy. These findings suggested that CPT1A might be a candidate target for overcoming chemoresistance and radioresistance in tumors.

Perspective

CPT1A is upregulated and associated with poor prognosis in the majority of cancers, such as GC, AML, HGSO, and BC; in contrast, CPT1A is decreased and correlates with good prognosis in renal carcinoma (Zhao *et al.*, 2019; Sawyer *et al.*, 2020; Wang *et al.*, 2020b; Mao *et al.*, 2021; Peng *et al.*, 2021; Tan *et al.*, 2021). The reasons why both activation and inactivation of CPT1A and FAO can promote tumorigenesis in different types of cancers are still fairly unclear.

Blocking CPT1A or FAO has recently shown potential therapeutic effects in many types of cancers; in particular, this approach has shown promise for the treatment of chemoresistant and radioresistant cancer cells. Nevertheless, the roles and mechanisms of CPT1A and FAO in resistance to chemo- or radiotherapy urgently need to be investigated exhaustively, and future studies should focus on the application of CPT1A- or FAO-based methods in cancer therapy. Owing to its important roles in the cancer-promoting microenvironment and immune suppression, CPT1A might be developed as a new target for tumor immunotherapy.

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Availability of Data and Materials: All data generated or analyzed during this study are included in this paper.

Ethics Approval: Not Applicable.

Conflicts of Interest: The authors declare that they have no conflicts of interest to report regarding the present study.

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