Ferroptosis, Acyl Starvation, and Breast Cancer

Rafał Bobiński, Mieczysław Dutka, Monika Pizon, Wioletta Waksmańska, and Anna Pielesz

Department of Biochemistry and Molecular Biology (R.B., M.D., W.W.) and Department of Microbiology and Environmental Technology, Institute of Engineering and Environmental Protection (A.P.), University of Bielsko-Biała, Bielsko-Biała, Poland; and Department of Research and Development, Transfusion Center Bayreuth, Bayreuth, Germany (M.P.)

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ABSTRACT

To maintain their growth rate, cancer cells must secure a supply of fatty acids, which are necessary for building cell membranes and maintaining energy processes. This is one of the reasons why tissues with intensive fatty acid metabolism, such as the mammary gland, are more likely to develop tumors. One natural or induced defense process against cancer is ferroptosis, which interferes with normal fatty acid metabolism. This leads to the oxidation of polyunsaturated fatty acids, which causes a rearrangement of the metabolism and damages cell membranes. As a consequence of this oxidation, there is a shortage of normal polyunsaturated fatty acids, which disturbs the complicated metabolism of fatty acids. This imbalance in metabolism, resulting from the deficiency of properly structured fatty acids, is called, by these authors, “acyl starvation.” When cancer cells are exposed to alternating hypoxia and reoxygenation, they often develop resistance to neoadjuvant therapies. Blocking the inhibition of fatty acid desaturase leads to the formation of toxic phospholipid hydroperoxides in ferroptosis, whereas on the other hand, the inhibition of fatty acid–binding protein 4 and translocase leads to a reduced uptake of fatty acids and disruption of the cellular transport of fatty acids, resulting in intracellular acyl starvation. The disruption in the metabolism of fatty acids in cancer cells may augment the effectiveness of neoadjuvant therapy.

SIGNIFICANCE STATEMENT

Regulation of the metabolism of fatty acids in cancer cells seems to be a promising therapeutic direction. Studies show that the induction of ferroptosis in cancer cells, combined with use of neoadjuvant therapies, effectively inhibits the proliferation of these cells. We link the process of ferroptosis with apoptosis and SCD1-FABP4-CD36 axis and propose the term “acyl starvation” for the processes leading to FA deficiency, dysregulation of FA metabolism in cancer cells, and, most importantly, the appearance of incorrect proportions FAs.

Introduction

In addition to the growth, differentiation, and proliferation of cells, the fourth process that completes the cycle of life is the death of the cells. The cause of death may be the activation of self-destruction mechanisms or the occurrence of disturbances in the cell metabolism caused by external or intracellular factors. An example of regulated cell death is ferroptosis—iron-dependent lipid peroxidation resulting from disruption of intracellular iron metabolism. As a result, the redox potential of the cell is disturbed, which leads to the oxidation of cellular lipids (Jiang et al., 2021). This causes damage to the cell membranes, a loss of stimuli, an increase in the entropy of the cell, and, eventually, its death. The key compounds in the regulation of ferroptosis are glutathione (GSH) and glutathione peroxidase 4 (GPX4). Glutathione is the most common reductant in mammalian cells. It is, first of
all, a cofactor of GPX4, a selenoperoxidase, whose main role is to protect cells against oxidation by peroxides generated during biochemical processes such as hydrogen peroxide and phospholipid hydroperoxide (PLOOH), among others. Glutathione deficiency or a decrease in GPX4 activity exacerbate ferroptosis (Dixon et al., 2012). The mechanism of ferroptosis regulation, however, is much more complicated. There are numerous metabolic pathways involved, such as the transsulfuration pathway, the mevalonate (MVA) pathway, the lipid peroxidation pathway, the stearoyl-coenzyme A (CoA) desaturase-1 (SCD1) pathway, the fatty acid (FA) membrane transport pathway, the transferine/ferritine pathway, the \( \chi_c \) cistine/glutamate antiporter system, and many others. These processes directly or indirectly regulate the level of cellular glutathione and, thus, intensify or inhibit ferroptosis.

In recent years, ferroptosis has become a subject of interest for oncologists, especially in terms of supporting hormone or drug therapy. Ferroptosis interferes with many biochemical pathways, but, most importantly, it interferes with the normal metabolism of fatty acids, which are used in large quantities for the construction of cell membranes and energy processes of rapidly dividing tumor cells. Therefore, tissues with intensive fatty acid metabolism, such as the mammary gland, are more likely to develop tumors. It has been observed that cancer cells tend to become resistant to neoadjuvant therapies. The reason for the successful survival of cancer cells is the ease with which they adapt to metabolic and oxidative stress. Although the mechanism is not fully understood, it is known that resistance is connected with the occurrence of hypoxia in tumor cells. There are two types of hypoxia. Chronic hypoxia is located mainly around the necrotic areas of the cancer tumor and is the result of the increasing distance between the proliferating cancer cells and the blood vessel (diffusion-limited hypoxia) (Rofstad et al., 2007). Cyclic (transient, acute) hypoxia is characterized by the occurrence of alternating states of hypoxia and reoxygenation, and it appears in different areas of the tumor as a result of changes in blood flow, the presence of nonfunctional vessels, and the process of vascular remodeling during angiogenesis (perfusion-limited hypoxia/intermittent hypoxia) (Carmona-Bozo et al., 2021). Both types of hypoxia lead to the cancer cells becoming more aggressive and have an adverse effect on the success of the therapy (Muz et al., 2015). In studies involving various drugs, small molecule–induced ferroptosis has been shown to have a strong inhibitory effect on tumor growth in a drug-resistant environment, which may increase the sensitivity of the tumor to chemotherapeutic treatment (Luís et al., 2021). The question is, however, how does ferroptosis reduce the resistance of cancer cells to classic neoadjuvant therapies? This review is an attempt to answer this question. The first part will discuss the mechanisms that lead to ferroptosis, and the second part will introduce the concept of using ferroptosis in the treatment of breast cancer.

**Cysteine Metabolism.** Although the concept of ferroptosis was suggested by Stockwell in 2012, (Dixon et al., 2012), this pioneering work on disruption of the cysteine metabolism, which is crucial to the process of ferroptosis, was started in the 1950s by Harry Eagle. He showed that depriving cells of cysteine resulted in their death (Eagle 1955), whereas endogenous cysteine synthesis inhibited this process of self-destruction (Eagle et al., 1961). These observations indicated that cysteine, as the main substrate for the biosynthesis of reduced glutathione, is an important factor in maintaining the level of intracellular oxidation potential, and its presence inhibits ferroptosis. Due to the key role of glutathione in cellular metabolism, its biosynthesis from cysteine has been evolutionarily secured by several pathways. The source of cysteine may be cystine collected from the environment surrounding the cell via the \( \chi_c \) cystine/Glu antiporter system (Fig. 1). This is a transmembrane protein complex, consisting of the subunits solute carrier family 7 member 11 (SLC7A11) and solute carrier family 3 member 2 (SLC3A2), which replace Glu with cystine at a ratio of 1:1. (Bannai and Kitamura 1980; Lin et al., 2020). In this mechanism, the availability of Glu, which is formed from glutamine, is important. The glutamine released from tissues is carried into the cell by means of the solute carrier family 1 member 5 (SLC1A5) transporter and then converted to Glu by means of glutaminase 1 (GLS1) and glutaminase 2 (GLS2). During the deamination reaction, Glu forms \( \gamma \)-ketoglutarate (\( \gamma \)-KG), which is then degraded in the mitochondrial tricarboxylic acid (TCA) cycle. This reaction is catalyzed by the amino-transferase glutamic-oxaloacetic transaminase (GOT)-1. It has been proven that the knockdown of GLS2, which inhibits the glutamine degradation pathway (Gao et al., 2019), as well as the inhibition of GOT1 by amino-oxyacetate (AOA) (Villar et al., 2015) may secondarily inhibit ferroptosis. It should be added here that an important factor influencing ferroptosis is the ratio of intra- and extracellular Glu concentrations. When the extracellular concentration of Glu is abnormally high, the uniform exchange of Glu and cystine is disrupted, which indirectly affects the amount of available cysteine and ultimately leads to ferroptosis due to the accumulation of oxidized lipids (Lin et al., 2020). The second source of cysteine is the transsulfuration pathway, a multistep sequence of reactions in which cysteine is formed from methionine via \( S \)-adenosylmethionine, \( S \)-adenosylhomocysteine, homocysteine, and cystathione. A third possible source of cysteine is the blockage of cysteinyl-tRNA biosynthesis by inhibiting cysteinyl-tRNA synthetase (CARS) or a knockout of the gene encoding it. This situation causes the inhibition of protein synthesis but then increases the amount of free intracellular cysteine. The inhibition of CARS additionally induces the transsulfuration pathway, thus inhibiting ferroptosis induced by cystine deficiency (Hayano et al., 2016).

**The Role of GSH and GPX4**

GSH and GPX4 are part of the \( \chi_c \)-GSH-GPX4 pathway responsible for the inhibition of ferroptosis. This pathway inhibits lipid oxidation, i.e., the formation of PLOOH—a form of reactive oxygen species (ROS) that destroys the cell. Formed from cysteine, GSH is an intracellular antioxidant buffer that maintains redox balance with the help of GPX4. The reduction of PLOOH and cholesterol to the corresponding alcohols by GPX4 requires the catalytic selenocysteine residues of GPX4 and two electrons mainly supplied by GSH but also by other low-molecular-weight thiols or even protein thiols (Maiorino et al., 2018). In other words, GPX4 is responsible...
for the reduction of PLOOH to phospholipid alcohols (PLOH) (Lv et al., 2019). The substrates are two GSH molecules, which are the reducers of PLOOH to PLOH (Ursini et al., 1982; Ursini et al., 1985). In addition to PLOH, this reaction produces oxidized glutathione (GSSG). This form of glutathione must be reduced so that glutathione can be reused in the...
Lipid Peroxidation Metabolism

Although it is known that the level of unsaturation of lipid bilayers is a key determinant of ferroptosis, it is still unclear how the lipid peroxidation process is initiated. It is known that it proceeds in two different ways—nonenzymatic and enzymatic. Failure to control the lipid peroxidation process chain leads to the rise of innumerable byproducts, the breakdown of membrane integrity, and, ultimately, disruption of the membranes of organelles and cells. Thus, membranes with a high content of polyunsaturated fatty acid–containing phospholipids (PUFA-PL), as seen in neurons, are particularly prone to peroxidation. Nonenzymatic peroxidation is a spontaneous process—an oxygen-dependent free radical chain reaction. It is divided into three stages: initiation, propagation, and termination (Frank, 1950). The initiation process is associated with the generation of a free radical, formed in the Fenton reaction with the participation of iron (Lai and Piette, 1978). Next, the bis allylic hydrogen atom is removed between the two carbon-to-carbon double bonds in the polyunsaturated acyl molecules. At the next stage, acyl molecules react with molecular oxygen, resulting in the formation of a phospholipid peroxy radical (PLOO). (Bateman, 1954; Conrad and Pratt, 2019). This PLOO removes hydrogen from another polyunsaturated fatty acid (PUFA), turning itself into PLOOH. With the participation of GPX4, PLOOH is converted into PLOH. If this does not happen, PLOOH reacts with further PUFA molecules (Davies and Guo, 2014). In the presence of oxygen, another hydrogen atom is removed from PUFA, and further PLOOH molecules, which are pathognomonic for ferroptosis, are formed. However, enzymatically controlled lipid peroxidation seems to be of greater importance for ferroptosis. At least some enzymes are involved in regulating this process. Research on enzymatic lipid peroxidation has mainly focused on lipoxygenase (LOX), acyl-CoA synthetase long-chain family member 4 (ACLS4), and lysophosphatidylcholine acyltransferase 3 (LPCAT3) (Golej et al., 2011; Yang et al., 2016; Doll et al., 2017). 

The Role of Iron in Ferroptosis

Iron is a biochemically active element of such cofactors as heme, iron-sulfur centers [Fe-S], and 1- or 2-atom iron centers, which, in turn, determine the activities and functions of many proteins necessary for the proper course of key biologic processes. Proteins containing iron in their active centers participate in the transportation of electrons in the respiratory chain, the transportation and storage of oxygen, and the regulation of gene expression, as well as in the synthesis of DNA, microRNA, and collagen. The regulation of iron metabolism is controlled by numerous genes, whose expression products are involved in maintaining the iron homeostasis.
An example of such molecules is iron regulatory proteins (IRPs) (Volz, 2008). By regulating the expression of transferrin receptor (TFRC) and ferritin heavy chain 1, etc., IRP1 and IRP2 stabilize the cell’s labile iron pools composed of Fe$^{2+}$ (Lin et al., 2020). One of the disruptions to iron metabolism is ferroptosis. Ferroptotic cell death correlates with an increase in iron stores in the cell, which ultimately leads to the oxidation of cell membrane fats. As mentioned earlier, lipid peroxidation takes place during enzymatic and nonenzymatic Fenton reaction. The latter is considered to be the key mechanism of ferroptosis (Conrad and Pratt, 2019; Jiang et al., 2021). The Fenton reaction, as well as the action of LOX, is regulated, inter alia, by the pool of intracellular iron. The main regulators of this pool, and thus of ferroptosis, are transferrin and TFRC (Gao et al., 2015a). Increasing TFRC activity to enrich the cellular iron pool can lead to ferroptosis (Yang and Stockwell, 2008; Lin et al., 2020). In the cell, iron binds to ferritin and is deposited in this form. The release of iron from the deposits occurs in the lysosomes. The process is controlled in three stages—phagocytosis of ferritin bound to iron, the reduction of iron, and its release into the cytoplasm. The key factor regulating phagocytosis of ferritin is nuclear receptor coactivator 4 (NCOA4). The combination of ferritin with NCOA4 forms autophagosomes, which are then internalized into lysosomes. Studies have shown that reducing the content of NCOA4 in the cytoplasm inhibits the internalization of ferritin into lysosomes and reduces susceptibility to ferroptosis (Mancias et al., 2014). The second stage, i.e., the reduction of Fe$^{3+}$ to Fe$^{2+}$, takes place with the participation of metalloreductase (six-transmembrane epithelial antigen of prostate 3) (STEAP3) (Zhang et al., 2012). STEAP3 activity has been proven to be dependent on farnesioid anemia complementation group D2 (FANCD2), a nuclear protein involved in DNA damage repair, which protects against ferroptosis-mediated injury in bone marrow stromal cells (Song et al., 2016). Knockdown of the FANCD2 gene inhibits STEAP3 expression and releases Fe$^{2+}$ (Song et al., 2016) and thus reduces the cytoplasmic labile iron pool and susceptibility to ferroptosis. The third stage, the release of Fe$^{2+}$ into the cytoplasm, occurs with the participation of the divalent metal transporter 1 (DMT1). Many other factors, such as iron responsive element-binding protein 2 (IREB2) (Dixon et al., 2012), autophagy-related protein 13 (ATG13) (Gao et al., 2016), heme oxygenase-1 (HMOX1) (Kwon et al., 2011), heat shock protein β-1 (HSPB1) (Sun et al., 2015), and ferroportin (Fpn) (Li et al., 2018), etc., also participate in the cytoplasmic metabolism of iron.

Glutamine, Mitochondria, and Ferroptosis

Mitochondria are involved in the implementation of various types of regulated cell death, such as extrinsic and intrinsic apoptosis and autophagy, thus playing a major role in tissue homeostasis (Mattson et al., 2008; Xie et al., 2018; Bebber et al., 2020). They are essential for most normal cell types due to their role in generating ATP via the mitochondrial oxidative phosphorylation system (Gao et al., 2015b; Gao et al., 2019). The involvement of mitochondria in ferroptosis thus emphasizes its metabolic nature. Characteristic mitochondrial changes in ferroptosis include rupture of the mitochondria, reduction of mitochondrial membrane density, and reduction of mitochondrial ridges (Lin et al., 2020). It has been shown, for example, that the experimental induction of ferroptosis by pharmacological inhibition of Xc− causes mitochondrial fragmentation, production of mitochondrial ROS, the loss of mitochondrial membrane potential, and depletion of ATP (Yagoda et al., 2007; Xie et al., 2016; Yuan et al., 2016; Neitemeier at al., 2017; Zhou et al., 2020a). The inhibition of the mitochondrial oxidative phosphorylation system or mitochondrial loss produced by mitophagia impedes the ferroptosis either induced by erastin or by the lack of cysteine. The metabolism of glutamine and, especially, its conversion to Glu are crucial for cysteine starvation–induced ferroptosis and the mitochondrial Krebs cycle. In other words, without glutamine, erastin-induced ferroptosis, in the absence of cysteine, is also inhibited. (Gao et al., 2015b). One of the factors regulating glutamine decomposition is AOA (Wu et al., 2021), an inhibitor of GOT1, an enzyme that mainly takes part, inter alia, in the biosynthesis of keto acids, principally 2-ketoglutaric acid, which is necessary in the mitochondrial process of ATP production. The action of AOA inhibits ferroptosis, but it can be restored by the supplementation of 2-KG (Gao et al., 2015b, Jennis et al., 2016; Luo et al., 2018). Research indicates that further mitochondrial metabolites of 2-KG such as succinate, fumarate, and malate could modulate cysteine deprivation–induced ferroptosis (Gao et al., 2016). It is believed that the electron transport assisted by the glutaminolysis-TCA cycle may facilitate lipid peroxidation by generating ROS, which are produced as an inevitable byproduct of mitochondrial respiration. Sensitivity to ferroptosis may also be determined by the modulation of adenosine monophosphate–activated protein kinase (AMPK) activity by the glutaminolysis-TCA cycle and the associated production of ATP in the electron transport chain (Ma et al., 2020). The AMPK, activated in this mechanism, phosphorylates and thus inhibits acetyl-CoA 1 (ACC1) and 2 (ACC2) carboxylase, which leads to a reduced conversion of acetyl-CoA to malonyl-CoA necessary for PUFA biosynthesis (Lee et al., 2020). It is possible that this mechanism reduces the level of lipid peroxidation and slows down ferroptosis (Li et al., 2020a; Lee et al., 2020; Wu et al., 2021). It seems, however, that endogenous biosynthesis can be replaced by the transport of FAs from the tumor microenvironment (TME), hence the influence on the inhibition pathway of ACC1 and ACC2 may be of less importance in the regulation of ferroptosis. Additionally, AMPK activation also triggers another mechanism. Due to the AMPK phosphorylation, there is upregulation of sterol regulatory element–binding protein 1 (SREBP1) and the downstream SCD1, and this results in a decrease in the amount of MUFA that inhibit ferroptosis (Zhao et al., 2020; Wang et al., 2018).

Breast Cancer

Breast cancer is a disease that is molecularly and clinically extremely heterogeneous. Unlike normal tissue, cancer cells develop under conditions of metabolic and oxidative stress. This situation may be favorable or unfavorable to their growth, depending on whether they are exposed to moderate or excessive levels of stress and the internal mechanisms of both antioxidant protection and the stress defenses of the tumor (Harris, 2002; Ackerman and Simon, 2014; Manda et al., 2015; Reczek and Chandel, 2017). Changes in oxygen and nutrient levels in a hypoxic TME may limit tumor growth but can also alter the tumor phenotype and provoke...
conversion to more malignant tumor types (Sanna and Rofstad, 1994). The TME is key to the growth of the tumor. In the breast cancer TME, the role of adipocytes has received great attention due to their proximity to a developing breast tumor. Clinical trials clearly indicate an increased invasiveness of breast cancer, leading to worse treatment outcomes and prognosis (Dirat et al., 2011; Wang et al., 2012). Adipocytes influence the growth of cancer cells through two main mechanisms. First, adipocytes secrete adipocytokines (adipocyte-secreted growth factors) and cytokines, which activate growth-promoting signaling pathways in tumor cells and stimulate various oncogenic processes. Interleukin-6 (IL-6) and leptin secreted by adipocytes induce and regulate epithelial-mesenchymal transition in cancer cells (Lee et al., 2015; Gyamfi et al., 2018; Gyamfi et al., 2019). The secreted leptin activates pathways that increase stem cell renewal and also increase drug resistance (Ayob and Ramasamy, 2018). Second, adipocytes release metabolites and biomolecules that remodel the metabolism of cancer cells to increase tumor growth. It should be added that adipocytes in close/direct contact with tumor cells are commonly called cancer-associated adipocytes (CAAs) and have different characteristics from adipocytes not associated with tumor cells. The adipose tissue infiltrated by breast cancer has a substantially reduced lipid droplet (LD) size. Importantly, CAAs have a greatly increased expression of IL-6 and leptin. The CAAs release increased amounts of IL-6 and leptin, which are important factors in boosting the growth of tumors (Gior dano et al., 2016; Balaban et al., 2017; He et al., 2018; Zaoui et al., 2019). This proximity of the adipocytes to the cancer cells means that the breast cancer cells can parasitize their energy substrates and obtain metabolites, including lactate, glutamine, and FAs, that are restricted in the environment of the growing tumor (DeBerardinis et al., 2008; Dias et al., 2019; Wang and Li, 2019). The metabolites thus obtained support metabolic needs and provide a selective advantage for cancer survival and progression in a difficult microenvironment. The reprogramming of energy metabolism is therefore a key hallmark of tumor growth (Hanahan and Coussens, 2012; Dias et al., 2019; Wang and FAs, that are restricted in the environment of the growing tumor (DeBerardinis et al., 2008; Dias et al., 2019; Wang and Li, 2019). The metabolites thus obtained support metabolic needs and provide a selective advantage for cancer survival and progression in a difficult microenvironment. The reprogramming of energy metabolism is therefore a key hallmark of tumor growth (Hanahan and Coussens, 2012; Dias et al., 2019; Wang and Mahvi et al., 2019). Systemic therapies have improved overall survival for many cancers. However, relapses are the most common problem among many primary cancer treatments (Mahvi et al., 2018). Small tumors remaining after chemotherapy or targeted therapies can survive under conditions of constant change between hypoxia and reoxygenation in the TME during treatment and later cause a relapse and/or the development of aggressive tumors (Cardenas-Navia et al., 2008). Uncontrolled proliferation overloads the existing vessels and causes the tumor to become hypoxic (Brown and Giaccia, 1998), and neoadjuvant therapies may exacerbate tumor hypoxia, which may drive drug resistance (McIntyre and Harris, 2015). Alternating hypoxia and reoxygenation lead to chronic oxidative stress destabilizing the cell's redox potential (Semenza, 2017). As a consequence, this affects genomic instability, changes in tumor metabolism, the progression of malignancy (Brown and Wilson, 2004; Zhang et al., 2015; Li et al., 2015), and, ultimately, resistance to neoadjuvant therapies.

It should be clearly emphasized that ferroptosis is only one of several pathways through which tumor cells may be killed therapeutically. Unfortunately, this same process may be
induced, in parallel, in normal cells, which may be the basis for adverse effects. So, the questions arise: how to increase or induce ferroptosis in cancer cells during cancer treatment without causing ferroptosis in normal cells and how to suppress the repair mechanisms in cancer cells that inhibit ferroptosis. The starting point for the answers to these questions should be the identification of the factors that promote ferroptosis. The key compounds involved in ferroptosis are FAs. A number of macro- and micromolecules, involved in the transport and biosynthesis pathways of FAs, are involved in their metabolism, biosynthesis, and penetration into cells (Table 1).

**The SCD1-FABP4-CD36 Axis**

The SCD1 pathway and FA membrane transport pathway deserve special attention. These pathways disrupt the metabolism in the specific microenvironment of the tumor, and this disruption is crucial in inhibiting the tumor regrowth process. This applies, inter alia, to the biosynthesis of FAs, in which SCD1 participates. According to many authors, de novo biosynthesis of FAs (Sounni et al., 2014; Iwamoto et al., 2018) is emerging as a key driver of cancer malignancy dependent on the hypoxic and metabolic stress induced by antiangiogenic treatment. Expression of SCD1 (EC 1.14.19.1) has been detected in recurrent human breast cancer samples and has been correlated with a worse prognosis in patients with different types of cancer (Luis et al., 2021). SCD1, also called Δ9-desaturase, is an endoplasmic reticulum–related enzyme that catalyzes the formation of MUFA s from de novo synthesized or food-supplied FAs. SCD is a four-transmembrane domain protein composed of 359 amino acids, with a mass of 37 kDa (Paton and Ntambi, 2009; Kucharski and Kaczor, 2014). In humans, there are two homologs of the gene encoding SCD. One is on chromosome 10 (SCD1), and the other is on chromosome 17 (SCD5). Both isoforms differ in structure.
and size of the transcripts (Zhang et al., 1999). SCD1 catalyzes the reaction of introducing a first double bond, at the cis-position between carbon atoms 9 and 10, into saturated fatty acids such as palmitic acid (C16:0) and stearic acid (C18:0). The MUFAs, such as palmitoleic acid (16:1) and oleic acid (C18:1), resulting from this reaction competitively disturb the activity of PUFAs, thus inhibiting ferroptosis (Yang et al., 2016; Magtanong et al., 2019; Tesfay et al., 2019). PUFAs, unlike MUFAs, are a preferential substrate for lipid peroxidation. The inhibitory effect on ferroptosis is due to the fact that MUFAs do not have bis-allylic carbon atoms and are therefore much less prone to peroxidation. The bis-allylic position seems to be crucial to the progress of the ferroptosis process. Research has shown that deuterated at the bis-allylic position PUFAs reduce oxidative stress and protect against ferroptosis caused by erastin or RSL3 (Yang et al., 2016). This mechanism suggests that PUFA-induced ferroptosis may depend on the structure of these FAs. The regulation of ferroptosis in cancer via SCD1 also involves the lactate-activated hydroxycarboxylic acid receptor 1 (HCAR1)/monocarboxylate transporter 1 (MCT1) system. Lactate-rich cancer cells show increased resistance to ferroptotic damage induced by commonly used ferroptosis inducers such as RSL3 and erastin. The uptake of extracellular lactate by MCT1 may promote ATP production as lactate has the ability to support ATP production via the Krebs cycle (Martinez-Reyes and Chandell, 2017). On the other hand, blocking HCAR1/MCT1 by gene knockdown or the use of MCT1 inhibitor AZD3965 slows ATP biosynthesis, which results in increasing the AMP:ATP ratio (Fig. 2). A change in the energy status of a cell may initiate phosphorylation of AMPK, which leads to inhibition of the expression of SREBP1 (Bertolino et al., 2019; Zhao et al., 2020) and the eventual repression of SCD1. The inhibition of SCD1 results in a decrease in MUFAs amount, a decrease in tumor cell resistance to ferroptosis, and an increase in the accumulation of cytotoxic lipid ROS in the cytoplasmic membrane. The intracellular concentration of MUFAs is therefore one of the key factors in the regulation of ferroptosis. Studies have shown that the administration of SCD1 products such as palmitoleate (C16:1) and oleate (C18:1) with simultaneous inhibition of HCAR1/MCT1 reduces the susceptibility of cells to ferroptosis (Zhao et al., 2020). The partial restoration of cancer cells proves that other nonferroptotic mechanisms of cell regulation, such as apoptosis, may be involved (Li et al., 2017; Ma et al., 2017; Tesfay et al., 2019; Zhao et al., 2020). An example is the regulation of AMPK/mammalian target of rapamycin (mTOR) pathway by sodium-glucose cotransporter-2 (SGLT-2) (Zhou et al., 2020b). SGLT-2 is the primary cotransporter involved in renal glucose reabsorption (Cowie and Fisher, 2020). It belongs to the sodium/glucose cotransporter-1 family (SLC5A) and is responsible for creating a Na⁺ gradient in cells located in the proximal tubule, which drives glucose transport from the renal tubules into the cells. Physiologically, SGLT-2 is found only in the kidneys. Pathologically, SGLT-2 expression has been observed in, inter alia, breast cancer (Zhou et al., 2020b). Studies have shown that blocking SGLT-2 with specific inhibitors stops the cellular cycle of breast cancer cells at the G1/G0 phase and induces apoptosis. Canagliflozin and dapagliflozin, hypoglycemic and cardioprotective drugs, have been used as SGLT-2 inhibitors. It has been observed that SGLT-2 inhibitors cause a decrease in glucose uptake and an increase in AMPK phosphorylation, i.e., its activation. A further effect of this is the inhibition of p70S6K phosphorylation, which means mTOR inhibition (Zhou et al., 2020b). Canagliflozin and dapagliflozin reduce ATP production, inhibit oxidative phosphorylation, and decrease the intracellular concentration of ATP in breast cancer cells. This results in a large increase in the AMP:ATP ratio and thus the activation of AMPK, which is a sensor of cellular energy and nutrition levels in eukaryotic cells. This signaling pathway leading from the activation of AMPK to the inhibition of mTOR is believed to be, at least partially, responsible for inhibiting the proliferation, arresting the cellular cycle at the G1/G0 phase, and inducing apoptosis in breast cancer cells by canagliflozin and dapagliflozin (Zhou et al., 2020b). The activation of AMPK inhibits protein synthesis and cell proliferation. Zakikhanl et al. (2012) also showed that another diabetes medication, metformin, inhibits the proliferation of breast cancer cells by activating AMPK, resulting in an inhibition of mTOR signaling. Thus, the mTOR signaling axis has emerged as a promising area in breast cancer therapy (Kennedy et al., 2020). The activation of AMPK also influences the activity of SCD1 as previously described. Thus, the action of canagliflozin and dapagliflozin must inhibit the biosynthesis of MUFAs, which directly connects the SGLT-2 inhibition pathway with ferroptosis. The MUFAs, a product of this reaction, inhibit ferroptosis by competitively interfering with the activity of PUFAs. In contrast to MUFAs, PUFAs are preferential substrates for lipid peroxidation. Thus, the inhibition of SCD1 induced by SGLT-2 connects the AMPK activation and SREBP1 inhibition pathway to ferroptosis. SCD1 inhibition causes diminished production of MUFAs, resulting in a surplus of PUFAs and increased lipid peroxidation. This, then, causes the ferroptosis to intensify.

In addition to the previously discussed lactate, ACLS4 is also involved in the process of regulating ferroptosis. Lactate can inhibit ACLS4 via other pathways (Brown et al., 2017; Pucino, et al., 2019; Xie et al., 2020) and reduce the production of oxidizable PUFAs (Doll et al., 2017; Li et al., 2019). Relative changes in SCD1 and ACLS4 levels after lactate entry into the cell suggest that lactate-induced rearrangement in the biosynthesis of MUFAs and PUFAs may act synergistically—enhancing ferroptosis resistance in cancer cells. That is, lactate may protect tumor cells from ferroptotic cell death through highly regulated mechanisms.

Another important macromolecule involved in cancer ferroptosis is fatty acid–binding protein (FABP)-4. FABPs are intracellular lipid chaperones—a group of molecules that coordinate lipid responses in cells (Haunerland and Spener, 2004; Makowski and Hotamisligil, 2005; Chmurzyńska, 2006). FABPs are abundantly expressed 14 to 15 kDa proteins that reversibly bind hydrophobic ligands, such as saturated and unsaturated long-chain fatty acids, eicosanoids, and other lipids, with high affinity (Coe and Bernlohr, 1998; Zimmerman and Veerkamp, 2002). In addition to the intracellular transport of FAs, FABP4 is responsible for the organization of LDs in the cell, which, in the case of cancer cells, is important in the process of sensitizing them to ferroptosis. Studies have shown that FABP4 derived from adipocytes or endothelial cells present in TME can promote the uptake of PUFAs necessary for tumor regrowth and stimulate the formation of LDs in cancer cells, which is essential for cell survival under hypoxic conditions (Luis et al., 2021). The administration
of FABP4 inhibitors caused a dose-dependent increase in ROS production in cells and inhibited clinical recurrence of breast cancer. However, the best efficacy was when SCD1 and FABP4 inhibitors were administered simultaneously. The inhibition of SCD1 led to a halt in FA desaturation, and thus the pool of FAs, necessary for the formation of PLOOHs, was increased, which, in turn, increased ferroptosis. Moreover, the inhibition of FABP4 decreased the transport of FAs to the tumor cells and inhibited LD formation in response to hypoxia.

Fatty acid translocase/fatty acid translocase (CD36) plays an important role in the SCD1-FATP4 axis, which regulates FA metabolism in tumor cells and TME. CD36 is a key membrane glycoprotein involved in importing adipocyte-released fatty acid into breast cancer cells (Febbraio et al., 2001; Pepino et al., 2014; Liang et al., 2018). The primary functions of CD36 include FA uptake, cell adhesion, and regulation of inflammatory processes. In the adipocyte–breast cancer cell interaction, CD36 plays a role in reprogramming the metabolism with a shift toward increased fatty acid oxidation (Wang and Li, 2019). Thus, CD36 may be a unique FA receptor and regulate various oncogenic processes. In patients with breast cancer, the expression of CD36 is increased, with a simultaneous increase in the expression of lipid transport receptors Low Density Lipoprotein and FABP4. (Gyamfi et al., 2021). An increased expression of CD36 and FABP4 worsens the prognosis in breast cancer. An appropriate expression of CD36 and FABP4 maintains homeostasis at the rate of FA import and metabolism, ensuring that imported FAs are efficiently transported to subcellular locations (mitochondria and peroxisomes). This collaboration between the two transport proteins is probably as a result of the presence of similar amino acid sequences creating possible motives for the interaction between CD36 and FABP4 as well as other proteins. Presumably, CD36 acts as a transmembrane FA importer. In contrast, FABP4 interacts with CD36 to transport FAs to various cell locations. In all likelihood, these interactions are responsible for the reprogramming of the metabolism, which induces the drug resistance seen in breast cancer cells cultured with adipocytes (Bochet et al., 2011; Iwamoto et al., 2018). Studies have shown that the chemical inhibition of CD36 and FABP4 induces apoptosis in breast cancer cells. The use of CD36 and FABP4 inhibitors, sulfofuscinimidyl oleate and BMS309403, respectively, greatly decreased the lifespan of breast cancer cells and also notably reduced the proliferative, migratory, and invasive abilities of breast cancer cells (Gyamfi et al., 2021).

**Acyl Starvation.** More than 100 years of cancer research have provided an enormous amount of information on the role of FAs in tumorigenesis (Koundouros and Poulogiannis, 2020). It is known that due to their exceptional growth dynamics,

![Fig. 3](image-url) In breast cancer cells, there is an increased synthesis and uptake from the environment of FAs necessary for energy and building purposes. Blocking this synthesis and transport from the TME leads to a reduction in the number of available FAs for metabolic purposes and, particularly, to the construction of cell membranes. Regardless of the overall FA deficiency, when fat metabolism inhibitors are administered, a change in the reciprocal ratios of different types of FA is observed, which may promote, for example, ferroptosis. An example of such a mechanism may be the inhibition of SCD1, as a result of which the number of FAs susceptible to oxidation increases. Disruption of the physiologic ratios of the different types of fatty acids present in TAG and phospholipids and the formation of their damaged forms leads to a loss of cell membrane fluidity and, ultimately, to its disintegration. Most of the FA of cell membranes is incorporated into derivatives such as TAG or phospholipids; therefore, the mechanisms presented in this figure are called “acyl starvation.”

<table>
<thead>
<tr>
<th>Molecules involved in the promotion of apoptosis in breast cancer cells</th>
<th>Therapy</th>
<th>Type of Evidence</th>
<th>Reference</th>
</tr>
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<tbody>
<tr>
<td>Erastin</td>
<td>Cell culture</td>
<td>Li et al., 2020b</td>
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<tr>
<td>Siramesine</td>
<td>Cell culture</td>
<td>Ma et al., 2016</td>
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<tr>
<td>Lapatinib</td>
<td>Cell culture</td>
<td>Ma et al., 2016; Yang et al., 2020</td>
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<td>Sulfasalazine</td>
<td>Cell culture</td>
<td>Yu et al., 2019</td>
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<td>Sorafenib</td>
<td>Cell culture</td>
<td>Luiz et al., 2021</td>
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<tr>
<td>SCD1 Inhibitor</td>
<td>Cell culture</td>
<td>Luiz et al., 2021</td>
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<td>FABP4 inhibitor</td>
<td>Cell culture</td>
<td>Luiz et al., 2021</td>
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<td>CD36 inhibitor</td>
<td>Cell culture</td>
<td>Liang et al., 2018</td>
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<tr>
<td>SGLT2 inhibitor</td>
<td>Cell culture</td>
<td>Zhou et al., 2020b</td>
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SGLT2, sodium-glucose cotransporter 2.
cancer cells consume large amounts of FAs for building and energy purposes, thus maintaining a high proliferation rate, especially under metabolic stress conditions associated with alternating hypoxia and reoxygenation. The source of FAs in cancer cells is de novo synthesis from nutrients such as glucose or glutamine and exogenous uptake from the surrounding microenvironment. The above-mentioned macromolecules, such as SCD1, CD36, FATP, or FABP and many others, participate in these processes, especially in the uptake from the surrounding environment. Appropriate regulation of their expression or activation/inhibition promotes tumor growth. The spread of breast cancer metastases is also stimulated by the presence of adipocytes located in periglandular regions. Adipose tissue functions as an endocrine system, which secretes growth factors and cytokines as well as releasing FAs after lipolysis (Nieman et al., 2013). It also serves as a reservoir of FAs and other fats for the cancer cells, which is why people with obesity have a higher propensity to develop cancer (De Pergola and Silvestris, 2013). Adipocytes activate the endogenous lipolysis of triglycerides to produce free FAs, which can then be secreted and taken up by FABP4-overexpressed metastatic cells (Nieman et al., 2011). Thus, adipose cells perpetuate a network of reciprocal interactions and function as active mediators of endocrine and paracrine signaling. Adipokines, secreted by adipocytes, stimulate cancer cells to release exosomes containing prolipolytic factors such as miRNA-144 and miRNA-126, which in turn promote lipolysis in adjacent adipocytes by activating AMPK signaling and inducing autophagy (Lengyel et al., 2018; Wu et al., 2019). Ultimately, increased lipolysis and the release of free FAs fundamentally change the metabolic dependence of the migrating cancer cells, shifting their reliance onto exogenous lipid uptake and β-oxidation for energy (Balaban et al., 2017; Wu et al., 2019). The main effect of this increased uptake of exogenous FAs is their subsequent storage in LDs, which sequester excess FAs as TAGs and sterol ester (Olzmann and Carvalho, 2019). Consequently, the accumulation of LDs in cancer cells is not only used to maintain lipid homeostasis and prevent lipotoxicity but also provides valuable ATP and NADPH during metabolic stress (Petan et al., 2018; Pizon et al., 2018; Olzmann and Carvalho, 2019). This is mainly due to the β-oxidation of stored lipids, which leads to the production of acetyl-CoA. The acetyl-CoA produced in each round of β-oxidation can then enter the TCA cycle to produce, in turn, NADH and FADH2 for the electron transport chain. Thus, the β-oxidation of FAs contained in LDs provides a sufficient amount of ATP to drive the metastatic cascade and generate NADPH, which is essential for anabolic metabolism and detoxification of ROS (Lu, 2009; Mitsuishi et al., 2012; Samovski et al., 2015; Pascual et al., 2017). This is particularly important in the case of hypoxic cells, which have an increased FA uptake and LD accumulation following the action of the cellular oxygen-sensing and hypoxia-inducible factor (HIF)-1α-dependent expression of FABP3 and FABP7 (Bensaad et al., 2014). Thus, the proliferation capacity of cancer cells as well as their metastasis is closely related to FA metabolism not only in the cancer cells but also in adjacent tissues, especially adipose tissue. Studies show that dysregulation of lipid metabolism in TME contributes to a reduction in or successful treatment of metastasis (Koundouros and Poulogiannis, 2020). However, cancer cells have the ability to bypass the major pathways by activating other pathways that allow them to synthesize or take up FAs from the environment. It is therefore more effective in the fight against cancer to intervene at multiple levels in the FA metabolism of cancer cells, such as supporting neoadjuvant therapies with induced ferroptosis. This leads to a blockade of FA biosynthesis, their abnormal metabolism, PLOO- production, disruption of FA transport into the cell, and the loss of proper biochemical communication between cancer cells and the TME, especially adipocytes. The result is a lack of FAs needed to maintain the proper rate of tumor growth. Apart from energy and general metabolic issues, FAs are necessary for the construction of cell membranes, so any deficiency and, particularly, incorrect proportions constitute a key obstacle in uncontrolled proliferation of cancer cells. The deficiencies in question concern short-, medium-, and long-chain saturated, monounsaturated, polyunsaturated, n-3, and n-6 acids, etc., and lead to FA starvation. However, due to the fact that those FAs present in cells, especially in cell membranes, occur in combination with other compounds such as glycerol to form mono-, di-, and triacylglycerols, or are part of phospholipids, sphingolipids, etc., a more precise term is “acyl starvation” (Fig. 3). It can therefore be assumed that “acyl starvation” is a consequence of, among other things, ferroptosis. Ferroptosis disturbs the delicate balance in the correct proportion and number of FAs by generating useless PLOO- which additionally causes heavy metabolic stress on a cancer cell and leads to its death. Studies show that inducing ferroptosis in tandem with neoadjuvant therapy gives much better results in cancer treatment than neoadjuvant therapy alone because it reduces the cells’ invasiveness and inhibits the spread of metastases to distant tissues.

Breast Cancer and Other Cancers

Tumors differ in location, tissue of origin, metabolism, etc. However, they all consist of rapidly dividing cells. They require building materials to maintain their rate of proliferation. The main component of their cell membranes is fatty acids and, especially, their acyl derivatives such as phospholipids and triacylglycerols. Ferroptosis and the subsequent acyl starvation affect the supply of these acyl derivatives in the overall metabolic process but, above all, affect the rate of construction of the cell membranes. This may be of particular importance in tissues with intensive FA metabolism, such as the mammary gland.

Despite a relatively good understanding of ferroptosis, it is still not known how cells die. There are already quite a few publications that present the results of studies supporting neoadjuvant therapies with induced ferroptosis. However, the vast majority of these are in vitro studies. Ferroptosis has been studied in several types of cancer. These include hepatocellular, gastric, ovarian, pancreatic, and colorectal carcinomas, among others. Of particular interest, however, seem to be the results of studies on ferroptosis in association with FABP4 and SCD1 inhibition in breast cancer cells. There, drastically reduced tumor recurrence (Luis et al., 2021) was observed, as well as the inhibition of tumor growth. The interference of FABP4, SCD1, and CD36, to a very large extent, disrupts the normal metabolism of fatty acids. This leads to the development of their defective forms such as PLOO- as well as abnormal ratios and quantities of FAs. Uncontrolled peroxidation of PUFA-PLs is one of the mechanisms explaining the inhibition of tumor growth. Peroxidized phospholipids cause membrane damage and pore formation, thereby compromising membrane integrity. This is especially true for phospholipids that have two
chains of PUFAs and that are particularly prone to ferroptosis leading to acyl starvation and membrane damage. However, it should be added that at least some of these described mechanisms inhibit tumor growth in other tissues. For example, it is known that canagliflozin downregulates SCD1 in hepatocellular carcinoma cells, resulting in the inhibition of fatty acid synthesis and the proliferation of these cells (Nakano et al., 2020). Downregulation of SCD1 is also known to inhibit prostate cancer cell proliferation by suppressing the production of MUFA s (Fritz et al., 2010).

**Conclusion**

Ferroptosis is a form of cell death driven by iron-dependent lipid peroxidation. Its complicated mechanism is gradually becoming better understood, but many aspects still remain unclear, such as the role of cell organelles in the development of ferroptosis. The use of ferroptosis in the treatment of cancer, and especially in supporting classic neoadjuvant therapies, gives hope for effective anticancer therapies (Pizon et al., 2022). Cancers, adaptively, create mechanisms that inhibit lipid oxidation, which leads to disease relapse. This adaptation is driven by alternating hypoxia and reoxygenation as well as the specific structure and metabolism of TME, which all support tumor growth. A major role in both the development of cancer and in the process of ferroptosis is played by FAs. These FAs play both an energetic and a formative role (cell membranes) in tumor development. In the process of ferroptosis, they are oxidized, causing cell damage. Therefore, the regulation of the FA metabolism in cancer cells seems to be a promising therapeutic direction. In this study, we have focused mainly on the SCD1-FABP4-CD36 axis because both cell line studies and clinical trials show the effectiveness of therapies acting on these biochemical pathways (Table 2). The inhibition of SCD1 causes an increase in the amount of long-chain PUFAs, which can further be used for the formation of PLOOH. The inhibition of FATP4 and CD36 in cancer cells and TME causes dysregulation of both the transport of FAs in the TME and the intracellular transport of FAs and also inhibits the formation of LDs in tumor cells. FATP4 and CD36 are also involved in the apoptosis of cancer cells through other mechanisms such as the SGLT-2 cotransporter and the AMPK/mTOR pathway. Ferroptosis reduces cell resistance to classic neoadjuvant therapies by rearranging the metabolism of FAs, which are in great demand in the rapidly growing tumor cells. Limiting the consumption and biosynthesis of the relevant FAs in tumor cells results in a deficiency of FAs and an inhibition of the tumor progression. We suggest that this mechanism should be named “acyl starvation.” The tumor’s dependency on lipids and its sensitivity to FAs oxidation by ferroptosis are the starting points for designing new treatment strategies to prevent tumor recurrence. Cancer cells should be the sole target for ferroptosis-inducing therapies. It is also important to monitor any possible adaptation processes of cancers to ferroptosis.

**Authorship Contributions**

Participated in research design: Bobiński.

**Conducted experiments:** Bobiński, Pizon.

**Contributed new reagents or analytic tools:** Bobiński, Pilelsz.

**Performed data analysis:** Bobiński, Dutka, Waksmanisaka.

Wrote or contributed to the writing of the manuscript: Bobiński, Dutka.

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**Participated in research design:** Bobiński.
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