

Effects of cuproptosis and its application in inflammatory bowel disease (Review)

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Abstract. Inflammatory bowel disease (IBD), which includes ulcerative colitis and Crohn's disease, is a common, recurring, chronic intestinal inflammatory illness that is considered to be impacted by the immune system, gut microbiota and genetic factors. Copper (Cu), a crucial metal ion in cuproptosis, contributes to IBD, with studies revealing that its dysregulation contributes to oxidative stress, intestinal inflammation, gut dysbiosis and disruption of barrier integrity. Additionally, cuproptosis-related genes have been implicated in the pathogenesis of IBD, characterized by defects in barrier integrity and enhanced immune responses. These genes have been identified as biomarkers of IBD, providing novel therapeutic strategies for exploring their treatment. The present review highlights the mechanism of cuproptosis and the role of Cu in IBD. The review also highlights the cuproptosis-related genes in the pathogenesis of IBD, as well as their applications as biomarkers for therapeutic purposes. These biomarkers may provide a reference for IBD for clinical decision-making. The primary challenge is the lack of standard clinical medications for treating IBD associated with cuproptosis-related genes. Consequently, researchers are employing molecular docking and other techniques to identify potential drugs aimed at these genes for therapeutic purposes.

Contents

1. Introduction
2. Mechanism of cuproptosis

3. Key features between cuproptosis and ferroptosis, apoptosis, pyroptosis and necroptosis
4. Cuproptosis is a unique type of cell death distinct from other forms
5. IBD overview
6. Role of Cu in IBD
7. Cuproptosis-related genes in IBD pathogenesis
8. Therapeutic applications of cuproptosis in IBD
9. Limitations and future directions
10. Conclusion

1. Introduction

A recently discovered type of cell death, known as cuproptosis, results from an excessive accumulation of copper (Cu) within cells (1). Through enzymatic activity and nuclear magnetic resonance analysis, Tsvetkov *et al* (2) discovered that elesclomol targets ferredoxin 1 (FDX1) and induces Cu-dependent cell death. Elesclomol and disulfiram are examples of Cu ionophores that raise intracellular Cu levels (3). This increase causes oxidative stress and consequent cell death, which may have consequences for cancer treatment (3). Additionally, Cu ionophores contribute to Cu toxicity and cell death by interfering with protein lipoylation and mitochondrial respiration (3). Cuproptosis is a Cu-dependent cell death that differs from the well-known programmed cell death (PCD) (4). Typical modes of PCD include ferroptosis, necroptosis, autophagy, pyroptosis, apoptosis and neutrophil extracellular traps (5). However, cuproptosis has unique molecular mechanisms and signaling pathways that differentiate it from other forms of cell death, such as apoptosis, necroptosis and ferroptosis (6).

Cuproptosis results from disruptions to Cu homeostasis, which is dependent on the Cu transporter (7). Inflammation, oxidative stress and apoptosis are among the pathogenic processes in which cuproptosis is now known to be involved (8). Attention has recently been drawn to the part that Cu and Cu-induced cell death play in the etiology of cancer (9). Due to its immense potential for cancer therapy, cuproptosis has attracted a lot of attention from cancer research communities (9). Cu-based therapy inhibits the growth of malignancies and may make it possible to treat tumors that are resistant to

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chemotherapy (9). Cuproptosis is a highly investigated topic in the field of cancer research (8). In the setting of inflammatory bowel disease (IBD), cuproptosis has not been well studied (10). Additionally, numerous studies have now demonstrated that genes linked to cuproptosis are essential for the initiation, spread and prognosis of a wide range of malignancies, such as breast cancer, lung adenocarcinoma and uterine corpus endometrial carcinoma (11-14). Nevertheless, the precise function of genes linked to cuproptosis in ulcerative colitis (UC) (14) and Crohn's disease (CD) remains unclear. Current evidence indicates that these genes are involved in the pathophysiology of IBD (15). Despite this, limited clinical treatments target these genes in IBD, which justifies the search for new drugs that can cure IBD caused by cuproptosis-related genes. Consequently, the present review emphasizes the cuproptosis mechanism, related genes, their pathogenesis and their use as biomarkers for IBD, aiming to explore therapeutic strategies targeting these genes.

2. Mechanism of cuproptosis

The type of cell death known as cuproptosis was discovered in 2022 and depends on the precise delivery of Cu ions to lipoylated tricarboxylic acid (TCA) cycle proteins (16). A study by Huo *et al* (17) showed that the creation of the Cu ionophore elesclomol causes cuproptosis in cardiomyocytes, implying that Cu ions may be involved in cuproptosis. Solute carrier family 31 member 1 (SLC31A1) importers and ATPase Cu transporting β (ATP7B) exporters of Cu modulate intracellular Cu^{2+} levels to regulate cuproptosis (18). The first three metal-binding domains and the Cu chaperone antioxidant 1 Cu chaperone (ATOX1), which transports Cu to ATP7B, are essential for controlling ATP7B activity (19). Notably, excess Cu causes cuproptosis through the TCA cycle's Cu-dependent aberrant oligomerisation of lipoylation proteins and subsequent reduction in iron-sulphur cluster protein levels, leading to proteotoxic stress and, eventually, cellular death (7,16). During the TCA cycle, Cu binds to acyl-CoA synthetase, causing cuproptosis (20). In the formation of the pyruvate dehydrogenase (PDH) complex, FDX1 stimulates the lipoacylation of dihydrolipoyl transacetylase (DLAT) and inhibits iron-sulfur cluster proteins by converting Cu^{2+} to Cu^+ , which results in cell death (7). Additionally, FDX1 interacts directly with lipoyl synthase (LIAS) to support its function in lipoylation of cellular proteins, which is necessary to keep cells viable in low-glucose environments (21). FDX1 is both a critical regulator of Cu ionophore-induced cell death and an upstream regulator of cellular protein lipoylation, a post-translational modification based on mitochondrial lipids that occurs spontaneously on four mitochondrial enzymes necessary for TCA cycle function (21).

In summary, the core regulatory axis of cuproptosis includes Cu increase, FDX1 stimulation, LIAS upregulation, and DLAT, as the executioner of cuproptosis. Elesclomol increases intracellular Cu levels (3), but FDX1 is a reductase that converts Cu^{2+} to a more hazardous Cu^{1+} (22). Furthermore, FDX1 directly interacts with LIAS to facilitate its role in cellular protein lipoylation (21). LIAS enhances the lipoylation of DLAT, thereby altering DLAT and facilitating Cu binding to it (23). Finally, DLAT conducts cuproptosis by aggregation

and oligomerization. Proteotoxic stress-induced cuproptosis results from this, as well as the decrease in iron-sulfur cluster protein levels (23). Fig. 1 illustrates the pathways in more detail.

Possible regulatory mechanisms of cuproptosis in immune cells. Cu plays a vital role in immune function, and a lack of Cu can impair immune performance, making the body more susceptible to microbial infections (24). The metal can influence the activation of cells linked to innate immunity, such as macrophages and neutrophils, during bacterial infections, as well as the processes of leukocyte differentiation, maturation and migration (25,26). Furthermore, the presence of Cu within tumors has been shown to influence PD-L1 expression and tumor immune evasion (27). These indicate that Cu may play a role in regulating the immune system and its checkpoints. Consequently, this section will explore the potential modulatory effect of cuproptosis on immune cells and the checkpoints that govern them.

FDX1-lipoylation axis and metabolic rewiring. Cuproptosis, a new form of Cu-dependent cell death that relies on the precise delivery of Cu ions to lipoylated TCA cycle proteins and that is dependent on mitochondrial respiration regulation, is mediated by FDX1 (7,28,29). Cells that rely on mitochondrial respiration are more susceptible to the Cu ionophore elesclomol, which causes cuproptosis (30). More mitochondria and a higher rate of oxygen consumption are characteristics of M2-polarized macrophages (31). M2 macrophages often use glutamine to power the TCA cycle, in contrast to M1 macrophages, which rely on glycolysis (32). Therefore, M2 polarization is unaffected by glucose deprivation as long as oxidative phosphorylation (OXPHOS) and mitochondrial activity are maintained (33). As a result, inflammatory M1 macrophages exhibit decreased mitochondrial activity and increased glycolytic metabolism. On the other hand, anti-inflammatory M2 macrophages exhibit increased spare respiratory capacity and strong mitochondrial OXPHOS (31). Consequently, M2 macrophages (34), T cells in a resting state (35,36) and memory T cells (37) utilize OXPHOS. This suggests that these immune cells may exhibit increased sensitivity to the Cu ionophore elesclomol, which induces cell death through cuproptosis.

Transmembrane Cu flux mediators (SLC31A1 vs. ATP7A/B). i) SLC31A1 influx. The process of 'cuproptosis' is associated with SLC31A1, known as a Cu importer (38). Studies have shown that SLC31A1 exhibits higher expression in macrophages, chondrocytes and fibroblasts (39), in chronic apical periodontitis (40), and in CD (10). In CD, SLC31A1 is positively correlated with the relative abundance of resting natural killer (NK) cells and M1 macrophages (10). This shows that macrophages and NK cells expressing SLC31A1 may be susceptible to Cu-induced cell death.

ii) ATP7A and ATP7B efflux. ATP7A and ATP7B play a crucial role in regulating Cu levels in cells by facilitating the removal of excess Cu (41). Cu^+ ions are transferred from delivery to acceptor proteins across the membrane via ATP7A/B without creating a free Cu^+ gradient (42). Prior research demonstrated that bactericidal activity against a non-pathogenic strain of *Escherichia coli* was reduced when ATP7A expression was silenced in RAW264.7

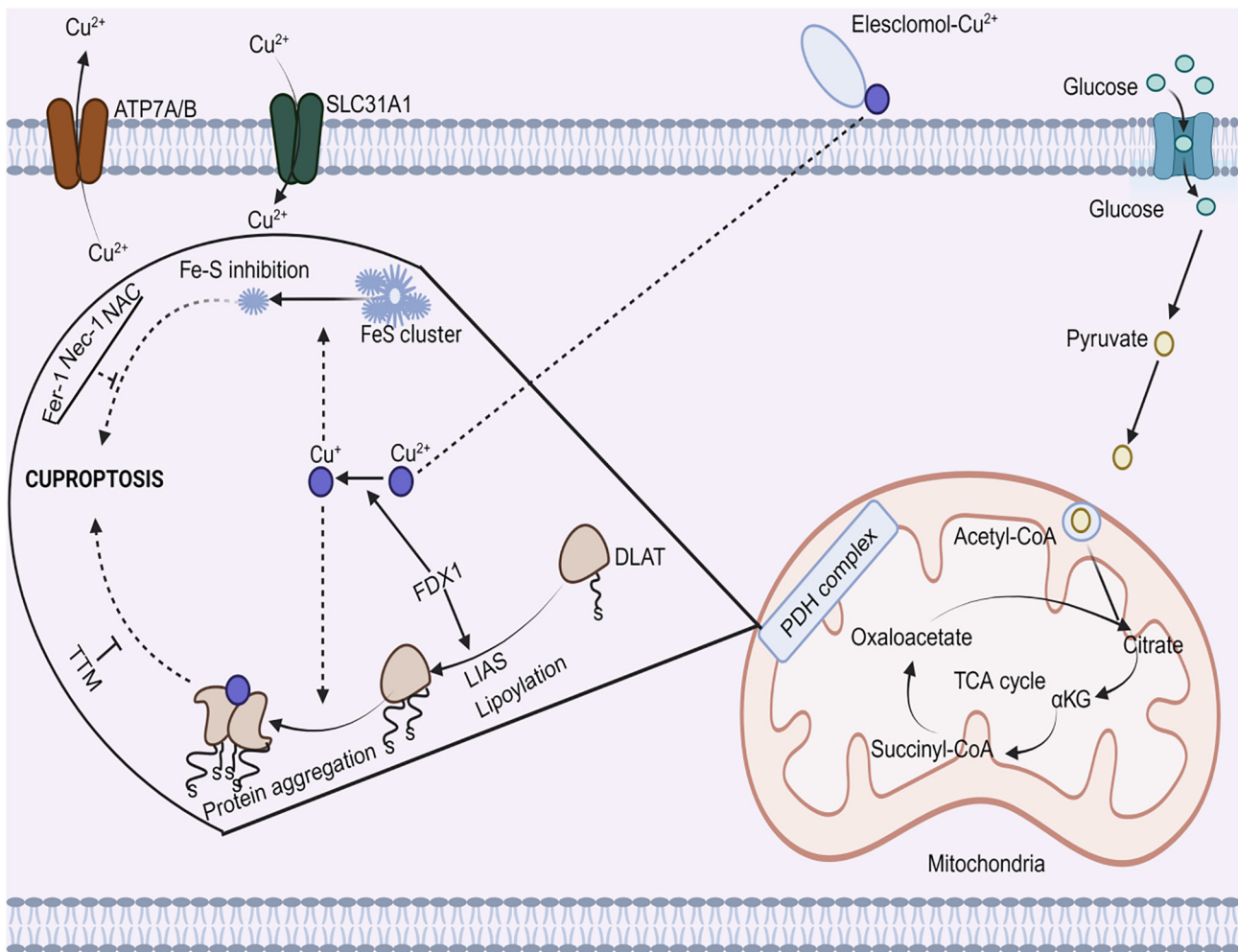


Figure 1. Cuproptosis route. Excess Cu^+ causes cuproptosis in the TCA cycle. Fer-1, Nec-1 and NAC do not inhibit cuproptosis, however, TTM does. Created using BioRender.com. αKG , α ketoglutarate; Cu^+ , copper ion; DLAT, dihydrolipoyl transacetylase; Fer-1, ferrostatin-1; Fe-S, iron-sulfur; LIAS, lipoyl synthase; NAC, N-acetyl cysteine; Nec-1, necrostatin-1; TTM, tetrathiomolybdate; ATP7A/B, ATPase Cu transporting α/β ; SLC31A1, solute carrier family 31 member 1; PDH, pyruvate dehydrogenase; TCA, tricarboxylic acid; FDX1, ferredoxin 1.

macrophage-like cells (43). Additionally, in comparison to macrophages separated from wild-type mice, primary macrophages isolated from ATP7A^{lysMcre} (mice with the ATP7A gene specifically deleted) showed reduced Cu transport into phagosomal compartments and a lower capacity to kill *Salmonella enterica* serovar Typhimurium (44). These findings suggest that increased ATP7A expression in macrophages may enhance Cu transport into phagosomes, thereby helping to fight infection. This suggests that extracting more Cu from macrophage cytosol may help prevent cuproptosis in these cells by inhibiting mitochondrial Cu entry.

Glutathione (GSH) and intracellular Cu buffering. i) The GSH-cuproptosis brake. GSH chelates Cu to prevent cuproptosis (45,46). By contrast, cell cuproptosis is enhanced when GSH concentration is decreased (46). Cu chelators, such as tetrathiomolybdate (TTM), can be used to lessen cuproptosis (47). ROS produced by activated T cells activate the GSH response, which is required to buffer the increasing ROS and prevent cellular damage (48). GSH controls metabolic activity, which is crucial for T-cell effector functions (48). Since GSH inhibits cuproptosis by chelating Cu, the loss of the antioxidant GSH may likely perpetuate cuproptosis in cells, including T cells.

p53-glycolytic switch. OXPHOS is a critical component of mitochondrial respiration and is responsible for cuproptosis, a recently discovered mechanism of cell death (49). Cells with high OXPHOS capacity are more prone to cuproptosis (50). Notably, in cancer cells, the tumor suppressor p53 is an essential metabolic regulator that prevents glycolysis and promotes a metabolic shift towards OXPHOS (51). Furthermore, this tumor suppressor may be involved in cuproptosis, as p53 regulates the production of iron-sulfur clusters and the Cu chelator GSH, both of which are required for cuproptosis (51). Thus, by inhibiting glycolysis and promoting the switch to mitochondrial metabolism, p53 may make cells more vulnerable to cuproptosis (30). High levels of glycolysis flux via the pentose phosphate pathway and an increase in some Krebs cycle intermediates, such as succinate, citrate and itaconic acid, are characteristics of M1 macrophage metabolism (32). However, M2 macrophages have high levels of OXPHOS and fatty acid oxidation in their metabolism (52,53). As a result, immune cells most likely undergo cuproptosis as they transition from glycolysis to OXPHOS. Anti-inflammatory macrophages (M2 subtype) may undergo cuproptosis via p53 glycolytic switch to the OXPHOS phase compared with M1 macrophages.

Crosstalk with immune checkpoints and the microenvironment. Programmed death ligand 1 (PDL1) has been recognized as the ligand for the immunological suppressive receptor programmed death 1 protein (PD1). PDL1 may suppress T-cell responses by triggering apoptosis when it binds to PD1 on active T cells. PD-L1 is therefore considered a therapeutic target for malignant tumors, as it promotes immune evasion and contributes to tumor growth (54). PD-L1 expression in cancer cells is affected by Cu levels within the tumor. A study found that Cu-chelators significantly inhibited neuroblastoma tumor growth, improved survival rates in mice, and increased the number of CD8⁺ T cells and NK cells infiltrating the tumors (27). This suggests that Cu may increase tumor immune evasion by increasing PDL1 expression, which inhibits T-cell and NK responses while facilitating tumor growth. High T-cell infiltration, elevated interferon- γ signaling, PD-L1 expression and a high tumor mutational burden are characteristics of immune-inflamed tumors, commonly referred to as 'hot tumors' (55) and immune checkpoint inhibitors (ICIs) typically have a greater effect on tumors with an inflammatory nature (56,57). Conversely, cold tumors also contain immunosuppressive cell populations, such as myeloid-derived suppressor cells, regulatory T cells and tumor-associated macrophages (55), and ICI monotherapy is rarely effective for treating 'cold tumors' (56).

Possible regulatory mechanisms of cuproptosis on gut microbiota. The intestinal microbiota contributes significantly to immune homeostasis. Numerous immune-related inflammatory disorders, such as systemic lupus erythematosus, rheumatoid arthritis, diabetes and IBD, have been linked to changes in the gut microbiota and its metabolites (58). An unregulated immunological response to dysbiosis of the gut microbiome is one cause of IBD (59). The effects of Cu oxide (CuO) nanoparticles (NPs) on the intestinal microbiota and their metabolite levels have been shown to mediate their intestinal immunotoxicity (60). Additionally, CuO NPs can strongly activate the FDX1-LIAS-DLAT cuproptosis pathway and penetrate mitochondria, damaging their structure. Intestinal homeostasis is disrupted, and the gut microbiota is altered by a decrease in Firmicutes and Fusobacteria, and an increase in Proteobacteria and Actinobacteria (61). CuO has also been shown to raise Proteobacteria levels while lowering those of Bacteroidetes and Firmicutes (62). These findings imply that cuproptosis may alter the gut microbiota and intestinal homeostasis, potentially leading to dysbiosis and unregulated immune responses.

3. Key features between cuproptosis and ferroptosis, apoptosis, pyroptosis and necroptosis

Cuproptosis is a type of cell death triggered by excessive Cu accumulation within cells (1), and key regulatory genes include negative regulators [glutaminase (GLS), cyclin-dependent kinase inhibitor 2A (CDKN2A) and metal regulatory transcription factor 1] and positive regulators [FDX1, LIAS, lipoyltransferase 1, dihydrolipoamide dehydrogenase (DLD), DLAT, pyruvate dehydrogenase E1 subunit α 1 (PDHA1) and pyruvate dehydrogenase E1 subunit β (PDHB)] (63,64), whilst ferroptosis, which is a non-apoptotic cell death that

is iron-dependent, involves a deficiency in GSH or glutathione peroxidase 4 (GPX4) (65,66). The expression levels of GPX4 (67), FDX1, LIAS, DLAT, PDHA1 and DLD (15,68) in the inflamed gut are all decreased. Also, necroptosis is driven by receptor-interacting protein kinase 1 (RIPK1), RIPK3 and mixed lineage kinase domain-like protein (MLKL), leading to cell expansion, membrane disintegration, leakage of intracellular content and cell death, along with inflammation (69). Deficiency in caspase-8 leads to activation of RIPK3 and MLKL (70,71). In the inflamed gut, RIPK3 and MLKL levels are increased when caspase-8 is reduced or deficient (70). Conversely, adaptor proteins such as TNF receptor-associated death domain protein (TRADD) and Fas-associated death domain protein, along with caspase-8 and caspase-10, are essential for apoptosis signaling through death receptors. Within the inflamed gut environment, the expression of Fas and Fas ligand (72), which are part of the extrinsic route, is increased, while in the intrinsic route of apoptosis, the expression of BAX and caspase 3 is increased (73). Pyroptosis is an inflammatory cell death triggered by inflammasomes; it degrades gasdermin D (GSDMD) and activates cytokines such as IL-1 β and IL-18 (74,75). The pyroptosis effector is GSDMD (76). In the inflamed gut environment, GSDMD, as well as other markers of pyroptosis, such as NOD-like receptor family pyrin domain-containing 3 (NLRP3), IL-1 β and caspase-1, are increased (77).

To summarize, in terms of core elements, cuproptosis depends on Cu ions, ferroptosis on iron, apoptosis on death receptors and caspase 8, necroptosis on RIPK1, RIPK3 and MLKL in the absence of caspase 8, and pyroptosis on GSDMD. Furthermore, cuproptosis does not require caspases but relies on lipoylation proteins, whereas apoptosis and pyroptosis require caspases. The morphological alterations in cuproptosis, as well as the genes involved, differ from other cell death processes. This suggests that therapeutic approaches for other types of cell death, such as ferroptosis, necroptosis, pyroptosis and apoptosis, may differ from cuproptosis due to distinct cell death pathways.

Although Table I (7,16,69,78-97) highlights the key differences between cuproptosis and other forms of cell death, there are also key overlapping features among them. Cuproptosis and ferroptosis, for example, share a link to GSH depletion. Notably, when comparing ferroptosis and cuproptosis, GSH works at the crossover point of the regulation network (98). Therefore, GSH depletion may lead to cuproptosis and ferroptosis. Additionally, the cystine-glutamate antiporter xCT allows free cystine to enter cells; however, plasma GSH-disulfide may be the primary source of cystine in the body (99). Reduced cystine and glutamine levels interfere with GSH synthesis in acute myeloid cells, which causes glutathione peroxidase-4 (GPX4), a cofactor that keeps lipid peroxidation homeostasis, to malfunction (100). Thus, blocking the cystine-glutamate antiporter xCT (SLC7A11/SLC3A2) may diminish GSH and GPX4 and, in the presence of elevated Cu levels, might lead to cuproptosis and ferroptosis. Additionally, SLC31A1 downregulation and mitochondrial Cu depletion in cardiac fibrosis (CF) are associated with lower Cu concentrations (101). SLC31A1 deficiency specific to fibroblasts increases mitochondrial Cu depletion, increases glycolysis, stimulates fibroblast proliferation and causes CF (104). This suggests that SLC31A1

Table I. Key differences between cuproptosis, ferroptosis, apoptosis, pyroptosis, and necroptosis.

Parameter	Cuproptosis	Ferroptosis	Apoptosis	Pyroptosis	Necroptosis	(Refs.)
Trigger(s)	Cu ²⁺ buildup	-Iron buildup -GSH-GPX4 failure -Excessive peroxidation of lipids	Either extrinsically by death signals from the outside of the cell or intrinsically through mitochondrial membrane permeabilization	-Damage-associated molecular patterns -Pathogen-associated molecular patterns	-Virus sensors -Pattern-recognizing receptors -Death receptor activation with caspase-8 deficiency	(16,78-84)
Key executioners	Lipoylation of DLAT	-Fe ²⁺ , -GPX4 failure -PUFAs	Caspase 3, 6, 7	-GSDMD -Caspase 1, 4, 5, 11	-RIPK-1, 3 -MLKL	(7,16,79, 82,83,85)
Mechanism	Excess Cu causes cuproptosis, a process in which the TCA cycle's Cu-dependent aberrant oligomerization of lipoylation proteins reduces iron-sulfur cluster protein levels, resulting in proteotoxic stress and cell death.	When the GPX4 function is inhibited, lipid peroxidation occurs, and ferroptosis may be induced.	Both extrinsic and intrinsic mechanisms of apoptosis activate a family of proteases known as caspases, which are responsible for the final cell death during the execution process of apoptosis.	The last step of pyroptosis requires the cleavage of GSDMD at D275 (numbering after human GSDMD) into N- and C-termini by caspase 1 in the canonical pathway and caspase 4/5/11 (caspase 4/5 in humans, caspase 11 in mice) in the noncanonical pathway. Upon cleavage, the N-terminus of GSDMD forms a transmembrane pore that releases cytokines such as IL-1 β and IL-18 and disturbs the regulation of ions and water, eventually resulting in strong inflammation and cell death	The stimuli stimulate RIPK3 via RHIM-containing proteins. RIPK3 binds and phosphorylates MLKL, resulting in alterations in cell shape.	(7,81,82, 84,86,87)
Morphological features	-Cell membrane rupture -Mitochondrial shrinkage -Mitochondrial stress	-Condensed density of the mitochondrial membrane in smaller-than-normal mitochondria -Diminished or absent mitochondrial cristae -Disruption of the outer membrane of the mitochondria	-Condensation of the nucleus and cytoplasm. -Cell fragmentation into well-preserved, membrane-bound fragments	-Ballooning morphology of cells -Breakdown of the cell/plasma membrane and the production of inflammatory mediators such as HMGB1, IL-1 β and IL-18	-Cell expansion and rupture of the cell/plasma membrane -Intracellular content leakage -Cell death and the creation of inflammation	(69,84, 88-92)

Table I. Continued.

Parameter	Cuproptosis	Ferroptosis	Apoptosis	Pyroptosis	Necroptosis	(Refs.)
Inflammatory profile	Yes/immunogenic reaction	Yes	No (silent)	Yes	Yes	(91, 93-96)
Caspase dependency	No	No	Yes	Yes	No	(84,93,97)

Cu, copper; DLAT, dihydrolipoyl transacylase; GPX4, glutathione peroxidase-4; GSH, glutathione; IL, interleukin; PUFA, polyunsaturated fatty acids; TCA, tricarboxylic acid; HMGB1, high mobility group protein B1; Fe²⁺, ferrous iron; RIPK, receptor-interacting protein kinase; MLKL, mixed lineage kinase domain-like protein; GSDMD, gasdermin D; RHIM, RIPK homology interaction motif.

upregulation may increase mitochondrial Cu accumulation, leading to cuproptosis. Lysine demethylase 5B (KDM5B) is activated by intracellular α -ketoglutarate buildup caused by SLC31A1-mediated cuproptosis (102). Activated KDM5B, in particular, demethylates H3K4me3 marks at the promoter of the ferroptosis regulator ferritin heavy chain 1 (FTH1), inhibiting transcription and making keratinocytes more susceptible to ferroptotic cell death, thereby increasing inflammatory tissue damage (102). These results demonstrate a basic pathogenic SLC31A1/KDM5B/FTH1 molecular axis that connects cuproptosis and dysregulated Cu metabolism to the execution of ferroptosis (102). Thus, cuproptosis and ferroptosis could overlap or intersect via SLC31A1, GSH depletion and the cystine-glutamate antiporter xCT (SLC7A11/SLC3A2).

Cuproptosis can also overlap with apoptosis in terms of mitochondrial damage. One of the roles of cytochrome *c* in living cells is to catalyze lipid peroxidation in the inner mitochondrial membrane, which triggers apoptosis (103). According to a previous study, Cu buildup in cardiomyocyte mitochondria causes mitochondrial damage, and exposure to cytochrome *c* causes apoptosis, further damaging the heart (104). Additionally, mitochondrial damage has been identified as a characteristic of cuproptosis (105). This implies that mitochondrial damage may occur in both cuproptosis and apoptosis. Furthermore, cuproptosis can coexist with apoptosis by producing ROS. Oxidative stress refers to elevated intracellular ROS levels that harm proteins, lipids and DNA (106). Overproduction of ROS overwhelms the cells' antioxidant defenses, resulting in either cell death or functional damage (107). Cu ionophores that increase intracellular Cu levels include disulfiram and elesclomol. This rise results in oxidative stress, which leads to cell death (3). This implies that ROS may overlap with the cuproptosis and apoptosis pathways. Finally, p53 activities may also overlap with cuproptosis and apoptosis. For instance, Cu buildup results in apoptosis, which appears to be mediated by p53 activation and DNA damage (108). At physiological concentrations, Cu can directly interact with p53 and prevent it from binding DNA (109), but high Cu levels in hepatocytes result in increased p53 mRNA and apoptotic cell death (110). p53 regulates a variety of metabolic pathways to help cells maintain metabolic homeostasis and adapt to stress (111). In Fanconi anemia hematopoietic stem cells, p53 inactivation inhibits the switch from glycolysis to OXPHOS (112), implying that p53 activation may stimulate this switch. Given that OXPHOS is an essential component of cuproptosis (46), p53 may play a role in regulating cuproptosis (51).

Cuproptosis and pyroptosis may overlap via the NLRP3 pathway. Cu exposure causes NLRP3-dependent cellular pyroptosis, which promotes inflammatory reactions and neurotoxicity (113). Cu has been shown to mediate macrophage pyroptosis and participate in the control of the inflammatory response through the NLRP3 inflammatory vesicle-initiation pathway (114). In a mouse model of acute inflammation that was pretreated with the Cu chelator TTM, serum caspase-1-dependent cellular factors were decreased, but caspase-1-independent cellular factors were unaffected (114,115). Dong *et al* (116) demonstrated that NLRP3, cleaved caspase-1, apoptosis-associated speck-like protein containing a CARD and IL-1 β protein levels increased in a

time-dependent manner when CuCl_2 and lipopolysaccharide were administered to primary microglia in non-mutant control mice. CuCl_2 exposure has been indicated to trigger NLRP3 activation-mediated inflammation and the resultant neurotoxicity in microglia (116). Additionally, hepatocyte toxicity is mediated by caspase-1-dependent cellular pyroptosis, which is triggered by excessive Cu exposure. CuSO_4 -treated hepatocytes cocultured with N-acetylcysteine exhibited increased expression of the caspase-1 protein and mRNA levels of genes linked to Cu^{2+} -induced pyroptosis. Treatment with the caspase-1 inhibitor Z-YVAD-FMK reduced Cu^{2+} -induced increases in lactate dehydrogenase, aspartate aminotransferase and alanine aminotransferase activities, mitochondrial membrane potential and apoptotic activity. These findings suggest a link and signaling pathway interaction between pyroptosis and apoptosis caused by Cu exposure (116,117).

Cuproptosis and necroptosis may overlap due to the activation of the necroptosome. When cells are exposed to high levels of Cu, they allow MLKL infiltration and increase MLKL levels, triggering the formation of necroptosomes. This causes MLKL to translocate to the nucleus, where it regulates NF- κ B transcriptional activity and provides components for MLKL pore assembly. Cu overload also activates downstream tumor necrosis factor (TNF)/TNF receptor regulators, such as cellular inhibitor of apoptosis 1/TRADD/RIPK1/TNF-receptor-associated factor-2 complexes that control NF- κ B essential modulator (NEMO) and TAK1-binding protein 2/3 protein levels and inhibitor of NF- κ B α activity, which in turn affects NF- κ B transcription. Additionally, the linear ubiquitin chain assembly complex ligates linear chains to NEMO after being drawn to the activated TNF receptor complex by identifying ubiquitin chains produced by other E3 ubiquitin ligases. When the ubiquitin binding in ABIN and NEMO structural domain of NEMO in another I κ B kinase (IKK) complex identifies the linear chains attached to NEMO, the IKK complex dimerizes, IKK2 is autophosphorylated and NF- κ B is activated (118).

4. Cuproptosis is a unique type of cell death distinct from other forms

Cell death entails signaling pathways and molecularly specified effector processes (119), including necroptosis (120), apoptosis (121), ferroptosis (122,123) and pyroptosis (124,125). According to previous studies, elesclomol causes ROS-dependent apoptosis in cells (126-128). However, neither the cleavage of caspase 3 nor its activation, which is indicative of apoptosis, occurred in elesclomol-induced cell death (129). Similarly, when the two main apoptotic effectors, BAX and BAK1, were removed or cells were co-treated with pan-caspase inhibitors (Z-VAD-FMK and Boc-D-FMK), the ability of elesclomol to kill cells was preserved, demonstrating once again that Cu-induced cell death is distinct from apoptosis (16). Additionally, Cu ionophore-induced cell death was not prevented by treatment with inhibitors of other recognized cell death pathways, such as ferroptosis (ferrostatin-1), necroptosis (necrostatin-1) or oxidative stress (N-acetyl cysteine), indicating a process different from established cell death routes (16). As a result, treatment for cuproptosis-induced IBD may differ from other types of controlled cell death.

5. IBD overview

A long-term and recurrent inflammatory condition of the gut is known as IBD (130), with the two main types being CD and UC (131). Depending on the type, location and intensity of the ailment, symptoms may include diarrhea, bleeding, abdominal pain, fever and weight loss (132). It is considered that a patient's immune system, gut microbiota and genetic composition all significantly influence IBD (133). IBD is a prevalent ailment in Europe and America, and its incidence rate is increasing in Asia due to dietary changes (134). Although colorectal cancer (CRC) cases have been less common recently, patients with IBD are at a higher risk of developing CRC (135). The complications of IBD include a toxic megacolon (136), strictures (137), intestinal fibrosis (138), fistulas, abscesses and colitis-associated neoplasia (139). Balloon dilatation of strictures has been replaced by endoscopic stricturotomy, strictureplasty, stenting, fistulotomy, sinusotomy and neoplasia ablation as the methods for treating complications (139). These endoscopic procedures have made it possible to treat certain complications using minimally invasive procedures (139). Additionally, extra-intestinal manifestations (EIMs) of IBD are linked to intestinal activity and can negatively impact quality of life (140). EIMs usually impact the skin, joints and eyes, while the kidneys, liver and pancreas are less frequently affected (140). Studies have shown the efficacy of aminosalicylates (141,142), corticosteroids (143-145), immunomodulators (146-148), small molecule inhibitors (149,150) and biologics (151-155) in treating IBD.

6. Role of Cu in IBD

Cu levels in patients with IBD. Cu levels in patients with IBD have been reported to vary in studies. According to certain studies, Cu levels are higher in IBD groups than in healthy control groups (156-159), while other studies have reported a deficiency in patients with IBD (160,161). Notably, Makevic *et al* (162) found that the terminal ileums and cecums of patients with IBD have lower Cu levels than those of controls; however, serum Cu level increased in CD. In another study, Skalny *et al* (163) also found higher Cu/Zn ratios and lower serum Zn levels in children with attention deficit/hyperactivity disorder than in controls. Common risk factors for Cu deficiency include foregut surgery, dietary deficiency, enteropathies with malabsorption, prolonged intravenous nutrition (total parenteral nutrition) (164) and Zn overload (165). Conversely, an increase in Cu in patients with IBD may be due to systemic inflammation (161). The Cu levels in IBD are summarized in Table II.

Dual roles of Cu

Beneficial roles. i) Antioxidant defense. A family of enzymes called superoxide dismutases (SODs) contains Cu and plays a role in the metabolism of ROS by converting superoxide anion radicals into hydrogen peroxide and oxygen (166). The Cu ion that is active in redox reactions drives catalysis. In most cases, SODs have a zinc (Zn) ion at the active site, which enhances Cu catalytic processes and preserves protein structure (166). The periplasm of bacteria and almost every organelle in a human cell contains these bimetallic Cu,

Table II. Summary of Cu levels in inflammatory bowel disease.

Authors, year	Cu levels	Sample	(Refs.)
Schneider <i>et al</i> , 2020	Decreased	Serum	(161)
Xing <i>et al</i> , 2021	Increased	Serum	(156)
Ritland <i>et al</i> , 1979	Increased in UC, normal in CD	Liver	(157)
Mohammadi <i>et al</i> , 2017	Increased	Serum	(158)
Piątek-Guziewicz <i>et al</i> , 2021	Increased	Serum	(159)
Kamel <i>et al</i> , 2024	Decreased	Serum or whole blood	(160)
Makevic <i>et al</i> , 2023	Increased in CD Decreased	Serum Intestinal mucosa	(162)

Cu, copper; CD, Crohn's disease; UC, ulcerative colitis.

Zn-SODs. Nevertheless, a novel class of SODs that contain Cu and do not require Zn has just surfaced (166). The body's antioxidant defense against oxidative stress is based on metalloenzymes known as SOD (167). Therefore, SOD supplementation may activate the body's natural antioxidant system to counteract excess free radicals and be applied in pathological situations (167). Studies have shown decreased SOD levels in IBD (168), collagen-induced arthritis (169) and cognitive impairment after mild acute ischemic stroke (170), implying that increased SOD may mitigate several diseases. A recent study found that mice with colitis exhibited fewer symptoms when SOD mimics Mn1 and Mn1C were injected into lactic acid bacteria (171). Additionally, Cu ion-luteolin nanocomplexes have been shown to enhance anti-inflammatory and antioxidant effects of cells by regulating the NF- κ B signaling pathway and the nuclear factor erythroid 2-related factor 2/heme oxygenase-1 oxidative stress pathway, increasing SOD activity/content, and reducing intestinal inflammation (172). Other nanocomposites composed of Cu and carbon have shown promise in increasing antioxidant defenses, hence decreasing intestinal inflammation (173). These studies show that Cu may enhance antioxidant defenses to curb intestinal inflammation.

ii) Regulation of inflammation and gut microbiota in intestinal health. Numerous biological functions, including Cu transport, have been linked to Cu metabolism MURR1 domain-containing 1 (COMMD1) (174). COMMD1 selectively binds with NF- κ B components to suppress their transcriptional activity (175,176). Colon inflammation has been linked to the NF- κ B pathway (177,178). COMMD1, a negative regulator of NF- κ B, regulates intestinal inflammation and prevents colitis-associated cancer, according to genetic research on mice and humans (179). Prolonged NF- κ B activation leads to intestinal epithelial cell death and upregulation of proinflammatory cytokines, resulting in mucosal inflammation and barrier breakdown (180). As a result, COMMD1, a Cu transporter, may modulate inflammation. Li *et al* (181) found that circulating leukocytes and colon biopsy specimens from patients with IBD had lower levels of COMMD1 expression; thus, myeloid cells expressing COMMD1 exhibited anti-inflammatory properties, and the pathophysiology of IBD may involve reduced COMMD1 expression or function.

Cu has been shown to enhance the stability and accumulation of hypoxia-inducible factor 1 α (HIF-1 α) (182). The transcriptional control of anti-inflammatory or cellular responses to hypoxia is mediated by the master regulator HIF-1 α (183). A study found that after infection with *Citrobacter rodentium*, transgenic mice with selective inactivation of the HIF-1 α gene in innate retinoic acid receptor-related orphan receptor- γ t-positive cells experienced more severe colitis, primarily since they could not upregulate IL-22 (184). Additionally, HIF-1 α -mediated stimulation of type 1 innate lymphoid cells prevents elevated inflammation and fibrosis during persistent gut injury, even though it is detrimental during acute colitis (185). Hence, the ability of Cu to enhance HIF-1 α may help regulate inflammation in the colon. Other studies suggest that HIF-1 α expression is linked to reduced colon inflammation (186,187).

In addition to regulating inflammation, Cu has been shown to improve intestinal barrier function, support bacterial populations and reduce intestinal damage. For instance, Li *et al* (188) found that Cu/Zn-montmorillonite administration reduced the potentially harmful bacteria (*Streptococcus* and *Pseudomonas*) in the colon of weaned pigs, increased the relative abundance of core bacteria (*Lactococcus* and *Bacillus*) at the genus level, and elevated expression levels of tight junction proteins [zonula occludens-1 (ZO-1) and claudin-1]. Similarly, Jiao *et al* also (189) found that in weaned pigs, dietary Cu/Zn-Mt enhanced barrier function, reduced intestinal inflammation and affected the toll-like receptor 4-myeloid differentiation primary response 88 and transforming growth factor- β 1 signaling pathways, thereby decreasing LPS-induced intestinal damage. Dietary Cu deficiency is associated with colonic injury, and these alterations occur together with disruption of the intestinal barrier, inflammatory response activation and dysbiosis of the gut microbiota (190).

iii) Iron regulation. Ceruloplasmin (CP) is a ferroxidase found in the blood plasma of mammals. This protein, which belongs to the multiCu oxidase family, carries >95% of the Cu present in plasma (191). Iron homeostasis is dependent on CP, and abnormal activity of this protein results in iron accumulation (192). CP is considered to have evolved from cupredoxin, a multi-Cu blue protein with three mononuclear and trinuclear Cu binding sites (193). Ferrous iron is oxidized to ferric iron

by multiCu ferroxidases (194). Iron insufficiency is correlated with low vitamin D levels in IBD. By decreasing hepcidin and increasing CP, vitamin D may improve intestinal iron absorption and treat iron insufficiency (195). Additionally, in a previous study, ferroxidase CP expression was highly increased in Caco-2 cells by 1,25(OH)D (195). Baykalir *et al* (196) also found that lycopene helps prevent colitis by increasing SOD activity, CP and iron levels. IBD-related iron deficiency and anemia are frequently treated with intravenous iron, which can cause hypophosphatemia (197), implying that iron may be required to treat anemia. This suggests that increased CP may improve iron sufficiency and absorption.

iv) Other beneficial roles: Connective tissue formation. A cuproenzyme called protein-lysine 6-oxidase is necessary for the enzymatic cross-linking of collagen and elastin, which stabilizes extracellular matrices (198). Also, Cu-dependent monoamine oxidases known as lysyl oxidases (LOXs) are essential for the remodeling of the extracellular matrix (199). Other biological roles of the LOX and LOX-like proteins include tumor suppression, cellular senescence, and the regulation of development and growth (199). To stabilize the crosslinks between collagen and/or elastin during the development or remodeling of the extracellular matrix, Cu-dependent LOX proteins catalyze the oxidation of lysine residues within these fibrous proteins (200).

v) Other beneficial roles: Neurotransmitter synthesis and central nervous system function. The Cu-containing enzyme dopamine β -hydroxylase (DBH) is crucial for preserving the balance between the two neurotransmitters, dopamine and noradrenaline, within cells (201). DBH is an oxygenase that contains Cu and uses molecular oxygen ascorbate as a cofactor to catalyze the hydroxylation of the β -carbon of a broad range of phenylethylamine derivatives (202). DBH is found in immunocytes as well as the catecholaminergic neuron system, and it contributes to the immunological responses of vertebrates (203). Numerous neuropsychiatric disorders are linked to DBH functional polymorphisms, which also affect serum DBH protein levels and DBH enzymatic activity (201).

vi) Other beneficial roles: Melanin production. Tyrosinases are abundant in nature. These Cu-containing oxidases, along with hemocyanins and catechol oxidases, belong to the type 3 Cu protein family (204). In 2011, Matoba *et al* (205) presented a chemical mechanism that uses a metallochaperone, caddie, to help move two Cu ions to the catalytic core of tyrosinase. The pigmentation of mammalian skin and hair is a result of tyrosinases, which are essential enzymes in the production of melanin (204). Two other enzymes, known as tyrosinase-related proteins, also play a role in the pathway (204).

Detrimental roles. i) Oxidative stress. Oxidative stress has a significant impact on IBD, as chronic inflammation in the gut produces an excess of ROS, causing oxidative stress (206). Numerous lines of evidence indicate that oxidative stress results from excess ROS or reduced antioxidant activity, and that IBD is associated with this imbalance (206). According to previous studies, exposure to Cu/Cu sulphate causes oxidative stress, apoptosis and a decline in antioxidant function, which can result in lung lesions and dysfunction (207), hepatic apoptosis (208) and spermatogenesis disorders (209). These results suggest that Cu may cause oxidative stress. Additionally, Cu ion carriers have been shown in studies to block anti-apoptotic

NF- κ B signaling, generate ROS and activate pro-apoptotic signaling pathways, including the c-Jun N-terminal kinase and mitogen-activated protein kinase pathways (210,211). Moreover, Cu complex nanoparticles exhibit stimulus-responsive Cu complex discharge, which causes mitochondrial dysfunction and promotes lipoylated DLAT aggregation, ultimately resulting in cuproptosis (212). Diseases such as IBD and cancer are marked by alterations in mitochondrial function and the activation of the unfolded protein response (213). A bioenergetic crisis occurs when mitochondrial function is impaired. This impairment weakens the epithelial barrier, increasing the risk of cuproptosis, reducing the production of secretory barrier factors, and hindering the repair process following injury (214-216). As a result, using pharmaceuticals or natural agents to combat oxidative stress may aid in the prevention of IBD.

ii) Impact of Cu on inflammation, intestinal integrity and gut microbiota. Results from animal models have shown that the gut microbiota plays a variety of context-specific roles in health and disease, from pro-inflammatory to protective. Furthermore, data from these experimental models indicate that while gut bacteria frequently trigger immunological stimulation, persistent inflammation also influences the gut microbiota, leading to dysbiosis (217). Cu has been demonstrated in studies to decrease barrier function, affect gut flora and trigger inflammatory reactions. For instance, Liao *et al* (218) found that excessive Cu resulted in decreased expression of tight junction proteins (ZO-1, claudin-1 and junctional adhesion molecule-1), increased inflammatory cytokines and increased levels of *Streptococcus*, *unidentified_Enterobacteriaceae* and *unidentified_Muribaculaceae*, but decreased levels of *Lactobacillus* and *Methanobrevibacter*. Also, Ma *et al* (219) found that early-life exposure to both Cu and florfenicol leads to visceral damage, inflammatory responses and alterations in the gut microbiota associated with disease and energy intake. Notably, at the phylum level, exposure to Cu only increased *Bacteroidetes* levels, while decreasing *Spirochaetae*, *Actinobacteria* and *Verrucomicrobia* levels when compared with the control group. In another study, exposure to Cu was shown to decrease *Lactobacillus*, *Bifidobacteria* and *Romboutsia* levels, and alter the ratio of *Firmicutes* to *Bacteroidetes* and the abundance of bacteria linked to intestinal inflammation and fat metabolism, suggesting that prolonged Cu exposure weakens the gut barrier and elevates permeability due to gut microbial disorders, which may trigger an inflammatory reaction (220). These findings suggest that Cu may cause impaired barrier integrity, intestinal dysbiosis and inflammation. These findings may support the dual involvement of Cu in IBD. Fig. 2 shows the dual roles of Cu in IBD.

7. Cuproptosis-related genes in IBD pathogenesis

Preclinical studies. Genetic factors play an important role in IBD. Notably, preclinical studies have demonstrated that downregulation of cuproptosis-related genes contributes to the development of IBD by damaging the intestinal epithelium, reducing junctional protein expression and increasing inflammatory cell infiltration (15,68,221). Additionally, these processes lead to a reduction in colon length, increased weight

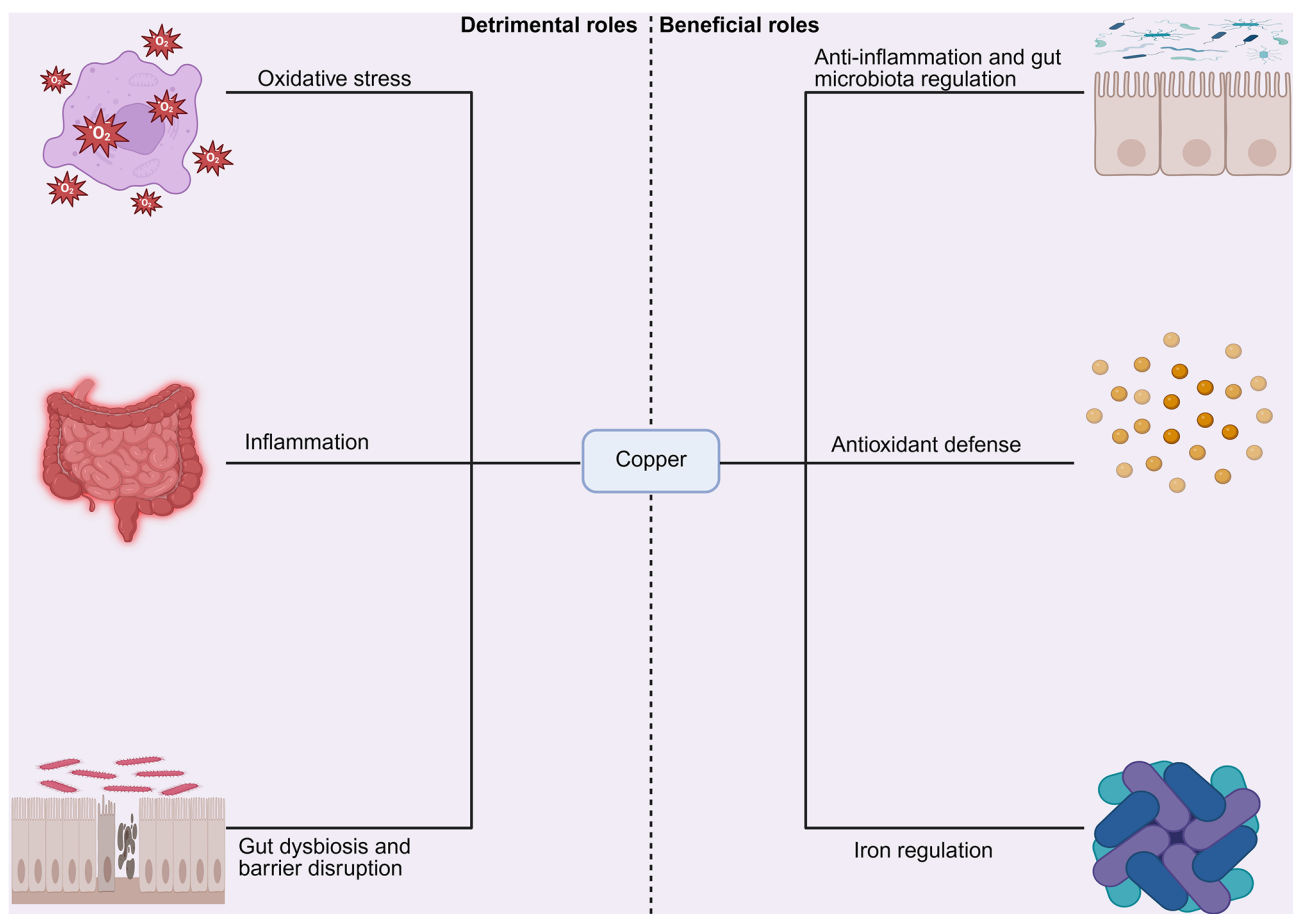


Figure 2. Dual roles of Cu in IBD. Cu plays a beneficial role in IBD, contributing to antioxidant defense, regulating inflammation and managing iron levels, while also having detrimental effects such as inducing oxidative stress, promoting gut dysbiosis, disrupting barriers and activating the intestinal immune system. Created using BioRender.com. CU, copper; IBD, inflammatory bowel disease.

loss and a higher disease activity index, all of which are characteristic signs of IBD (15,68,221). Emerging evidence suggests that in DSS-induced colitis, levels of FDX1, DLAT, dihydrolipoamide branched chain transacylase E2 (DBT), LIAS, DLD and PDHA1 are markedly lower than in the control group (15,68,221). These findings suggest that genes related to cuproptosis may be involved in the pathophysiology of IBD. Notably, these genes are downregulated in IBD. As a result, drugs that upregulate these genes may prevent IBD in tandem with Cu chelation agents. As shown previously, systemic inflammation can lead to increased Cu levels (161). Therefore, to prevent cuproptosis-induced IBD, this Cu must be removed to prevent excess Cu, which may trigger cuproptosis by the conversion of Cu^{2+} to Cu^{+} by FDX1. Additionally, safely increasing the cuproptosis-related genes helps transition from the glycolytic phase to mitochondrial OXPHOS, which is associated with M2 macrophage polarization. M2 macrophages have been shown to reduce inflammation, restore intestinal tissue, interact with the gut microbiota and prevent IBD (222,223). Thus, the combination of Cu chelation agents and upregulation (safely) of critical cuproptosis genes may effectively prevent cuproptosis-induced IBD. Increasing these cuproptosis genes could lead to the functional activation of the PDH complex (16). The first and most crucial enzyme in the conversion of pyruvate into acetyl-CoA, which enters the TCA cycle to generate ATP and electron

donors, is PDH (224). Additionally, when the PDHA1 gene is overexpressed, PDH activity rises, improving mitochondrial OXPHOS and ATP production (225). According to one study, tight junction proteins are disrupted by ATP deficiency (226), implying that the assembly of the PDH complex and its increased activity may provide energy via ATP for the repair of the mucosal barrier by increasing tight junction proteins. Fig. 3 depicts the role of cuproptosis-related genes in preclinical studies of IBD.

Clinical studies involving cuproptosis-related genes, immune infiltration and biomarkers. Bioinformatics and machine learning techniques have revealed that cuproptosis-related genes show differential expression in IBD. Moreover, these genes are associated with immune cell infiltration and can act as biomarkers for IBD. For instance, a study identified the hub genes associated with cuproptosis in active UC, including sulfatase modifying factor 1 (SUMF1), metallothionein 1G (MT1G), antioxidant 1 Cu chaperone (ATOX1), ATP7B, FDX1 and LIAS, with corresponding area under the curve values of 0.877, 0.864, 0.823, 0.803, 0.799 and 0.752, respectively (227). The genes displayed reduced expression, except for ATOX1, which displayed elevated expression in active UC (227). The study found that SUMF1, MT1G, ATP7B, FDX1 and LIAS showed a marked positive association with CD8^{+} T cell infiltration, whereas ATOX1 had

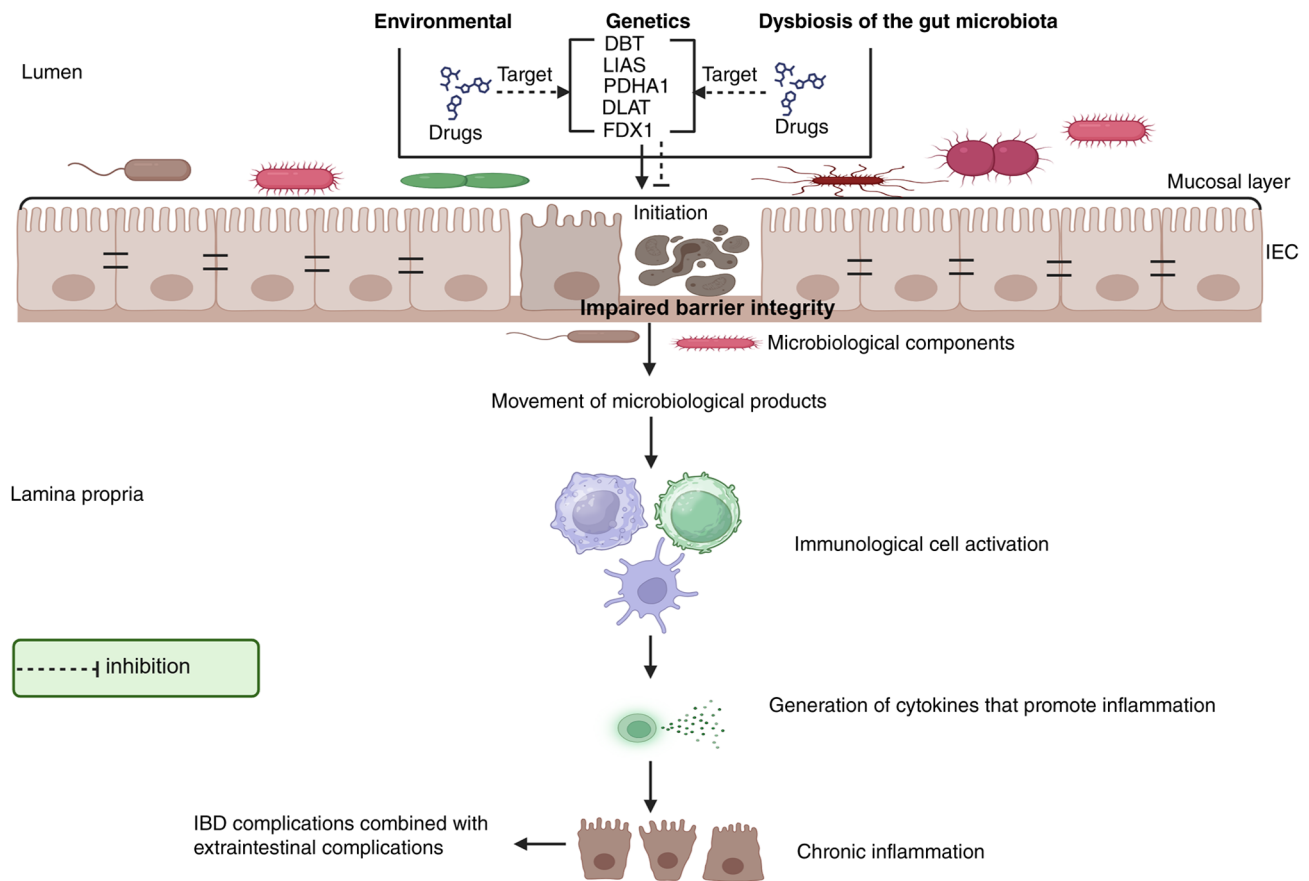


Figure 3. Role of cuproptosis-related genes in the pathogenesis and potential therapeutic targets in IBD. Cuproptosis-related genes are downregulated in preclinical studies, compromising the gut integrity. This causes increased immune cell infiltration and the generation of pro-inflammatory cytokines, which exacerbate the illness (chronic inflammation) and lead to IBD and extraintestinal problems. Molecular docking techniques have been used to identify potential drugs that target specific cuproptosis-related genes for IBD remission. These prevent barrier disruption, immunological reactions, the generations of cytokines, chronic inflammation and IBD complications. Created using BioRender.com. IBD, inflammatory bowel disease; DBT, dihydrolipoamide branched chain transacylase E2; LIAS, lipoyl synthase; PDHA1, pyruvate dehydrogenase E1 subunit α 1; DLAT, dihydrolipoyl transacetylase; FDX1, ferredoxin 1; IEC, intestinal epithelial cell.

a marked negative link (227). Other studies have also found cuproptosis genes, including PDHA1, PDHB, LIAS, FDX1, DLD, DLAT, ATP7B and DBT (68), metallothionein 1M, β -secretase 1, ATP binding cassette subfamily B member 6, GLS, FDX1, PDHA1 and LIAS (228), DBT, LIAS, PDHA1 and DLAT (221), and DLD, DLAT, PDHB and DBT (10), respectively, which serve as diagnostic markers for IBD. These genes have been shown to correlate with immune cell infiltrations such as macrophages and neutrophils, activated CD4 and CD8 T cells, and T17 cells. It is noteworthy that while these cuproptosis genes are differentially expressed in IBD, comparable observations have also been made in its complications, such as CRC, which can be exploited for diagnostic purposes (229,230). Table III shows that the expression of key cuproptosis-related genes (positive regulators: FDX1, LIAS, PDHA1 and DLAT) was downregulated in IBD and CRC, which is consistent with preclinical investigations in IBD models. The negative regulators (such as CDKN2A) were increased in CRC. However, GLS (a negative regulator) was downregulated in IBD but elevated in CRC. Other associated genes were either upregulated or downregulated. These results suggest that the core regulatory genes involved in cuproptosis (FDX1, LIAS and DLAT) are downregulated in IBD.

Summary of potential biomarkers from other diseases. Table IV (11-13,231-237) summarizes the potential indicators of cuproptosis-related genes in different illnesses, including sepsis-induced myocardial dysfunction, diabetic nephropathy, atherosclerosis, acute myeloid leukemia, sarcopenia, hepatic ischemia and reperfusion injury, lung adenocarcinoma, severe community-acquired pneumonia, breast cancer and uterine corpus endometrial carcinoma.

8. Therapeutic applications of cuproptosis in IBD

Chelation therapy is the preferred method of treatment for Cu overload or poisoning (238). Cu chelators have been used at the cellular and organismal levels to study Cu acquisition, distribution and disposition (239). One of the most effective ways to maintain physiological Cu concentrations is by using Cu-chelating agents (240). TetrathiomolybdateTM, trientine (triethylenetetramine dihydrochloride), 5,7-dichloro-2[(dimethylamino)methyl]quinoline-8-ol, 2,3-dimercaptosuccinic acid and D-penicillamine [(S)-2-amino-3-mercapto-3-methylbutanoic acid] are the primary Cu-chelating agents (240). Numerous chelating medications have been shown to alter Cu levels by various processes. Specifically, tetrathiomolybdate encourages Cu biliary

Table III. Summary of potential biomarkers of cuproptosis-related genes in IBD and related CRC.

Authors, year	Cuproptosis gene	Condition	Diagnosis	Parameter/AUC	Prognostic	Parameter	(Refs.)
Zou <i>et al.</i> , 2023	↓SUMF1, ↓MT1G, ↑ATOX1, ↓ATP7B, ↓FDX1, ↓LIAS	UC	✓	0.877, 0.864, 0.823, 0.803, 0.799, 0.752	-	-	(227)
Huang <i>et al.</i> , 2022	↓FDX1, ↓LIAS, ↓DLAT	UC, DSS-induced UC	✓	0.889	-	-	(68)
Chen <i>et al.</i> , 2022	↓DBT, ↓LIAS, ↓PDHA1, ↓DLAT	DSS-induced UC, IBD	✓	0.743	-	-	(221)
Yuan <i>et al.</i> , 2022	↓MT1TM, ↑BACE1, ↑ABC6, ↓GLS, ↓FDX1, ↓PDHA1, ↓LIAS	CD	✓	0.759, 0.720, 0.649, 0.730, 0.631, 0.685, 0.678	-	-	(228)
Shi <i>et al.</i> , 2025	↓DLD	IBD + MDD	✓	-	-	-	(10)
Wu <i>et al.</i> , 2022	↑CDKN2A, ↓DLAT	CRC	-	-	✓	OS (HR, 1.14); OS (HR, 0.53)	(229)
Du <i>et al.</i> , 2022	↑CDKN2A, ↑GLS, ↓DLAT	CRC	-	-	✓	0.616, 0.681, and 0.677 in the 1st, 3rd and 5th years, respectively	(230)

CD, Crohn's disease; CRC, colorectal cancer; DSS, dextran sulfate sodium; HR, hazard ratio; IBD, inflammatory bowel disease; MDD, major depressive disorder; OS, overall survival; AUC, area under the curve; HR, hazard ratio; UC, ulcerative colitis; DBT, dihydrolipoamide branched chain transacylase E2; LIAS, lipoyl synthase; PDHA1, pyruvate dehydrogenase E1 subunit α 1; DLAT, dihydrolipoyl transacetylase; FDX1, ferredoxin 1; SUMF1, sulfatase modifying factor 1; MT1G, metallothionein 1G; ATOX1, antioxidant 1 Cu chaperone; ATP7B, ATPase Cu transporting β ; MT1TM, metallothionein 1M; BACE1, β -secretase 1; ABC6, ATP binding cassette subfamily B member 6; GLS, glutaminase; DLD, dihydrolipoamide dehydrogenase; CDKN2A, cyclin-dependent kinase inhibitor 2A.

excretion, whereas penicillamine, trientine and dimercapto-succinic acid produce complexes that are eliminated in the urine (240). As a result, using medications to help regulate Cu levels in IBD may help alleviate cuproptosis. Preclinical studies have shown that Cu chelators TM (241), TM + cetuximab (242) and disulfiram + oxaliplatin (243) can be used in treating breast cancer, head and neck carcinoma, and CRC, respectively. Additionally, other clinical trials or studies have also shown that trientine plus carboplatin and pegylated liposomal doxorubicin (244), bis-choline tetra-thiomolybdate or trientine tetrahydrochloride (245,246), D-penicillamine with Cu sulfate (247), and TM combined with irinotecan, 5-fluorouracil and leucovorin (248) can be used to treat relapse of epithelial ovarian, tubal and peritoneal cancer, Wilson disease, glioblastoma multiforme and metastatic CRC, respectively. Nonetheless, research into Cu chelators and ionophores in the treatment of IBD is ongoing, and there is no concrete evidence that Cu chelators can control Cu levels in IBD. Notably, differentially expressed cuproptosis-related genes have been shown to contribute to

the etiology of IBD. As a result, drugs that target these genes using molecular approaches may prevent IBD. For example, molecular docking and other techniques have been used to identify potential medications targeting cuproptosis genes in IBD and provide therapeutic benefit (10,68,221,227). These prospective medication breakthroughs could help prevent IBD in the future.

Potential cuproptosis-related gene drug discoveries

Methotrexate (MTX). The synthetic folic acid analog methotrexate is prized for its anti-inflammatory and anti-proliferative qualities. MTX is frequently used to treat steroid-recalcitrant inflammatory diseases and is regarded as one of the first immune-modifying drugs (249). Intracellular metabolites of MTX, known as MTX polyglutamates, play a crucial role in the efficacy of the drug and influence its toxicity (250). The most important enzyme in the cuproptosis-regulatory pathway is FDX1. Chen *et al.* (221) used computational simulation to study the molecular interactions between FDX1 and IBD medications. Based on molecular

Table IV. Summary of potential biomarkers of cuproptosis-related genes in other conditions.

Authors, year	Cuproptosis-related genes	Condition	Diagnosis	Parameter/AUC	Prognostic	Parameter/AUC	(Refs.)
Shi <i>et al</i> , 2025	↓PDHB	Sepsis-induced myocardial dysfunction	✓	0.995, 0.960, 0.864, 0.984 (AUC values from different data sets)	-	-	(231)
Chen <i>et al</i> , 2024	↑FSTL1, ↑CX3CR1, ↑AGR2	Diabetic nephropathy	✓	0.911, 0.935, 0.922	-	-	(232)
Chen <i>et al</i> , 2023	↑SLC31A1, ↑SLC31A2, ↓SOD1	Atherosclerosis	✓	0.800, 0.779, and 0.798 respectively (for one data set), 0.736, 0.838 and 0.848 respectively (for another data set)	-	-	(233)
Li and Kan, 2024	↑MTF1, ↑LIPT1	Acute myeloid leukemia	✓	-	✓	0.953, 0.795	(234)
Zhu <i>et al</i> , 2023	↓PDHA1, ↓DLAT, ↓PDHB, ↓NDUFC1	Sarcopenia	✓	0.83, 0.87 and 0.64 for validation	-	-	(235)
Xiao <i>et al</i> , 2024	↑NLRP3, ↓ATP7B, ↑NFE2L2	Hepatic ischemia and reperfusion injury	✓	0.832, 0.904 for validation	-	-	(236)
Li <i>et al</i> , 2024	↑DBT, ↑DLAT	Lung adenocarcinoma	-	-	✓	Poor prognosis (DLAT: HR, 6.103; DBT: HR, 4.985)	(11)
Chen <i>et al</i> , 2023	↓GCSH, ↓LIPT1, ↑DLD	Severe community-acquired pneumonia	✓	0.8359, 0.8724, 0.9566	-	-	(237)
Jiang <i>et al</i> , 2022	↑CDKN2A, ↑PDHA1, ↓MTF1, ↓DLD, ↓LIPT1, ↓FDX1	Breast cancer	-	-	✓	HR, 1.22 (poor OS); HR, 1.39 (poor OS); HR, 0.65 (better OS) ^a ; HR, 0.65 (better OS) ^a ; HR, 0.37 (better OS) ^a	(12)

Table IV. Continued.

Authors, year	Cuproptosis-related genes	Condition	Diagnosis	Parameter/AUC	Prognostic	Parameter/AUC	(Refs.)
Chen, 2022	↑CDKN2A, ↓GLS ↓LIPT1	Uterine corpus endometrial carcinoma	-	-	✓	HR, 3.58 (poor prognosis); HR, 3.23 (poor prognosis) ^b ; HR, 1.95 (poor prognosis) ^b	(13)

^aImproved survival when increased, ^bpoor prognosis when increased. AUC, area under the receiver operating characteristic curve; HR, hazard ratio; OS, overall survival; DBT, dihydrolipoamide branched chain transacylase E2; PDHA1, pyruvate dehydrogenase E1 subunit α 1; DLAT, dihydrolipoyl transacetylase; FDX1, ferredoxin 1; ATP7B, ATPase Cu transporting β ; GLS, glutaminase; DLD, dihydrolipoamide dehydrogenase; CDKN2A, cyclin-dependent kinase inhibitor 2A; PDHB, pyruvate dehydrogenase E1 subunit β ; FSTL1, follistatin-like-1; CX3CR1, C-X3-C motif chemokine receptor 1; AGR2, anterior gradient-2; SLC31A1/2, solute carrier family 31 member 1/2; SOD1, superoxide dismutase 1; MTF1, metal regulatory transcription factor 1; LIPT1, lipoyltransferase 1; NDUFC1, NADH:ubiquinone oxidoreductase subunit C1; NLRP3, NOD-like receptor family pyrin domain-containing 3; NFE2L2, nuclear factor, erythroid derived 2, like 2; GCSH, glycine cleavage system protein H.

docking studies, they discovered that MTX had the highest affinity for binding to the primary chain of significant regulators linked to cuproptosis when compared to other drugs. MTX had the highest binding potential among IBD drugs, including olsalazine, prednisone and tofacitinib; thus, it could be used as a target for cuproptosis genes to treat IBD. With its growing use in clinical practice, MTX, a folic acid antagonist, is one of the most commonly administered medications (251). However, due to its numerous side effects, which include bone marrow suppression, hepatic or renal dysfunction, gastrointestinal distress, mucocutaneous injury and neurotoxicity, the use of the medication needs to be monitored (251). The toxicity typically happens quickly and results in difficult-to-manage advanced renal failure, sepsis and severe neutropenia (251).

Barasertib and NTP-TAE684. Barasertib, a selective inhibitor of Aurora B kinase, serves as the prodrug for barasertib-hydroxy-quinazoline pyrazole anilide. This compound has shown early effectiveness against acute myeloid leukemia in clinical settings (252), inhibits T47D breast cancer cell lines resistant to fulvestrant (253) and influences the migration of hepatocellular carcinoma cells (254). It has recently been demonstrated that NTP-TAE684 and barasertib can target cuproptosis-related genes for therapeutic purposes in IBD. Barasertib and NTP-TAE684, which target DLAT, have been predicted to be the most effective drugs based on molecular docking and molecular dynamics simulation analyses. Additionally, Barasertib and NTP-TAE684 are the leading compounds with the most promise for treating MDD and IBD, providing fresh insights for treatment strategies in these intricate and crippling conditions, based on thorough molecular dynamics models using DLAT as the therapeutic target (10).

Golimumab, infliximab and vedolizumab. TNF antagonists have completely transformed the treatment of IBD. The first biological drugs used to cause and sustain remission in UC were infliximab and adalimumab (255). The transgenic anti-TNF monoclonal antibody known as golimumab mainly works by identifying and neutralizing TNF to stop inflammation (256). Research has demonstrated that golimumab helps patients with UC experience clinical remission and mucosal repair (257,258). Additionally, research has demonstrated that infliximab, an anti-tumor necrosis factor agent, can be used to treat IBD, albeit response rates have varied (152,259,260). Another anti-integrin monoclonal antibody effective for CD and UC is vedolizumab (261), and research (262-265) indicates that it is safe and effective in treating IBD. It is worth noting that golimumab, vedolizumab and infliximab have been shown to target cuproptosis-related genes associated with IBD, which improves outcomes. In patients with active UC, golimumab responders alleviate defective intestinal mucosal cuproptosis by controlling hub differentially expressed cuproptosis genes (227). In a previous study, golimumab injections improved SUMF1, MT1G, FDX1, ATP7B and LIAS levels while decreasing ATOX1 in patients with active UC, thereby promoting colonic mucosal healing (227). Similarly, infliximab therapy increased the expression of SUMF1, MT1G, FDX1 and LIAS in the colonic mucosa of patients with active UC while downregulating ATOX1 (227). Additionally, the differentially expressed cuproptosis genes exhibited expression patterns similar to those of golimumab after vedolizumab treatment (227). These findings suggest that drugs may modulate genes associated with cuproptosis, reduce inflammation and reduce colonic mucosal damage.

Other drugs. Antibiotics (latamoxef and clindamycin) (266), tricyclic antidepressants (clomipramine) (267), sulfonyleureas (glibenclamide) (268), organic acid/metabolite

(pyruvic acid) (269), corticosteroids (medrysone) (270), metabolic cofactor (flavin adenine dinucleotide) (271), vitinoin and caspan have been identified to target cuproptosis genes for IBD management. Therapeutics that target cuproptosis, a unique mechanism of Cu-induced cell death, are an emerging field. As a result, therapeutic compounds targeting cuproptosis-related genes have been investigated. According to the expected results, the target agents of cuproptosis-related genes may include latamoxef (PDHA1, FDX1, DBT, DLAT and LIAS), vitinoin (PDHA1, DBT, PDHB and DLD), clomipramine (DBT and LIAS), chlorzoxazone (PDHA1, FDX1, DLAT and DLD), glibenclamide (PDHA1, FDX1, DLAT and DLD), pyruvic acid (LIAS and DLD), clindamycin (PDHA1, FDX1, DLAT and LIAS), medrysone (FDX1, DLAT and LIAS), flavin adenine dinucleotide (DLD) and caspan (ATP7B, DLAT and DBT) (68). Fig. 3 depicts the potential role of prospective pharmacological agents targeting cuproptosis-related genes in IBD.

Potential drugs targeting cuproptosis-related genes from other studies. Other studies have discovered that cuproptosis-related genes can be targeted for therapeutic benefit. According to one study, PDHB expression, a gene linked to cuproptosis, was lower in patients with sepsis-induced myocardial dysfunction than in controls. Using immunohistochemistry, similar findings were discovered in sepsis-induced myocardial dysfunction animal models (231). Additionally, drug-gene interaction analysis was used to suggest prospective gene-targeting drugs. Using molecular docking, it was found that PDHB exhibits strong binding activity with ferric ammonium citrate, oxidopamine, imatinib, cube root extract, deferoxamine and vinblastine (231). Furthermore, Zhu *et al* (235) found that four genes associated with cuproptosis, PDHA1, DLAT, PDHB and NADH:ubiquinone oxidoreductase subunit C1 (NDUFC1), may serve as diagnostic indicators for sarcopenia, and that metformin shows great promise as a treatment for the condition. While no possible medications were found for the other three genes (PDHA1, DLAT and PDHB), metformin hydrochloride was identified as the therapeutic medication for NDUFC1 (235). Another study found that the occurrence and immune infiltration of septic cardiomyopathy are linked to the cuproptosis-related gene PDHB (272). However, rhodiolside, adenosine and pyruvic acid were predicted to be targets and to bind to PDHB (272). Therefore, these results suggest that possible medications that target genes linked to cuproptosis may be useful in treating a variety of illnesses, including IBD.

9. Limitations and future directions

Cuproptosis is a recently discovered type of cell death that warrants further investigation. Studies have reported increased Cu levels in IBD, while others have found lower Cu levels in the same condition. As a result, more research is needed to determine the specific pathways by which dysregulated Cu contributes to the pathogenesis of IBD. Moreover, the availability of Cu-targeting medications for IBD is currently limited. Notably, Cu has been shown to play a dual role in IBD, having both beneficial and harmful effects, which complicates the targeting of Cu ions as a therapeutic approach.

According to the present review, the majority of cuproptosis-related genes have a role in IBD pathogenesis. However, most of these genes were found via bioinformatic

analyses or public databases. Additionally, the complicated regulatory mechanisms of cuproptosis in IBD were also observed. The clinical and experimental data on cuproptosis in IBD are extremely scarce. A lack of raw sequencing data, which could lead to selection bias, and smaller sample sizes were also seen (10,68,227,228). Therefore, these findings provide additional clinical or experimental validation of cuproptosis-related gene expression levels in IBD pathogenesis. In addition, larger sample sizes are required for clinical investigations and well-designed prospective studies. Further research is needed to clarify the underlying mechanisms of cuproptosis genes in IBD. Also, prospective studies on cuproptosis dynamics during the transition from chronic inflammation to colitis-associated cancer are recommended. The use of molecular docking/methods, more IBD medications, natural products, stem cells and nanoparticles should be explored to target cuproptosis-related genes for therapeutic purposes. When it comes to natural products, stem cells and nanoparticles, these can help reduce the side effects of some IBD medications.

10. Conclusion

IBD is a chronic inflammatory disorder characterized by recurrent episodes and includes conditions such as UC and CD. Research has shown that IBD is associated with imbalances in Cu levels; while some studies indicate that Cu levels increase in patients with IBD, others report a decrease. Cu plays a complex role in IBD, complicating the development of effective therapeutic strategies. Recent studies have identified several cuproptosis-related genes that can serve as biomarkers in diagnosing and predicting the progression of IBD. These genes have also been linked to increased infiltration of immune cells. In response, emerging therapeutic approaches aim to regulate these cuproptosis-related genes. Researchers are exploring novel drugs through molecular docking and other methods to target these genes for treatment.

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Availability of data and materials

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Authors' contributions

LC, FAA and FM conceptualized the study. Funding acquisition and editing was performed by JG. BP and BW edited and reviewed the manuscript. LC and FAA wrote the original draft. FM reviewed and edited the manuscript. All authors have read and agreed to the final version of the manuscript. Data authentication is not applicable.

Ethics approval and consent to participate

Not applicable.

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Not applicable.

Competing interests

The authors declare that they have no competing interests.

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