REVIEW

Programmed cell death, redox imbalance, and cancer therapeutics

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Abstract

Cancer cells are disordered by nature and thus featured by higher internal redox level than healthy cells. Redox imbalance could trigger programmed cell death if exceeded a certain threshold, rendering therapeutic strategies relying on redox control a possible cancer management solution. Yet, various programmed cell death events have been consecutively discovered, complicating our understandings on their associations with redox imbalance and clinical implications especially therapeutic design. Thus, it is imperative to understand diferences and similarities among programmed cell death events regarding their associations with redox imbalance for improved control over these events in malignant cells as well as appropriate design on therapeutic approaches relying on redox control. This review addresses these issues and concludes by bringing afront cold atmospheric plasma as an emerging redox controller with translational potential in clinics.

Keywords Redox imbalance · Programmed cell death · Cold atmospheric plasma · Cancer therapeutics

Introduction

Cancer is a complex disease, the initiation and development of which requires intensive cross talks with its microenvironment and is highly regulated by cellular redox level. Reactive oxygen species (ROS) have been shown to play diverse roles in many critical transition stages of cancer cells such as the life/death transition, tumor angiogenetic switch, and epithelial mesenchymal transition (EMT) [\[1](#page-16-0)]. Cancer cells typically have a relatively higher redox level than normal cells due to their chaoticities in organizing cellular functionalities, rendering malignant cells more fragile under redox stress than healthy cells. On the other hand, cancer cells are naturally faced with oxidative stress as a result of imbalanced ROS production and disordered antioxidant defense ability [\[2\]](#page-16-1). That is, ROS are excessively generated in malignant cells due to increased metabolic

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rate, accumulated mitochondria dysfunction, elevated cell signaling, enhanced expression of oncogenes, and accelerated peroxisome activities [[3\]](#page-16-2), which is a required feature of malignant cells. Therapeutic strategies taking advantages of redox stress may kill cancer cells by triggering programmed cell death (PCD) events. PCD such as apoptosis, paraptosis, mitotic catastrophy, autophagic cell death, ferroptosis, necroptosis, and pyroptosis represents a set of highly ordered and programmed cellular death events that enable the elimination of cells running chaotic or being destined to die. Failed PCD may lead to uncontrolled cell proliferation that is one important cancer hallmark [\[4](#page-16-3)]. Thus, it is important to explore diferences and commonalities of these varied PCD programs as well as their diferential associations with cellular redox imbalance to enable our improved understandings and design on onco-therapeutic strategies relying on redox level control.

Among the various PCD programs identified so far, we selected apoptosis, paraptosis, mitotic catastrophy, autophagic cell death, ferroptosis, necroptosis, and pyroptosis in this review given their representativeness on the stimulating source and their prevalence in literatures. We focus on diferences of these diverse PCD events and their associations with redox imbalance in this review, with the aim of diferentiating these PCD events by the source of redox imbalance, identifying the link of these programs,

and pushing forward possible onco-therapeutic solutions that rely on redox control.

Programmed cell death associated with redox imbalance imposed by DNA damage

Apoptosis

Basics of apoptosis

Apoptosis is the most well-known PCD event that is carefully regulated by many cellular processes to balance cell turnover in proliferating tissues and selectively remove cells that hamper proper organ development and functioning [\[5](#page-16-4)]. Apoptosis is accompanied by membrane microvilli loss, cytoplasm condensation, nucleus segmentation, and chromosomal DNA degradation into 180 bp oligomers. During early apoptosis, cells shrink and undergo pyknosis [[6\]](#page-16-5) as a result of chromatin condensation [[7](#page-16-6)].Then, budding (i.e., forming a wide range of plasma membrane bubbles) occurs followed by nucleus break and separation of cellular debris corpuscles into the apoptosis body. These small apoptosis bodies are phagocytosed by macrophages, parenchymal cells, or neoplastic cells and degraded within phagolysosomes. Yet, the organelle integrity remains, which is enclosed within the intact plasma membrane.

One important feature of apoptosis is the fipping of phosphatidyl serine groups to the outer membrane surface that enables the common strategy of apoptosis detection through combined use of annexin V and cell-impermeable DNA staining dye such as propidium (PI) or 7-amino-actinomycin (7-AAD) followed by fuorescent microscopy or fow cytometry [[8\]](#page-16-7). Double-stranded breaks could be identifed through terminal de-oxynucleotidyl transferase (TdT)-mediated dUTP-biotin nick end labeling (TUNEL) technique and comet assay [[9\]](#page-16-8). Alternatively, caspase assay and poly-ADP ribose polymerase (PARP) cleavage assay [\[10\]](#page-16-9) could be used to evaluate the intermediate modulators of apoptosis.

Caspase-dependent apoptosis can be endogenous or exogenous.

Endogenous apoptosis pathway The endogenous pathway is originated from mitochondria that can be triggered by a variety of environmental and chemical stimuli capable of imposing oxidative stress. When cell redox homeostasis is disrupted, the mitochondrial outer membrane permeability alters that leads to the release of cytochrome C from mitochondria to the cytoplasm; cytochrome C forms complexes with Apaf-1 that further recruits caspase-9 to form the apoptosome in the cytoplasm through the CARD domain; caspase-9 is self-cut followed by caspase-3 activation to initiate apoptosis (Fig. [1](#page-1-0)).

Exogenous apoptosis pathway The exogenous pathway is mediated by death receptors. Taking Fas as an example, it trimerizes and recruits FADD and procaspase-8 through the cytoplasmic domain to form the death inducing signaling complex (DISC). Through self-cutting, procaspase-8 becomes caspase-8 that cuts procaspase-3 into caspase-3, the executioner of apoptosis (Fig. [1](#page-1-0)).

Apoptosis in response to DNA damage induced redox imbalance

A variety of factors or chemicals capable of initiating DNA damage signals such as ionizing radiation, ultraviolet radiation and H_2O_2 , etc., can cause redox imbalance and trigger apoptosis [\[11](#page-16-10)].

DNA damage is an inciting cause of endoplasmic reticulum (ER) stress that typically occurs when proteins are not or not properly folded. On ER stress, Bax and Bak in the ER membrane allow Ca^{2+} release from ER to the cytosol where it activates m-Calpain and subsequently caspase-12. This, on one hand, leads to a sequential activation of caspase family members including procaspase-9 and caspase-3; and, on the other hand, causes mitochondrial inner membrane depolarization and the release of cytochrome C to the cytoplasm. Consequently, apoptosome forms, a prerequisite for endogenous caspase-dependent apoptosis [[12\]](#page-16-11). In addition, ER stress can suppress the anti-apoptotic functions of Bcl2 and activate pro-apoptotic proteins such as Bim, Bax and Bak through activating c-Jun N-terminal kinase (JNK) and c/EBP homologous protein (CHOP) [\[13](#page-16-12)–[16\]](#page-16-13), linking caspase-independent apoptosis with the ROS/JNK pathway as reported in breast cancer cells [\[17](#page-16-14)]. Mammals express at

Fig. 1 Graphic illustration on the crosstalk and diferences of 3 example DNA damage associated PCD events regarding the mechanism and phenotype

least three diferent MAPKs, including extracellular signalregulated kinase (ERK), JNK and p38. These kinases share 60–70% similarity but difer in the signal they sense and the size of the avalanche they trigger. While ERK is stimulated by proliferative signals, JNK and p38 respond to environmental stimuli including ER stress [[18\]](#page-16-15).

Reactive oxygen intermediates (ROI) can react with all kinds of unsaturated fatty acids and cholesterols on the cell membrane to generate oxidative damage that can directly initiate cell apoptosis [[19](#page-16-16)]. On the other hand, ROI could cause DNA damage that leads to poly ADP-ribose polymerase (PARP) activation and p53 accumulation [\[20\]](#page-16-17). P53 accumulation could activate p21 transcription that arrests cells at the G1 phase until DNA damage is repaired. Otherwise, p53 will continue accumulating to trigger apoptosis through increasing the expression of the pro-apoptotic factor Bax and reducing that of the anti-apoptotic factor Bcl2 [[21\]](#page-16-18); and/ or induce apoptosis through activating death receptors such as TNF receptor and Fas [[21\]](#page-16-18).

Clinical relevance of apoptosis in cancer treatment

Tumor cells can develop resistance to apoptotic agents and suppress apoptosis by, e.g., up-regulating anti-apoptotic proteins such as Bcl-2 or down-regulating/mutating proapoptotic proteins such as Bax [[22\]](#page-16-19). Members of the steroid/ retinoid superfamily of ligand-activated transcription factors (SRTFs) could modulate the transcription level of Bcl-2 and Bcl-xL. For example, as Bcl-2 expression is estrogendependent in the mammary gland, anti-estrogens such as tamoxifen could inhibit Bcl-2 expression in breast cancer cells and thus promote the sensitivity of tumor cells to anticancer drugs [[22\]](#page-16-19). TNF family cytokines, TRAIL and agonistic antibodies against TRAIL receptors have been demonstrated to possess potent antitumor activity [\[23\]](#page-16-20). Synthetic triterpenoids such as CDDO and CDDO lm can sensitize solid tumor cells to TRAIL induced apoptosis that functions in both chemo-sensitive and chemo-refractory tumor cells [\[24–](#page-16-21)[26\]](#page-16-22).

Commercialized onco-therapeutic products triggering apoptosis in cancer cells include CDDO for solid tumor treatment [\[24](#page-16-21)–[26](#page-16-22)], and Venetoclax for treating acute myeloid leukemia and small lymphocytic lymphoma [[27\]](#page-16-23) (Table [1\)](#page-3-0). Many drugs have been under clinical trials, including ABBV-621 (NCT: 03082209) [[28\]](#page-16-24), GEN1029 (NCT: 3576131) [[29\]](#page-16-25), ALRN-6924 (NCT: 03725436) [\[30](#page-16-26)], BI907828 (NCT: 03449381) [[31\]](#page-16-27)for the treatment of malignant solid tumors, ABBV-155 (NCT: 03595059) for treating refractory solid tumors [\[32\]](#page-16-28), ABT-737 (NCT: 00902018) for treating small cell lung cancer and hematological tumors [\[33](#page-16-29)], APG-1252 (NCT: 03080311) for the treatment of solid tumors as represented by small cell lung cancer [[34\]](#page-16-30), Siremadlin (NCT: 04097821) for treating uveal melanoma [\[35](#page-16-31)],

SMACmimetic (NCT: 02890069) for the treatment of breast cancer [[36\]](#page-16-32), Lexatumumab (NCT: 00428272) for treating osteosarcoma, neuroblastoma and pancreatic cancer [[37](#page-16-33)], Mapatumumab (NCT: 00315757) for the treatment of multiple myeloma, renal carcinoma, bladder cancer, etc. [\[38](#page-16-34)], MIK665 (NCT: 02992483) for the treatment of multiple myeloma and lymphoma [[39\]](#page-17-0), Navitoclax (NCT: 01557777) [[40](#page-17-1)] and APG-2575 (NCT: 03913949) [\[41\]](#page-17-2) for the treatment of chronic lymphocytic leukemia, AMG176 (NCT: 02675452) for treating chronic lymphocytic leukemia and acute myeloid leukemia [[42\]](#page-17-3), APR-246 (NCT: 04214860) for treating myeloid malignancy [\[43](#page-17-4)], and AZD5991 (NCT: 03218683) for the treatment of blood tumors [[44\]](#page-17-5) (Table [1](#page-3-0)).

Paraptosis

Basics of paraptosis

Paraptosis is a form of PCD displaying mitochondria swelling and/or ER and cytoplasmic vacuolization [\[45,](#page-17-6) [46\]](#page-17-7). It difers from apoptosis in that it is not afected by caspase inhibitors or anti-apoptotic proteins such as Bcl2 [\[47](#page-17-8)]. Paraptosis is induced by insulin-like growth factor I receptor (IGF-IR) and suppressed by ALG-2-interacting protein (AIP1) (Fig. [1\)](#page-1-0). IGF-IR induced paraptosis is primarily mediated via mitogen-activated protein kinase (MAPK) family members.

No assay is so far available for paraptosis detection except for electron microscopy where the appearance of multiple single-membraned cytoplasmic vacuoles could be considered as a symbol of paraptosis [[48\]](#page-17-9).

Paraptosis in response to DNA damage imposed redox imbalance

Paraptosis could be induced through ER stress as a result of DNA damage signaling. Lots of studies have suggested the association of paraptosis with redox imbalance and accumulation of misfolded proteins in ER [[49,](#page-17-10) [50](#page-17-11)]. It was reported that ginger extract triggers cytoplasmic vacuolation, ER dilation, mitochondrial dysfunction, and DNA fragmentation in response to DNA damage induced ER stress that ultimately leads to paraptosis as a result of excess ROS generation [[51](#page-17-12)]. As a DNA damage response sensor, p53 was reported to suppress paraptosis through inhibiting IGF-IR and transactivating IGF-BP3 expression, whereas the binding of IGF-BP3 to IGFs suppresses IGF-IR signaling [[52,](#page-17-13) [53](#page-17-14)].

Clinical relevance of paraptosis in cancer treatment

Many natural compounds such as taxol, cyclosporine A, tunicamycin, procyanidins, curcumin, honokiol, ginsenosides, tocotrienols, celastrol, ophobiolin A, hesperidin,

Table 1 (continued)

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morusin, 6-shogaol, chalcomoracin, gambogic acid, plumbagin, 8-p-hdroxybenzoyl tovarol, cis-nerolidol, manumycin A, DL-selenocystine, 15-deoxy-Δ12,14-prostaglandin J2, yessotoxin and 1-desulfoyessotoxin have shown great promise and translational potential in triggering paraptosis in a variety of human cancer cell lines [\[54](#page-17-15)]. Among them, taxol [\[55](#page-17-16), [56](#page-17-17)] (for treating ovarian, breast, and lung cancers) and curcumin (for treating colorectal cancer) [\[54](#page-17-15)] have been commercialized for clinical use (Table [1\)](#page-3-0).

Mitotic catastrophe

Basics of mitotic catastrophe

Mitotic catastrophe is a form of PCD due to failed or incomplete mitosis, which is featured by chromosome breaks and poor karyokinesis [[57\]](#page-17-18). During mitosis, the CDK1/cyclin B1 complex promotes the G2/M cell cycle transition and plays essential roles in microtubule reorganization, chromatin condensation, and nuclear membrane breakdown [\[58](#page-17-19)] (Fig. [1](#page-1-0)). Over-activated CDK1 can lead to mitotic catastrophe [\[59](#page-17-20)]. Prolonged suppression of anaphase-promoting complex (APC) can result in mitotic catastrophe [[59\]](#page-17-20) as APC could degrade cyclin B to promote cells transit from the metaphase to anaphase [\[58](#page-17-19)].

Dis-functionalities of cell cycle checkpoint regulators are vital to initiate mitotic catastrophe. Inhibition of G2/M checkpoint regulators such as checkpoint kinase 1/2 (Chk1/2), ataxia telangiectasia mutated (ATM), ataxia telangiectasia mutated and Rad3 related (ATR) are known to induce mitotic catastrophe [\[60](#page-17-21), [61](#page-17-22)]. Chemotherapies such as 5-fuorouracil and doxorubicin were reported to trigger mitotic catastrophe through increasing cyclin B1 [[62](#page-17-23)]. CDK1 promotes mitotic catastrophe through inhibiting the phosphorylation of survivin, a protein that promotes mitotic progression and inhibits apoptosis [[63\]](#page-17-24).

Mitotic catastrophe has been conventionally detected via continuous observation under microscopy. An automated fuorescence videomicroscopy assay was developed for the real-time detection of mitotic catastrophe in a high-throughput fashion[\[64](#page-17-25)].

Mitotic catastrophe in response to DNA damage imposed redox imbalance

Mitotic catastrophe is triggered by DNA damage signals that can be sensed by p53. P53 is a gatekeeper of genome integrity and inhibits mitotic catastrophe through various pathways including, e.g., transcriptionally inhibiting CDK1 and cyclin B1 [[65,](#page-17-26) [66](#page-17-27)], and upregulating the expression of CDK1 inhibitors such as p21 [[67\]](#page-17-28). Thus, mitotic catastrophe occurs predominantly in p53-defcient cells as a result of genomic instability $[68]$ $[68]$ $[68]$. On the other hand, p53 may also play a promotive role in mitotic catastrophe as it could tran-scriptionally repress surviving [\[69\]](#page-17-30).

Clinical relevance of mitotic catastrophe in cancer treatment

Induction of mitotic catastrophe such as anti-mitotic agents has been implicated as an efficient strategy for cancer management. Microtubule destabilizers such as vinblastine [[70\]](#page-17-31) and vincristine [[71](#page-17-32)] have been used in the treatment of hematological malignancies; microtubule stabilizers such as taxanes drugs paclitaxel [[72](#page-17-33)] and docetaxel [[73\]](#page-17-34) have been applied in clinics for treating ovarian, breast cancer, peritoneal malignancy, and for treating breast cancer, ovarian cancer, and non-small cell lung cancer, respectively (Table [1\)](#page-3-0). Drugs taking advantages of mitotic catastrophe and are being under clinical trials include BI2536) for treating non-small cell lung cancer [[74\]](#page-17-35), ON01910) for treating chronic lymphocytic leukemia [[75\]](#page-17-36), and MK-1775) for the treatment of acute lymphoblastic leukemia and nasopharynx cancer [\[76](#page-17-37)] (Table [1\)](#page-3-0).

Programmed cell death associated with redox imbalance imposed by metabolic stress

Autophagic cell death

Basics of autophagic cell death

Autophagic cell death is a type of PCD as a result of autophagy [[45](#page-17-6)]. Autophagy is a regulated catabolic lysosomal-dependent process that facilitates cells to eliminate misfolded proteins, damaged or non-functional cellular components, etc. to maintain cellular homeostasis [[77\]](#page-17-38). When autophagy occurs, cytoplasmic contents are sequestered by phagophores to form autophagosomes that merge with lysosomes and form autophagolysomes to degrade engulfed materials, where ATG proteins and beclin-1 are well-known regulators of autophagy [[78](#page-17-39)] (Fig. [2\)](#page-12-0). Mammalian target of rapamycin (mTOR) can inhibit autophagy through suppressing ATG13 and ULK1 [[79](#page-17-40)], where the complex formed by ATG13, ULK1 and FIP200 plays essential roles in phagophore formation and autophagy [\[79](#page-17-40)]. Beclin-1 was shown to induce autophagic cell death by promoting autophagosome formation [[80\]](#page-17-41).

Autophagy is a self-protective phenomenon in response to cellular stress such as metabolic stress, whereas cells are committed to death if the cellular stress is irreversible. Autophagic cell death is featured by the presence of large intracellular

vesicles, membrane blebbing, enlarged organelles, and depletion of cytoplasmic organelles without chromatin condensation [\[81](#page-17-42)].

Autophagic cell death could be detected through direct autophagic activity measurement or indirect antibody (autophagy specifc) based analyses such as western blot, fuo-rescence microscopy and flow cytometry [\[82](#page-17-43)].

Autophagic cell death in response to metabolic stress associated redox imbalance

Metabolic stress is characterized by nutrient, oxygen and growth factor deprivation [\[83\]](#page-17-44). Autophagic cell death is regulated by the endocrine system on nutrient starvation that constitutes a primary source of metabolic stress in cancer cells. Specifcally, glucose concentration in malignant cells is estimated to be 3-to-10 folds lower than that in normal tissues [\[84,](#page-18-1) [85\]](#page-18-2). This nutrient defciency directly reduces ATP production and results in excess ROS generation [\[86](#page-18-3)].

In response to metabolic stress imposed redox imbalance, p53 plays dual roles in autophagic cell death depending on its cellular localization. While nuclear p53 promotes autophagy, cytoplasmic p53 suppresses it [\[87](#page-18-4)]. Nuclear p53 triggers autophagy by transactivating its target genes [\[87](#page-18-4), [88](#page-18-5)]. For example, nuclear p53 promotes autophagy through transactivating TSC2 and AMPK, both of which are upstream regulators of mTOR [\[88](#page-18-5), [89\]](#page-18-6). P53 can also upregulate the AMPK activators sestrins ½ [\[90\]](#page-18-7) and the autophagy activator DRAM [\[91\]](#page-18-8). Besides, apoptosis-associated genes under p53 regulation such as PUMA, BAX, Bnip3, and BAD are also involved in autophagy [\[92](#page-18-9)[–94](#page-18-10)]. On the other hand, cytoplasmic p53 suppresses autophagy through binding Beclin-1 that promotes its ubiquitination and degradation [\[95](#page-18-11)].

Clinical relevance of autophagic cell death in cancer treatment

Impaired autophagy has been associated with many diseases including human cancers [[96\]](#page-18-12). Inhibitors of autophagy such as chloroquine and hydroxychloroquine have been proposed for the treatment of multiple malignancies in clinics despite the questionable unresolved safety issues [[97\]](#page-18-13).

Clinical therapeutic strategies using autophagic cell death include everolimus [\[98](#page-18-14)] and CCI-779 [[99\]](#page-18-15) for the treatment of renal cell carcinoma, as well as vorinostat for treating cutaneous T-cell lymphoma [[100](#page-18-16)] (Table [1](#page-3-0)).

Ferroptosis

Basics of ferroptosis

Ferroptosis, an iron-dependent oxidative PCD, was frstly discovered in 2012 by Brent R. Stockwell et al. [[101\]](#page-18-17). Different from apoptosis, cells undergoing ferroptosis do not show cell shrinkage and chromatin agglutination, but exhibit increased lipid peroxidation, elevated ROS, shrinked mitochondria, increased mitochondria membrane density and decreased ridge amount. While inhibitors of cell apoptosis, autophagy, pyroptosis do not inhibit ferroptosis, this process can be suppressed by iron chelators, lipophilic antioxidants, lipid peroxidation inhibitors, and polyunsaturated fatty acid depletion [\[102\]](#page-18-18). Ferroptosis inducers such as erastin decreases cellular antioxidant capacity through acting on the glutathione peroxidase (GPXs) [[103\]](#page-18-19).

Essential ferroptosis suppressor genes have been identifed that can be used in ferroptosis detection. Glutathione peroxidase 4 (GPX4), an antioxidant defense enzyme, functions to repair lipid oxidative damage and plays a primary suppressive role in ferroptosis [\[104](#page-18-20), [105\]](#page-18-21). Ferroptosis suppressor protein 1 (FSP1) is a GSH-independent ferroptosis suppressor [\[106\]](#page-18-22) that co-operates with coenzyme Q10 [[107\]](#page-18-23) and acts in parallel with GPX4 to inhibit ferroptosis [\[108](#page-18-24)]. Several ferroptosis-promotive markers have also been reported. For example, acyl-CoA synthetase long-chain family member 4 (ACSL4) expression was remarkably lower in ferroptosis-resistant than -sensitive cells which, once knocked down, inhibited erastin-induced ferroptosis [\[109](#page-18-25)]. Other pro-ferroptosis factors include, e.g., cox-2, PTGS2, NOX1 [[110](#page-18-26)], and transferrin receptor 1 (TfR1) [[111\]](#page-18-27). The lethal accumulation of lipid peroxides in plasma membranes as characterized by ferroptosis makes it possible to detect ferroptosis through determining the amount of lipid peroxides in cellular membranes using BODIPY-C11 probe and flow cytometry $[112]$ $[112]$.

Ferroptosis has two primary pathways, i.e., the canonical GPX4-meidated GSH-dependent pathway and the newly identifed FSP1-meidated GSH-independent pathway.

GPX4‑mediated GSH‑dependent pathway When intracellular cystine transport proteins such as erastin are inhibited, intracellular GSH will be exhausted as a result of substrate shortage. This will eventually lead to the inactivation of GPX4, a GSH peroxidase and perhaps the only enzyme that catalyzes liposome peroxide reduction. When cellular redox level exceeds a certain threshold, this will result in lipid peroxidation accumulation that, ultimately, triggers cell ferroptosis [\[113](#page-18-29), [114](#page-18-30)] (Fig. [2\)](#page-12-0).

GPX4-mediated GSH-dependent ferroptosis can be initiated by directly eliminating GPX4 using inhibitors such as

Fig. 2 Graphic illustration on the crosstalk and diferences of 2 example metabolic disorder associated PCD events regarding the mechanism and phenotype

squalene synthase, HMG-CoA reductase, and RSL3 [[101\]](#page-18-17); inputting iron in the form of ferrous iron ions, or consuming GSH. Ferroptosis can also be triggered by inhibiting cystine/ glutamate antiporter, namely system x_c^- , which is a heterodimeric cell surface amino acid antiporter composed of the twelve-pass transmembrane transporter protein SLC7A11 (xCT) and the single-pass transmembrane regulatory protein SLC3A2 [[115](#page-18-31)]. System x_c [−] imports extracellular cysteine proteinase inhibitor 2 (Cys2) in exchange for intracellular GSH $[101, 116]$ $[101, 116]$ $[101, 116]$ $[101, 116]$. Through inhibiting system x_c^- , cysteine absorption is inhibited that leads to reduced GSH and GPX4 activity [\[117](#page-18-33)].

FSP1‑mediated GSH‑independent pathway FSP1 was recently identifed as a key component of a non-mitochondrial CoQ antioxidant system that acts in parallel to canonical GPX4-mediated GSH-dependent ferroptosis [[108\]](#page-18-24). In particular, FSP1 myristoylation allocates itself to the plasma membrane and lipid droplets where it reduces coenzyme Q10 (CoQ10) via functioning as an oxidoreductase, and this results in the generation of a lipophilic radical-trapping antioxidant (RTA) that ultimately halts lipid peroxide propagation (Fig. [2\)](#page-12-0).

Ferroptosis in response to metabolic stress associated redox imbalance

Lipid peroxidation is initiated as a result of chain oxidation of unsaturated lipids due to excess ROS accumulation and represents a lipid metabolic disorder [\[118](#page-18-34), [119\]](#page-18-35). Metabolic stress, in turn, hampers the homoeostasis between fatty acids synthesis and uptake [\[120,](#page-18-36) [121\]](#page-18-37).

The tumor suppressor p53 senses metabolic disorder associated redox stress [[122](#page-18-38)] and triggers ferroptosis through p53-mediated suppression on system x_c^- . By exposing p53-defcient H1299 cells to ROS, cell viability did not alter; yet cells carrying the wildtype p53 underwent

a mortality rate as high as 90% under ROS stress; by treating cells with ferrostatin 1 (a ferroptosis inhibitor), the mortality rate of cells dropped about 40% [\[123](#page-18-39)], suggesting the role of p53 played in ferroptosis and ROS stress response. The same study also reported a negative correlation between p53 and SLC7A11 [[123\]](#page-18-39), implicating that SLC7A11, a core component of system x_c^- , is a p53 target.

Clinical relevance of ferroptosis in cancer treatment

Erastin, the earliest discovered inhibitor, can efectively inhibit the growth of ovarian tumors cells in mice [[124](#page-18-40)]. Glutathione synthetase inhibitors such as L-Buthioninesulfoximine (L-BSO) can inhibit breast tumor growth in mice via suppressing GSH formation and thus triggering ferroptosis [[125](#page-18-41)]. Ferroptosis has also been applied in cancer diagnosis. For instance, a paper published in 2020 identifed a ferroptosis gene panel composed of 8 genes (ALOX5, CISD1, FTL, CD44, FANCD2, NFE2L2, SLC1A5, GOT1) that is diagnostic of low-grade glioma [[126\]](#page-18-42).

Cisplatin has been applied in clinics for treating solid tumors through triggering ferroptosis [[127\]](#page-18-43) (Table [1](#page-3-0)). Sorafenib [[128](#page-18-44)], sulfasalazine [\[129](#page-18-0)] and ferumoxytol [[130\]](#page-18-45) have been approved by FDA for the treatment of renal cell carcinoma and hepatocellular carcinoma, for the treatment of pancreatic cancer, and for the treatment of leukemia, respectively (Table [1\)](#page-3-0).

Programmed cell death associated with redox imbalance imposed by infammation

Necroptosis

Basics of necroptosis

Necroptosis is a programmed form of necrosis that is characterized by permeable and rupture of cell membranes, numerous cytoplasmic vacuoles containing cellular remnants, and infammation [\[131](#page-18-46)[–133\]](#page-18-47). It is also accompanied with moderate chromatin condensation and clumping, as well as random DNA degradation [[131–](#page-18-46)[133](#page-18-47)].

Necroptosis is initiated by the binding of tumor necrosis factor (TNF) or FAS to their receptors that promotes interactions between RIPK1 and RIPK3 [[134,](#page-19-1) [135\]](#page-19-2), followed by activation of these kinases that recruits MLKL to form the necrosome [[136\]](#page-19-3) (Fig. [3](#page-14-0)). RIPK3 phosphorylates MLKL at threonine 357 and serine 358 to enhance its oligomerization; and then MLKL oligomers are translocated from the cytosol to cell membranes to disrupt membrane integrity, triggering necroptosis [[137](#page-19-4)].

Necroptosis can be detected by examining the loss of membrane integrity through the use of cell-impermeable DNA binding dyes, measuring the release of cellular contents such as LDH, HMGB1 and cyclophilin A via western blot, evaluating mitochondrial potential by fuorescent probes, and observing necroptosis morphology features through electron microscopy [\[138\]](#page-19-5). Alternatively, necroptosis can be detected with the aid of necroptosis specifc inhibitors such as necrostatin-1 [[139\]](#page-19-6).

Necroptosis in response to infammation associated redox imbalance

Infammation and oxidative stress are interconnected. It was shown that infammatory macrophages release proteins in the glutathionylated form such as PRDX2 [[140](#page-19-7)]. Extracellular PRDX2 mediates infammation in a redox-dependent manner through the release of TNF α , a primary tumor necrosis factor involved in infammation, from macrophages [\[140\]](#page-19-7).

In response to infammation associated oxidative stress, p53 is accumulated in the mitochondrial matrix that enhances the opening of mitochondrial permeability transition pore (PTP) via direct binding of p53 with a PTP regulator cyclophilin D (cypD), and this leads to mitochondrial swelling and necroptosis induction [\[141](#page-19-8)]. Besides, p53 transcriptionally upregulates the lncRNA NRF (necrosis-related factor) that enhances PIRK1/PIRK3 translation via repressing miR-873, and elevated RIPK1/RIPK3 is a direct trigger of necroptosis [[142\]](#page-19-9).

Clinical relevance of necroptosis in cancer treatment

Triggering necroptosis has been recently proposed as a novel onco-therapeutic strategy, with the feasibility still being controversial. Conventional necroptosis inducers or chemotherapeutic agents can trigger necrosis in many cancer cells especially colorectal cancers and hematopoietic tumors such as leukemia and multiple myeloma [[143\]](#page-19-10). Traditional chemotherapy and molecular targeted drugs such as VEGFR inhibitors and m-TOR inhibitors have recently been identifed as cancer necroptosis triggers and approved for clinical trials [\[144](#page-19-11), [145\]](#page-19-12).

Natural products such as shikonin have been shown capable of triggering necroptosis and used in clinics for bladder cancer treatment [[146\]](#page-19-0). Pazopanib [\[147](#page-19-13)] and ponatinib $[148]$ $[148]$ have received FDA approval for treating advanced renal cell carcinoma and soft-tissue sarcoma, and for treating chronic myeloid leukemia. respectively (Table [1](#page-3-0)).

Pyroptosis

Basics of pyroptosis

Pyroptosis is another proinfammatory form of PCD that relies on the enzymatic activity of infammatory proteases belonging to the cysteine-dependent aspartate-specifc protease (caspase) family [\[149\]](#page-19-15). Destructed cell membrane structure integrity and release of intracellular substances into the extracellular space are the most notable features of pyroptosis. With the activation of caspases-1, ostioles are formed on cell membrane that leads to the outfow of intracellular contents including pro-infammatory cytokines, intracellular ions, endogenous ligands, alarmins etc., and fnally contributes to cell dissolvement. This feature is similar with caspase-independent PCD such as necroptosis, yet difers signifcantly from apoptosis that maintains intact cell membrane structure.

Both pyroptosis and necroptosis form pores on the cell membrane surface whereas apoptosis does not. Necroptosis is more like a burst of cells, and cells undergoing pyroptosis become tabular as a result of cytoplasm leak to the extracellular space. Both necroptosis and pyroptosis require the oligomerization and transfer of their execution proteins to the plasma membrane. However, during necroptosis, mixed lineage kinase domain like pseudokinase (MLKL) triggers specific ion influx through inducing the ion selective channel, which leads to cell osmotic swelling and burst; during pyroptosis, gasdermin D (GSDMD) forms holes that lack ion specifcity and selectivity, and this does not lead to increased intracellular osmotic pressure nor consequent cell infate or burst [\[150](#page-19-16)].

Pyroptosis can be detected via western blot using antibodies against GSDMD (53 Kd) that is cut into 30 Kd pieces during pyroptosis [\[151\]](#page-19-17). It can also be assayed through ELISA by detecting IL-1β and IL-18 that are released into cells when pyroptosis occurs [[149\]](#page-19-15). Pyroptosis can also be detected through detecting the activity of caspase-1 and caspase-4 using the corresponding kits based on spectrophotometry [[151\]](#page-19-17).

Pyroptosis can occur via canonical caspase-1 dependent pyroptosis or non-canonical caspase-1 independent pyroptosis.

Caspase-1 dependent pyroptosis In response to pathogen associated molecular patterns (PAMPs) such as viral pathogens toxins, bacteria, parasites, etc. and danger associated molecular patterns (DAMPs) such as uric acid sodium and silicon dioxide, pattern recognition receptors (PRRs) are triggered to activate caspase-1 (Fig. [3](#page-14-0)). PRRs can be categorized into two classes based on cellular localization. While C-type lectin receptors (CLRs) and Toll-like receptors (TLRs) are present on cell membranes to sense exter-

Fig. 3 Graphic illustration on the crosstalk and diferences of 2 example infammation associated PCD events regarding the mechanism and phenotype

nal stimuli, the nucleotide-binding domain and leucine-rich repeat-containing (NLR) proteins, the AIM2-like receptor (ALR), RIG-I-like receptor (RLR) are localized inside the cell to detect signals issued by PAMPs or DAMPs [[152\]](#page-19-18).

The canonical infammasome or namely pyroptosome that participates in the caspase-1-dependent pathway is composed of apoptosis-associated speck-like protein (ASCs), PRRs such as NLRs and ALRs, and procaspase-1 [[153](#page-19-19)]. ASCs contain a caspase-activation and recruitment domain (CARD) and are recruited by NLRs/ALRs to form a complex called 'SPECK' that takes on the most important function of pyroptosome, i.e., activating caspase-1 [\[153,](#page-19-19) [154\]](#page-19-20). The NLR family is further divided into NLR family PYD-containing protein (NLRP) and NLR family CARD-containing protein (NLRC) receptors based on diferences in the N-terminal domain composition [[153](#page-19-19)]. Among all NLR family members, NLRP1, NLRP3, NLRC4 are the most intensively studied in pyroptosis, where NLRP3 relies on ASC to recruit procaspase-1, and NLRP1 and NLRC4 do not [\[155](#page-19-21)].

Caspase‑1 independent pyroptosis The non-canonical caspase-1 independent pathway is primarily induced by caspase-4/5/11 other than caspase-1. Similar with caspase-1, caspase-4/5/11 also harbor the CARD domain at the N terminal. Caspase-4/5/11 directly interact with lipopolysaccharide (LPS) to form non-canonical pyroptosome that directly lyses the substrate and triggers pyroptosis [[156\]](#page-19-22) (Fig. [3](#page-14-0)). Activated caspase-11 can induce the formation of cell membrane pores through GSDMD cleavage, and the produced N terminus can also activate caspase-1 [[157\]](#page-19-23), rendering caspase-11 another trigger of caspase-1 activation and bridging the gap between canonical caspase-1 dependent and noncanonical caspase-1 independent pathways. Caspase-4 and 5 are crucial in caspase-1-independent pyroptosis in humans. While caspase-4 self-activates through direct interactions with LPS, caspase-5 is specifically regulated by IFN– γ and LPS [\[158](#page-19-24), [159](#page-19-25)].

Caspase-3 has also been reported capable of mediating pyroptosis (Fig. [3B](#page-14-0)). As caspase-3 is both an executioner of apoptosis and an upstream regulator of pyroptosis [[150,](#page-19-16) [160\]](#page-19-26), pyroptosis and apoptosis are interconnected. In response to TNF-α or chemotherapeutic agents, GSDME is directly cleaved by caspase-3, and the produced GSDME-N fragment takes on a similar function as the activated GSDMD to penetrate cell membrane and trigger pyroptosis [[161\]](#page-19-27).

Much more details of non-canonical caspase-1 independent pyroptosis still await to be deciphered.

Pyroptosis in response to infammation associated redox imbalance

Pyroptosis is typically triggered on pathogen invasion such as viruses, bacteria and parasites [\[162](#page-19-28)]. ROS play essential roles in host immune defenses against pathogen invasion [\[163,](#page-19-29) [164](#page-19-30)]. Apart from toxic molecules expressed by pathogens, excessive ROS production by activated immune cells on pathogen invasion creates cytotoxic signals that can be sensed by p53 [[163](#page-19-29)[–165\]](#page-19-31). The p53 protein plays essential roles in pyroptosis through up-regulating caspase-1 [\[166,](#page-19-32) [167](#page-19-33)].

Clinical relevance of pyroptosis in cancer treatment

It has been proved that ZnO nanoparticles (ZnO-NPs), ivermectin, etc., and some chemotherapy drugs can all induce pyroptosis in tumor cells. Specifcally, high concentrations of ZnO-NPs can activate pyroptosis in lung cancer cells [[168\]](#page-19-34).

Drugs capable of triggering pyroptosis and applied in clinics include ivermectin for the treatment of breast cancer [169], α -NETA for the treatment of ovarian [[170\]](#page-19-36), and cisplatin for treating solid tumors [\[171](#page-19-37)], respectively (Table [1](#page-3-0)).

Cold atmospheric plasma being redox level controller

Cold atmospheric plasma (CAP), being the fourth state of matter, is composed of ions, electrons, neutral particles and photons [[172](#page-19-38), [173](#page-19-39)]. It is featured by its multimodality nature, with the anti-cancer efficacy being firstly reported in 2007 [\[174](#page-19-40)]. Though the underlying mechanism is not fully understood, it has been widely accepted that the selectivity of CAP against cancer cells relies on its roles in modulating cellular redox level [[1\]](#page-16-0). By tuning cell oxidative level, CAP could make malignant cells more easily exceed the cell death threshold without breaking the redox homeostasis of normal cells [[175\]](#page-19-41). Cancer cells have higher baseline ROS levels than healthy cells and are thus more sensitive to elevated ROS production and turnover on CAP treatment. The exceeding of the anti-oxidant capacity in cancer cells forced them undergoing various PCD programs with apoptosis being the most intensively studied [[172](#page-19-38), [173](#page-19-39)]. Specifically, interactions between H_2O_2 and $NO₂$ (components that stably exist in CAP-activated medium) generate peroxynitrite (ONOO−) that can be protonated to peroxynitrous acid (ONOOH) when approaching membrane-associated proton pumps, and decomposed into $\cdot NO_2$ and $\cdot OH$ radicals; $\cdot OH$ reacts with H_2O_2 to generate peroxynitric acid (O_2NOOH) and peroxynitrate $(O₂NOO⁻)$ that lead to the generation of primary singlet oxygen (${}^{1}O_{2}$); primary ${}^{1}O_{2}$ triggers the production of high concentrations of secondary ${}^{1}O_{2}$, with $H_{2}O_{2}$ and ONOO being the source for sustained secondary ${}^{1}O_{2}$ generation, inactivates the protective membrane-associated catalase in tumor cells, and promotes aquaporin-mediated infux of extracellular H_2O_2 , all of which ultimately initiate redox imbalance triggered apoptosis [\[1,](#page-16-0) [176](#page-19-42), [177](#page-19-43)].

P53 is a pivotal switch controlling cells' fate towards diferent PCD programs [[178](#page-19-44)] in response to redox imbalance as a result of various stimuli including DNA damage signal, metabolic stress, and infammation (Fig. [4](#page-15-0)). Thus, these diverse types of PCD events are interconnected via this shared controller. Through gene expression profling and downstream functional studies, CAP was found to be able to activate the expression of p53 pathway-related genes [[179](#page-19-45)], rendering CAP a potential modulator of cells' life/death fate [[1](#page-16-0)] that is of critical clinical relevance if applied in cancer treatment.

On the other hand, one stimulus may potentially trigger multiple PCD events. For instance, ivermectin could simultaneously trigger pyroptosis, apoptosis and necroptosis in MDA-MB-231 cells through generating ROS, activating cytoplasmic calcium/calmodulin kinase II (CaMK II), opening mitochondrial permeability transition pore (MPTP) and forming caspase-1 mediated NLRP3 infammatory corpuscle [[180](#page-20-5)]. Therefore, CAP-induced selectivity against cancer cells may be resulted from multiple PCD programs far beyond just apoptosis that deserves intensive investigations.

Conclusion

PCD events are fundamental to the maintenance of cell redox homeostasis, normal tissue development and human health. Signals triggering redox imbalance and consequently PCD might be originated from DNA damage signaling such as in apoptosis, paraptosis and mitotic catastrophe, might be from metabolic disorder such as in autophagic cell death and ferroptosis, and might be from infammation such as in necroptosis and pyroptosis. As uncontrolled cell proliferation,

Fig. 4 Conceptual illustration on CAP being a redox controller in resembling various stress signals in the trigger of varied PCD events via p53

metabolic reprogramming and tumor-associated infammation are essential cancer hallmarks, disordered PCD events as a result of disrupted redox homeostasis are essential for cells to become malignant that, once being under control, might push chaotic cells towards the death state or rewire them towards the healthy state.

CAP could generate and deliver controlled doses of reactive species to cells that selectively triggers redox imbalance in malignant cells. Thus, CAP represents a promising onco-therapeutic approach, alone or being combined with other therapeutic strategies, through selectively inducing PCD events in cancer cells that is not limited to apoptosis. With our incremental understandings on varied types of PCD, underlying mechanism and associated disorders, it is the time to explore other CAP-triggered PCD events beyond apoptosis. Importantly, these PCD events orchestrate the selectivity of CAP against cancer cells through cross-talking due to, e.g., the shared regulator $p53$. Thus, the efficacy of CAP as a redox controller and an emerging onco-therapeutic strategy is a synergistic result from multiple PCD events that relies on appropriate dosing. Deciphering the precise mechanism underlying the efficacy of CAP against a particular type of cancer type and ultimately translating it into clinics require intensive eforts from both bench and bed sides and involve experts from multiple research domains such as biology, chemistry, physics, bioinformatics, materials and medicine.

Author contributions X.F. Dai initiated this project and drafted the manuscript. D.J. Wang helped in literature searching, fgure drafting and table preparation. J.Y. Zhang and X.F. Dai fnanced this project. All authors have read and approved the submission of this paper.

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Declarations

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