

Chromosomal DNA fragmentation in apoptosis and necrosis induced by oxidative stress

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Abstract

Chromosomal DNA dysfunction plays a role in mammalian cell death. Oxidative stress producing reactive oxygen species (ROS) induces chromatin dysfunction such as single- and double-strand DNA fragmentation leading to cell death through apoptosis or necrosis. More than 1 Mbp giant DNA, 200–800 or 50–300 kbp high molecular weight (HMW) DNA and internucleosomal DNA fragments are produced by oxidative stress and by some agents producing ROS during apoptosis or necrosis in several types of mammalian cells. Some nucleases involved in the chromosomal DNA fragmentation in apoptosis or necrosis are classified. ROS-mediated DNA fragmentation is caused and enhanced by polyunsaturated fatty acids (PUFAs) or their hydroperoxides through lipid peroxidation. A reduction of intracellular GSH levels induced by the inhibition of cysteine transport or GSH biosynthesis leads to cell death through over production and accumulation of ROS in some types of mammalian cells. The ROS accumulation system has been used as a model of oxidative stress to discuss whether ROS-mediated DNA fragmentation associated with cell death is based on apoptosis or necrosis.

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Keywords: Apoptosis; Endonucleases; Giant DNA fragmentation; GSH depletion; Necrosis; Oxidative stress

1. Introduction

Cellular genomes are continually subjected to endogenous and environmentally-induced structural alterations. Our environment contains a multitude of substances which are carcinogenic and which, in many cases, are thought to act *via* direct damage to DNA. Such damage can manifest itself as gross chromosomal abnormalities inducing cell death. Cell death arises solely as a consequence of pathological processes, but it is now recognized that the death of certain cells is a physiological phenomenon necessary for normal development, maintenance of tissue shape and cell

renewal. Although the classification of cell death has proven difficult, two distinct patterns of cell death have been identified based on the morphology of dying cells, and on the DNA fragmentation or damage. These have been termed necrosis and apoptosis [1]. Mammalian cell death is induced through chromosomal DNA damage by ionizing radiation, ultraviolet (UV) radiation, anticancer drugs and various triggers of apoptosis.

ROS such as hydrogen peroxide (H_2O_2), hydroxyl radicals ($\bullet\text{OH}$) and superoxide anions (O_2^-) have been shown to damage chromosomal DNA and other cellular components, resulting in DNA degradation, protein denaturation, and lipid peroxidation. However, the mechanisms behind these cellular effects are rather complex, and are not yet fully understood. DNA damage induced by oxygen radicals occurs by oxidative nucleic acid base modification and scission of DNA strands. Most agents producing ROS induce cell death including apoptosis, by causing lipid peroxidation and DNA damage [2]. However, the implications of lipid peroxidation for ROS-induced DNA damage remain to be elucidated. There is a recent research review suggesting that amyloid β -peptide is heavily deposited in

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Abbreviations: AIF, apoptosis-inducing factor; BSO, L-buthionine-(S,R)-sulfoximine; CAD, caspase-activated DNase; DFF, DNA fragmentation factor; GSH, reduced glutathione; GSSG, oxidized glutathione; L, lipid radical; LO, lipid alkoxyl radical; LOO, lipid peroxy radical; 8-OH-dG, 8-hydroxy-2'-deoxyguanosine; HMW, high molecular weight; PARP, poly(ADP-ribose) polymerase; PUFA, polyunsaturated fatty acid; ROS, reactive oxygen species; TUNEL, terminal deoxynucleotidyl transferase-mediated dUTP-biotin nick end-labeling.

the brains of Alzheimer's disease patients, and free radical oxidative stress, particularly of neuronal lipids and proteins, is extensive [3].

Our purpose is to review the chromosomal DNA fragmentations such as giant DNA, HMW DNA, and internucleosomal DNA fragmentations and to reflect upon their significance in the cell death induced by oxidative stress.

2. Chromatin structure and pattern of chromosomal DNA fragmentation

A mammalian cell nucleus contains almost 50 cm of DNA requiring more than a 50,000-fold reduction in length to fit in the nucleus and nuclear matrix. The nuclear matrix is an important structural component in a variety of nuclear functions and nuclear morphology, including DNA organization, DNA replication, RNA synthesis and nuclear regulation. DNA loop domains of chromatin are attached to the nuclear matrix at their base and this organization is maintained throughout both interphase and metaphase. These loops are 50–150 kbp long and are equivalent in size to the replicon [4]. The haploid human genome contains 3000 megabase pairs (Mbp) of DNA with a mean chromosomal size of 130 Mbp.

Chromosomal DNA fragmentation is caused by two types of DNA breaks that are classified into single- and double-strand DNA breaks. Single-strand cleavage of DNA has been suggested to occur during apoptosis. At the level of the nuclear scaffold, single-strand DNA breaks were detected in HL-60 cells treated with camptothecin, a topoisomerase I inhibitor and inducer of apoptosis, but these were rapidly repaired after drug removal [5]. Internucleosomal DNA cleavage occurred after the repair of these single-strand cuts, suggesting that single-strand breaks at higher levels of DNA organization may not play an active role during apoptosis but can perhaps act as signals to induce the process. Clearly the role that single-stranded DNA breaks play during apoptosis requires additional studies. Double-strand DNA breaks are generally thought to have a greater biological consequence than single-strand DNA breaks because they can lead directly to chromosomal aberrations, and more frequently to the loss of genetic information [6]. Double-strand DNA breaks are 20 times less frequent than single-strand DNA breaks and are more difficult to measure at physiological doses. The application of gel electrophoresis to the measurement of double-strand DNA breaks has been described by some workers [7].

Chromosomal DNA fragments of more than 1 Mbp in size are double-strand DNA breaks and are classified as giant DNA fragments. DNA degradation accompanied by DNA fragmentation producing 1–2 Mbp and 200–800 kbp DNA fragments were observed during cell death in cells treated with some agents that can produce ROS [2,8], or under GSH depletion [9]. Chromosomal DNA fragments which are 200–800 and 50–300 kbp in size are called HMW

DNA fragments. The 1–2 Mbp giant DNA and 200–800 kbp HMW fragmentations that may represent features of high-order chromatin structure such as minibands and loops of DNA [10], lead to apoptosis ascertained by internucleosomal DNA fragmentation [11]. However, little is known about the mechanism of giant DNA and HMW DNA fragmentation during apoptosis induced by ROS.

3. Reactive oxygen species (ROS)-mediated chromosomal DNA fragmentation

DNA damage caused by ROS *in vivo* or in cultured cell systems is classified into DNA cleavages such as single-strand breaks, and double-strand breaks and nucleotide base oxidative modifications [12]. We know a little about the *in vivo* action mechanism of ROS produced by anticancer drugs, ionizing radiations and ultraviolet (UV) ray on chromatin DNA in the nuclei of cells. Ionizing radiation such as X-rays and γ -rays are, in general, thought to produce hydroxyl radicals from water molecules in or around the target sites in the DNA, and these in turn attack DNA and break it down [13]. The reaction of intracellular ROS with DNA results in numerous forms of base damage, and 8-hydroxy-2'-deoxyguanosine (8-OH-dG) is one of most abundant and the most studied lesions generated [14]. In addition, the involvement of ROS in the induction of apoptosis has been suggested in several cell lines [11,15,16].

Using pulsed-field gel electrophoresis, some groups have reported the size distribution of radiation-induced DNA fragments in mammalian cells such as Chinese hamster ovary cells [17] and L-1210 mouse leukemia cells [18]. In L-1210 cells irradiated at 1–50 Gy, double-strand DNA break fragments, calculated from marker chromosomes to be in the range of 0.1–12.6 Mbp, have been demonstrated [18]. In another X-ray irradiation study on T-24 human bladder carcinoma cells, similar DNA fragments to the DNA fragments found in the X-ray irradiated L-1210 cells were observed in the 1–2 Mbp but not the 0.1–1 Mbp range [2]. Giant DNA and HMW DNA fragments ranging from 100 kbp to 10 Mbp are distinctly produced by X-ray irradiation (Table 1). 1–2 Mbp giant and 200–800 kbp HMW DNA fragmentations prior to internucleosomal DNA fragmentation are caused by H_2O_2 [2,8]. All portions of the UV spectrum alone are capable of inducing the active oxygen-mediated formation of 8-OH-dG. UV radiation may generate ROS, which consequently induce DNA damage [19] including giant DNA fragmentation. However, the actual identities of ROS involved in UV radiation-induced oxidative DNA damage are still uncertain.

Some antibiotics that possess quinone moieties as part of their chemical structures are widely used as a drug to treat various human cancers. Most of these drugs produce ROS at various cellular sites *in vivo* [20–23]. Neocarzinostatin and bleomycin, both of which are anticancer drugs generating ROS *in vivo*, produce not only 1–2 Mbp and

Table 1
DNA fragmentation induced by oxidative stress and various agents in various cell types

Treatment	Cell type	Giant DNA (bp)	HMW DNA (bp)	Ladder DNA ^a	References
Ionizing radiation					
X-ray					
~50 Gy	L-1210 (mouse leukemia)	0.1–10 M		ND	[18]
1.5–12 Gy	EMT-6 (methotrexate-resistant)	3 M		ND	[76]
20–100 Gy	T-24 (human bladder carcinoma)	1–2 M	200–800 k	+	[2]
γ-Ray	HT-29 (colon adenocarcinoma)	~10 M, 2 M		ND	[25]
Ultraviolet C	T-24	1–2 M	100–800 k	+	[77]
Hydrogen peroxide					
>5 mM	T-24	1–2 M	200–800 k	–	[2]
1–5 mM	T-24	1–2 M	200–800 k	+	[2]
	U-937 (human myeloid leukemia)		50–500 k	+	[30]
1 mM	U-937	1–3 M	200–300 k	ND	[33]
GSH depletion					
Glutamate/BSO	C6 (rat glioma)	1–2 M	200–800 k, <50 k	+	[9,11]
Anticancer drugs					
BLM	Du145 (prostatic carcinoma)	>1 M	450–600 k, 30–50 k	+	[31]
	T-24	1–2 M	200–800 k	+	[2]
Neocarzinostatin	T-24	1–2 M		+	[2]
5-FdUrd	HT-29	~10 M, 2 M	200–800 k	–	[25]
Duocarmycins	HeLa (human uterine cervix carcinoma)	1–2 M	200–800 k	ND	[24]
Topoisomerase inhibitors					
VM-26	Thymocytes	800 k ~1 M,	200–600 k, <100 k	+	[32]
	U-937		50–100 k	+	[78]
mAMSA	Thymocytes	700 k ~1 M	30–80 k	+	[32]
	HeLa	1–2 M	900 k	ND	[24]
V-16 (etoposide)	Du145	>1 M	450–600 k, 30–50 k	+	[31]
	MCF-7 (breast adenocarcinoma)		50 k	+	[44]
	U-937	1–3 M	200–300 k	ND	[33]
TAS-103 ^b	HL-60 (human leukemia)	1–2 M	~50 k	+	[34]

ND: not determined.

^a Indicates internucleosomal DNA fragment and plus (+) is positive.

^b TAS-103 is 6-[[2-(dimethylamino)ethyl]amino]-3-hydroxy-7*H*-indeno[2,1-*c*] quinolin-7-one dihydrochloride.

200–800 kbp DNA fragments but also apoptotic internucleosomal DNA fragments during cell death (Table 1). Although DNA-crosslinking agents and mitotic inhibitors do not induce DNA fragmentation [24], 5-fluoro-2-deoxyuridine (5-FdUrd), an inhibitor of DNA synthesis, causes both giant DNA and HMW DNA fragmentations [25]. Cellular DNA cleavage into HMW DNA fragments during apoptosis is highly reminiscent of topoisomerase II-mediated HMW DNA fragmentation in cells [26,27]. In fact, the pattern of HMW DNA fragmentation by topoisomerase II poison, and that produced in apoptotic cells induced by other stimuli, is found to be similar [28]. However, the relationship between topoisomerase II and the excision of chromosomal loops during apoptotic cell death is still unclear. A major function of topoisomerase II is to regulate the topological state of DNA replication and chromosome condensation and segregation through its delicate act of breaking/rejoining DNA strands [27]. Recently, several new mechanisms including DNA structural modifications, enzyme modifications, oxidative stress and acidic pH environment have also been shown to activate topoisomerase II-mediated DNA cleavage [29,30]. Topoisomerase II inhibitors such as VM-26,

etoposide and TAS-103 also produced 1–3 Mbp or 800 kbp–1 Mbp giant DNA fragments together with 200–600 kbp and less than 100 kbp DNA fragments in thymocytes, Du145 human prostatic carcinoma cells, U937 human myeloid leukemia cells and HL-60 human leukemia cells [30–34]. Furthermore, although DNA damage caused by exogenously added ROS appears to activate apoptosis, it is important to elucidate the roles of ROS in the apoptosis. However, not only the mode of action of ROS but also the roles of such chromosomal giant DNA degradation remains to be elucidated.

4. Chromosomal DNA fragmentation in apoptosis or necrosis

Apoptosis and necrosis are two distinct forms of cell death that have profoundly different implications for the surrounding tissues. Apoptosis is characterized by chromatin condensation, activation of some caspases and fragmentation of DNA at internucleosomal linker sites giving rise to discrete bands of multiples of 180–200 bp [35]. This form of DNA degradation has been very widely observed in

apoptosis, although exceptions do exist. Different types of DNA fragmentation have been reported during apoptosis, in the presence or absence of the characteristic internucleosomal DNA cleavage (ladder-like) pattern. These enzymatic events encompass a vast array of chromosomal degradation states in the cell with the ultimate common consequence being cell death [36]. In contrast, necrosis is a passive process, typified by cell and organelle swelling with spillage of the intracellular contents into the extra cellular milieu. Necrosis is an uncontrolled event resulting from the loss of homeostasis and the cell contents which are dispersed, may then have adverse effects on neighboring tissues [37]. There have been some recent reports on apoptosis and necrosis caused under various conditions, including oxidative stress in some neuronal cells such as hippocampal neurons [38], cortical cell cultures [39], neonatal rat brain [40] and HT-22 hippocampus-derived cells [41].

One of the hallmarks of apoptosis is the digestion of genomic DNA by an endonuclease, generating a ladder of small fragments of double-stranded DNA. Single-strand nicks were found to be very frequent in the internucleosomal regions, but also to occur in the core particle-associated DNA. DNA fragmentation induced during apoptosis is not due to a double-strand cutting enzyme as previously postulated, but rather is the result of single-strand breaks. This ensures the dissociation of the DNA molecule at sites where cuts are found within close proximity [42]. There is a two-step process of DNA fragmentation in apoptosis: DNA is first cleaved into large fragments of 50–300 kbp that are subsequently cleaved into smaller oligonucleosomes in some, but not all cells. Significantly, only the first stage is considered essential for cell death since some cells, for example human MCF-7 breast carcinoma cells and human NT-2 neuronal cells, do not show this behavior but still display normal nuclear morphological apoptotic changes.

Some inducers of apoptosis such as etoposide and glucocorticoids have provided formations of 50–300 kbp HMW DNA fragments prior to internucleosomal DNA fragmentation [43] in apoptotic MCF-7 cells induced by etoposide [44], and in mouse L-929 cells induced by tumor necrosis factor (TNF- α) [26]. These DNA fragment formations have been observed in several human epithelial cells induced by serum deprivation [43], and in HeLa nuclei treated with apoptosis-inducing factor (AIF) [45]. Apoptosis has also been widely observed in some cells treated with anticancer drugs [46], and other cell death processes induced by some biological events such as depletion of nutrients [47]. However, little has been reported about the involvement of not only 1–2 Mbp giant DNA fragmentation but also HMW DNA fragmentation to 100–800 and 50–300 kbp fragments and their significance or roles in apoptosis. In some cases of apoptosis, ROS may be involved not only as inducers of DNA damage but also as specific second messengers in the signal transduction pathway, whereas in others they may be side effects of

either the experimental system or changes in the cellular redox status as a result of ROS-independent apoptosis signaling pathways [48]. Therefore, it is still unclear whether endogenous ROS are really involved in DNA degradation leading to apoptosis.

5. Nucleases involved in DNA fragmentation

In apoptosis, internucleosomal DNA degradation in which some endonucleases are involved has been observed [49] and several studies on the enzyme activation process are in progress [50,51]. Cells may also detach parts of their cytoplasm, which sometimes includes highly condensed fragments of the karyorrhectic nucleus. The dying cells also activate catabolic enzymes that ensure digestion of critical cellular components from the inside. Such catabolic hydrolases include a class of specific protein-cleaving enzymes (caspases), as well as DNA-digesting enzymes (DNases), both of which participate directly or indirectly in nuclear pyknosis [51]. This DNase sensitivity is specific to the chromosomal regions (Fig. 1). The single-strand-specific nuclease, DNase I, is thought to be specific for some type of DNA structure. Recently, a new type of endonuclease involved in apoptosis has been reported. This nuclease is endonuclease G, a mitochondrion-specific nuclease that translocates to the nucleus during apoptosis. Endonuclease G cleaves chromatin DNA into nucleosomal fragments independently of caspases [52]. Sahara *et al.* [53] have suggested that caspase-3 cleaves Acinus, which is the precursor of a chromatin condensation factor. Another chromatin condensation factor, caspase-activated DNase (CAD) [54], for example, uses its DNase activity to cleave chromatin at the boundaries between nucleosomes. In this way, CAD generates stretches of DNA about 200 bp long or multiples thereof. A few proteins responsible for caspase-independent chromatin condensation have, in fact, been identified. AIF is a flavoprotein that is normally confined to the space between the outer and inner mitochondrial membranes [45]. AIF translocates from the mitochondrion to the nucleus, where it causes partial chromatin condensation in the periphery of the nucleus. AIF causes degradation of DNA into fragments greater than around 50 kbp in length. Another chromatin condensation factor, which translocates from the cytoplasm to the nucleus, is L-DNase II. When added to isolated nuclei, L-DNase II causes marked chromatin condensation and cleaves the chromatin into nucleosome-sized fragments. Yet other proteins that might contribute to chromatin condensation and internucleosomal DNA fragmentation are endonuclease- γ [55] and cathepsin B [54]. These proteins could be activated on their release from the lysosomes of apoptotic cells.

The TUNEL assay has been used to label the 3' ends of nicked or fragmented DNA in apoptosis using [14-biotin]-dCTP and terminal deoxynucleotide transferase enzyme.

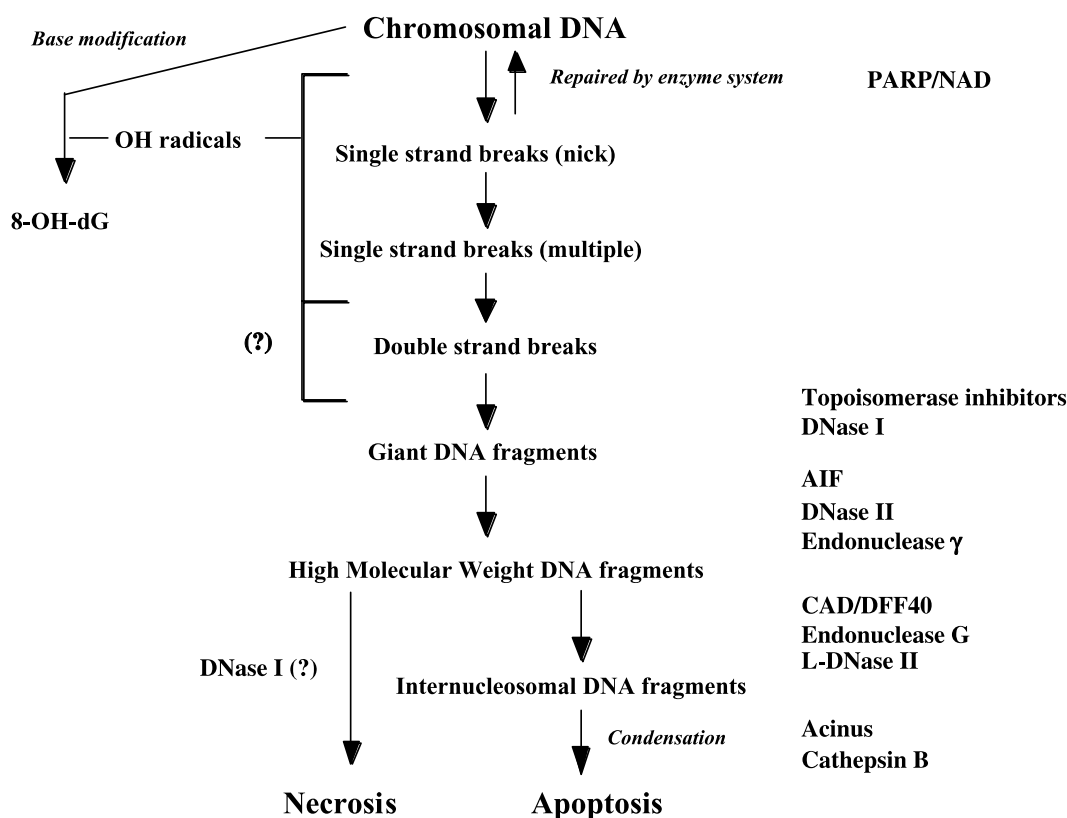


Fig. 1. Chromosomal DNA fragmentation induced by oxidative stress.

The labeled DNA is detected with horseradish peroxidase-conjugated streptavidin and diaminobenzidine. DNase I action can present a positive result in the TUNEL assay, and therefore, the TUNEL assay may be positive in both apoptosis and necrosis.

6. DNA fragmentation in apoptosis and necrosis by oxidative stress under GSH depletion

In addition to ROS such as H_2O_2 , O_2^- and $\bullet\text{OH}$, NO and lipid hydroperoxides are also considered to be important mediators of cytotoxicity in a variety of situations, including the apoptosis of neuronal cells [15,48,56]. Glutamate neurotoxicity has been postulated to contribute to the neuronal injury and death that underlie many central nervous system disorders both acute, for example, hypoxia, ischemia and hypoglycemia and chronic, for example, Huntington's [57], Parkinson's and Alzheimer's diseases [58] and Down's syndrome [59]. Amyloid-peptide is heavily deposited in the brains of patients, and free radical oxidative stress, particularly of neuronal lipids and proteins, is extensive. Recent research suggests that these two observations may be linked by amyloid-peptide-induced oxidative stress in Alzheimer's disease brains. There is current knowledge on phospholipid peroxidation and protein oxidation in Alzheimer's disease brains, one potential cause of this oxidative stress, and the

consequences of amyloid-peptide-induced lipid peroxidation and protein oxidation in Alzheimer's disease brains [3]. Besides the well-characterized receptor-mediated effects of excitatory amino acids such as glutamate, kainate and *N*-methyl-D-aspartate [40], it has also been proposed that high concentrations of exogenous glutamate inhibit the transport of cystine which is converted rapidly to cysteine followed by synthesis of glutathione (GSH) in cells. Consequently, intracellular GSH levels decrease *via* the depletion of intracellular cysteine [59,60] and thereby expose the cells to oxidative stress [61]. Most mammalian cells contain a high concentration of GSH (>4 mM) of which the majority is in the reduced form (>90%). Intracellular GSH depletion induced by BSO or glutamate causes apoptosis [9,11,61].

The GSH and GSH peroxidase system plays a major role in controlling cellular redox states and is the primary defense mechanism for peroxide removal from the brain protecting against the effects of ROS damage that may be involved in some neuropathological disorders [62]. 50–300 kbp HMW DNA fragments were also produced through rapid efflux of GSH during the apoptosis induced by anti-Fas/APO-1 antibodies [63]. In addition, not only 1–2 Mbp giant DNA and 100–800 kbp HMW DNA fragments but also internucleosomal DNA fragments were observed in C6 cells under glutamate or BSO-induced GSH depletion [9,11]. These DNA fragmentations were associated with intracellular accumulated ROS under

glutamate-induced GSH depletion [64]. However, the relationship between GSH depletion and active oxygen-induced DNA damage remains to be clarified. GSH depletion causes disturbance of cell membranes that releases phospholipase A₂ and phospholipase C [65]. Phospholipids contain mainly linoleic acid and arachidonic acid in position 2 which are mainly produced by phospholipase A₂. Polyunsaturated fatty acids with a homoconjugated *cis-cis*-pentadienyl system such as linoleic acid and arachidonic acid are substrates for lipoxygenases. Such polyunsaturated fatty acids enhance not only lipid peroxidation but also giant DNA fragmentation under both glutamate- and BSO-induced GSH depletion. The enhancements by these polyunsaturated fatty acids including linolenic acid and oleic acid are species-dependent [66]. Arachidonic acid is metabolized to some substances controlling cell survival and moreover is oxidized to its hydroperoxides not only by lipoxygenases or cyclooxygenases but also by a chemical reaction under aerobic conditions [67]. The lipoxygenase activity of lymphocytes and endogenous 15-hydroxyeicosatetraenoic acid (15-HETE), an arachidonate metabolite, are increased by X-ray irradiation of rats, stimulating internucleosomal DNA fragmentation [68]. 13-Hydroperoxy-octadecadienoic acid, a metabolite of linoleic acid and one of the lipid hydroperoxides, could cleave double-strand DNA at the position of guanosine

nucleotides in pBR322, but neither linoleic acid nor 13-hydroxyoctadecadienoic acid, were effective in the cleavage [69]. In spite of these facts, the production of lipid hydroperoxides is considered by most researchers to be initiated nonenzymatically. The superoxide anion O_2^- is postulated to be able to escape the enzyme complex in which it is produced, and either it or further reaction products, LOO^\bullet , H_2O_2 and $\bullet OH$, are suspected of attacking the double-allylic CH_2 groups of unsaturated fatty acids and initiating lipid peroxidation. Arachidonic acid converts apoptosis to necrosis representing the disappearance of internucleosomal DNA fragmentation under BSO-induced GSH depletion [70]. A decrease in GSH triggers the activation of neuronal 12-lipoxygenase leading to the production of peroxides, the influx of Ca^{2+} and ultimately to cell death [71]. In these cases, exogenous arachidonic acid can potentiate cell death by converting apoptosis to necrosis through lipid peroxidation and showing promotion of giant DNA fragmentation and reduction of internucleosomal DNA fragmentations [70]. Therefore, lipid metabolites, such as arachidonic acid-derived eicosanoids, may play a role in regulating cell survival [72]. We propose here, as has been suggested by many others, that lipid hydroperoxide production is a result of tissue injury. We suggest that lipid hydroperoxide formation in injured tissues is under the control of the GSH level.

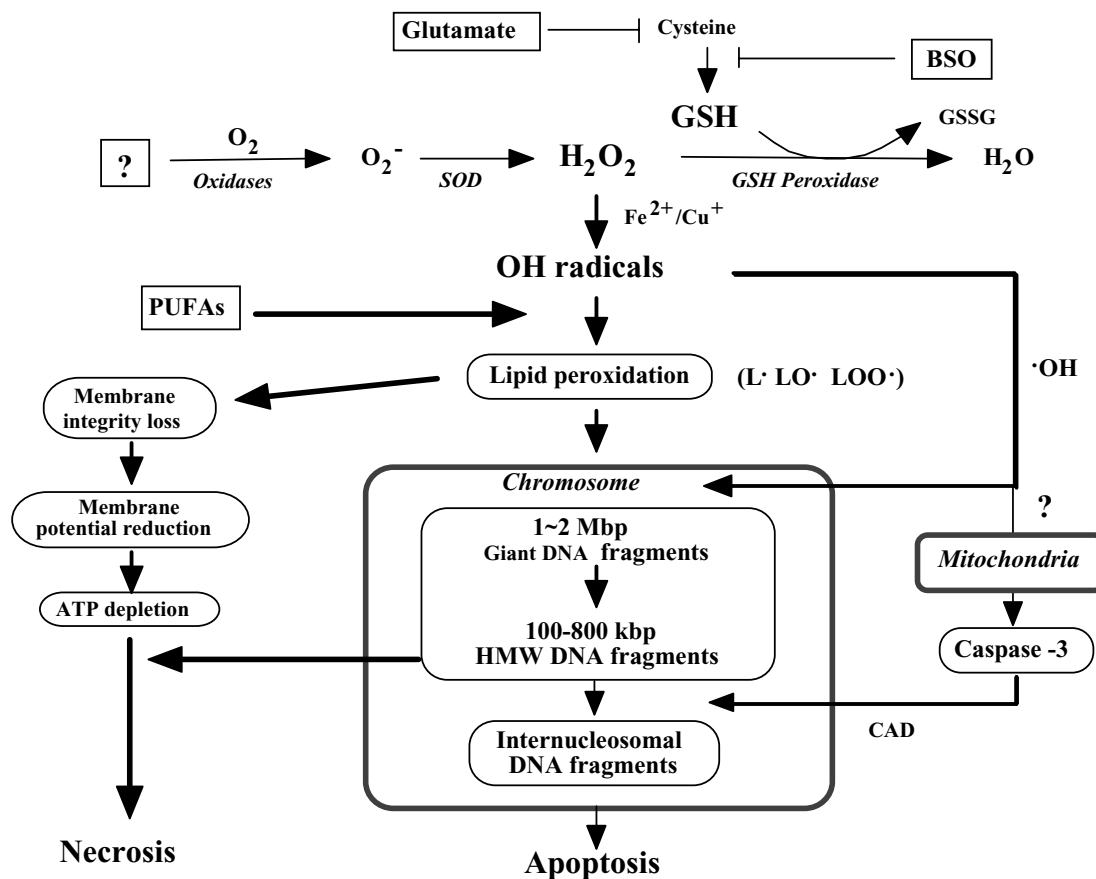


Fig. 2. Possible mechanism underlying the glutathione depletion-induced apoptotic or necrotic cell death in glioma cells.

7. Commentary remarks

We can consider that 1–2 Mbp giant DNA fragmentation under GSH depletion occurs by a few possible mechanisms (Fig. 2). First, lipid free radicals produced from PUFA directly attack chromatin DNA in nuclei. Second, lipid peroxidation in a cell leads to the loss of membrane integrity in cell membranes consisting of phospholipids and thereby may make suitable circumstances for other types of oxygen radicals, such as $\bullet\text{OH}$ radicals, produced from hydrogen peroxide by Fenton's reaction or from O_2^- by the Haber–Weiss reaction, to attack chromatin DNA. If the first case of the direct action mechanism of lipid free radicals is preferred, lipid peroxidation producing lipid free radicals might proceed not only in plasma membranes but also in the nuclear membranes close to the chromosomes, and such radicals might attack preferential cleavage sites in the hinge domain of chromatin. $\text{LO}\bullet$ or $\text{LOO}\bullet$ radicals may cleave DNA strands leading to giant DNA fragmentation in chromatin. $\text{LO}\bullet$ radicals are produced from lipid hydroperoxides by Fenton's reaction in the presence of iron or copper. However, it is also obscure whether PUFAs or their metabolites and derivatives act directly on the DNA in chromatin.

Intracellular iron and copper ions are known to be in close association with the chromatin in the nuclei. These metal ions may play an important role in the generation of hydroxyl radicals from H_2O_2 or O_2^- in or around the chromatin [73,74]. Hydroxyl radicals can cause single-strand DNA breaks associated with double-strand DNA breaks. Under the circumstance of membrane integrity loss induced by lipid peroxidation, hydroxyl radicals might attack and directly cleave chromosomal DNA into single-strand forms, consequently leading to double-strand DNA breaks. The location of specific DNA target site(s) attacked by $\bullet\text{OH}$ radicals may exist but is still unclear. On the mechanism of giant DNA fragmentation, $\bullet\text{OH}$ radical-mediated action is more possible and preferable to lipid radical-mediated action in providing 3'-OH-termini in single- or double-strand breakage. Lipid peroxidation induced under glutamate-induced GSH depletion promoted 8-OH-dG formation in chromatin DNA [75]. 8-OH-dG formation is thought to be caused by $\bullet\text{OH}$ radicals but not by $\text{LO}\bullet$ nor $\text{LOO}\bullet$ [76], and therefore, lipid hydroperoxides made from PUFA induce a loss of membrane integrity and thereafter may change the environment to make $\bullet\text{OH}$ radical attack on chromosomes easier.

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