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Redox Metabolism and Malignancy

Christina L. Grek and **Kenneth D. Tew**

Department of Cell and Molecular Pharmacology and Experimental Therapeutics, Medical University of South Carolina, Charleston, South Carolina, United States

Abstract

Redox balance underlies cellular homeostasis. Cancer initiation and progression has been linked to the disruption of redox balance and oxidative stress. Recent findings exemplify the distinctive roles of intra- and extraceullar redox state in the etiology and maintenance of oxidative stress associated with malignancy and metastasis. Within these compartments, redox sensitive cysteines play a critical role in regulating cell signaling events that act to promote the malignant phenotype via the activation of survival pathways, disruption of cell-death signaling, and increases in cell proliferation. New approaches that aim to accurately evaluate subcellular and microenvironment redox potential may be useful in developing cancer diagnostics and therapeutics.

Introduction

The balance between oxidation and reduction reactions plays an essential role in numerous cell signaling cascades including those associated with proliferation, inflammatory responses, apoptosis, and senescence. Reactive oxygen and nitrogen species (ROS; RNS) are invariable components of aerobic metabolism and are key contributors to cellular redox state. However, due to the fact that oxygen and nitrogen radicals readily interact with nucleic acids, proteins and lipids, the disruption of cellular redox homeostasis has emerged as a critical component in the etiology and prognosis of a variety of disease pathologies. Oxidative stress, defined as the result of the imbalance between the production rate of pro-oxidants and that of their removal by antioxidants, has been shown to play a major role in the origination, progression, and malignancy of a number of cancers [1,2]. Similarly, nitrosative stress occurs when the generation of RNS exceeds the ability to neutralize and eliminate them. Within these definitions, it is critical to incorporate the recently coined "redox hypothesis", which emphasizes the importance of non-radicals and thiols in oxidative and nitrosative stresses [3]. Despite emphasis on free radicals, disruption of redox signaling producing stress is largely non-radical based.

Elevated oxidative stress is observed in many solid tumors and carcinoma cell lines. Redox imbalance in cancer cells may be tied to a number of pathways including mitochondrial dysfunction, the activation of oncogenes, aberrant oxidative metabolism, and hypoxia/ reoxygenation cycles. Low levels of oxidative stress may be advantageous for cancer progression, as they may lead to increased rates of genetic mutation that could contribute to the acquisition of a malignant phenotype [4]. Higher levels of ROS are more likely to lead to

Corresponding author: Kenneth D. Tew, Department of Cell and Molecular Pharmacology and Experimental Therapeutics, Medical University of South Carolina, 173 Ashley Avenue, P.O. Box 250505, Charleston, SC 29425. Phone: 843-792-2514; Fax: 843-792-2475; tewk@musc.edu.

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cell senescence and/or death. Each may be influenced by subcellular localization. Recent studies have identified certain ROS as second messengers in signaling pathways, thus allowing the potential to regulate cell phenotype directly by acting as effector molecules [5]. Understanding the origin of various ROS/RNS, and their roles in cancer initiation and progression, as well as in the cell signaling pathways involved in these, could facilitate the development of therapies that might act to prevent and/or counteract malignancy.

Extracellular vs. Intracellular redox state

Intracellular sources of ROS/RNS

Endogenous ROS can regulate redox signaling and may have independent roles in malignancy as compared to those produced, for example, at the apical membrane corresponding to extracellular ROS. Intracellularly, ROS may be generated by a variety of sources, including non-mitochondrial electron transport chains and redox systems in the cytosol, nuclear envelope or ER, as well as phase I reactions through p450 metabolism, β-oxidation in peroxisomes and inflammatory cytokines. While each can contribute meaningfully to cellular redox homeostasis, mitochondria are traditionally considered the major endogenous source of ROS in mammalian cells. During aerobic respiration, mitochondrial ROS are formed via the univalent reduction of molecular oxygen mediated through the escape of electrons from complexes I and III in the mitochondrial electron transport chain. Of the oxygen consumed by mitochondria about 2% is reduced by these bifurcated electrons to form superoxide and subsequently hydrogen peroxide [6,7]. As such, mitochondrial DNA is intrinsically vulnerable to ROS-mediated injury, partially mitigated by the separate glutathione (GSH) pools maintained by active transport of the tripeptide across the mitochondrial membrane. Mutations in cancer cell mitochondrial DNA have not only been implicated in tumor pathogenesis and metastasis but have been linked to enhanced mitochondrial generation of superoxide as compared to their normal counterparts [8]. Novel methodologies permitting targeting of mitochondrial ROS have identified them as key regulators in NF-kB-dependent anti-apoptotic signaling [9]. Recent studies have focused on new methodologies to evaluate mitochondrial bioenergetics in attempts to use 'bioenergetic signatures' as cancer biomarkers and to further unravel the role of a family of inner mitochondrial membrane proteins, termed uncoupling proteins, in cancer progression [10,11]. These studies further emphasize the heterogeneous nature of the tumor microenvironment and support the underlying principles of individualized approaches to anticancer treatment.

Extracellular sources of ROS/RNS

Extracellular redox states are influenced by factors distinct from intracellular and are frequently a consequence of modifications of plasma membrane proteins and the proximal milieu around the cell. This includes ROS directly resulting from exposure to external environmental agents including irradiation, chlorinated compounds, metal ions, barbiturates, phorbol esters and peroxisome proliferating agents [12] or from membrane associated redox modulating proteins such as the NADPH oxidase family, in particular Nox1 [13]. Based on immunostaining, recent studies of the Nox family have not only identified a role for various Nox members as intracellular and/or extracellular signaling oxidases, but have also determined that based on sub-cellular location of oxidase components different ROS species can be produced [14]. Membrane associated γ-glutamyltransferase (GGT) also plays a critical role in controlling redox conditions by degrading extracellular GSH, thus providing cysteine to cells; or alternatively, by acting as a pro-oxidant. Beyond the plasma membrane, antioxidants such as extracellular superoxide dismutase (EC-SOD), glutathione peroxidase 3 (GPX3), and thioredoxin reductase-1 (TR1) as well as the extracellular supply of plasma thiol/disulfide couples, such as glutathione/glutathione disulfide (GSH/GSSG), play a major part in balancing redox homoestasis (reviewed in [15]). This balance is further impacted by glutathione-*S*-

transferases that are involved in maintaining glutathione homeostasis, as well as protein Sglutathionylation and kinase regulation [16,17].

The balance between extracellular and intracellular redox states in cancer metastasis has recently been discussed. Chaiswing et al. determined that extracellular redox-related proteins, GSH/GSSG levels, and the ROS/RNS levels of the extracellular space are altered in prostate cancer cells [18]. Furthermore, alterations in extracellular thiol/disulfide couples and GSH/ GSSG also affect proliferation of colorectal carcinoma and lung fibroblast cells [19,20]. It may prove viable to adapt the expression of certain extracellular redox parameters to use as potential biomarkers. For example, cancer patients with high levels of generalized oxidative stress markers in their sera also exhibit markers of constitutive oxidative stress within tumors. Therefore, assessing serum redox state may be useful in the prediction or prognosis of the response/progression of various human cancers (see Table 1).

Oxidative Stress in Cancer Initiation and Progression

Chronic oxidative stress in cancer cells

Low levels of superoxide or hydrogen peroxide can enhance cellular survival and stimulate proliferation. However, when this is concomitant with chronic ROS production, redox homeostasis can become imbalanced and normal cells may become transformed [5]. Current evidence supports the hypothesis that cancer cells are characterized by enhanced ROS generation, increased ROS accumulation, and the deregulation of antioxidant enzymes; thus existing in a state of perpetually elevated stress. Constitutively produced NOS have also been found in several human tumor cell lines, an observation further complicated by the fact that RNS can be chemically heterogeneous in different tumor cell types [21].

Methods currently used to evaluate redox status include measurements of pro-oxidants, quantification of antioxidants, detection of oxidized nucleic acids, or evaluation of redox potential based on thiol/disulfide couples via the Nernst equation. Markers of oxidative stress, such as DNA adducts e.g. 8-oxo-7,8 dihydro-2′-deoxyguanosine, as well as generalized biological anti-oxidant capacity of plasma might be developed as tools in disease prognosis. However, general quantification of redox remains a complicated analysis of a plethora of integrated pathways and cross talk imbued by the oxidation/reduction system. Moreover, the pathways are fluid and often unstable.

Chronic oxidative stress in cancer is influenced by numerous factors. Oncogene expression, including that of Ras2, Bcr-Abl, and c-Myc contribute to persistent ROS production in addition to the disruption of p53 function [22,23]. Recent studies have linked ROS produced as a result of chronic inflammation to the neoplastic process [24]. Furthermore, because oxidative stress plays a major role in the induced adaptive expression of antioxidants, malignant cells are often characterized by differential expression in the levels of a number of these enzymes, including superoxide dismutases (SOD), catalase, glutathione-S-transferases, GGT, and EC-SOD [25, 26]. Dysregulation in expression of such enzymes can influence cancer therapy and may contribute to metastasis and drug resistance. These characteristics further perpetuate a state of oxidative stress and result in the need to either adapt, or apoptose. Because oxidative stress may induce apoptosis, cell cycle arrest or cellular senescence, eventual cellular fate may be a delicate balance contingent upon factors such as cell type, tissue microenvironment and levels of free radical production/accumulation.

Results of chronic oxidative stress

Increases in ATP requirements in metabolically active cancer cells result from the need to support activities such as rapid proliferation. Such demands in association with ROS induced mitochondrial damage may result in amplified electron 'leakage' and ROS generation. In

Redox and thiol dependent cell signaling

Post-translational modification of proteins *via* redox sensitive cysteine residues can occur as a consequence of alterations in their oxidation state. There are over 200,000 unique cysteines in the human proteome and it is estimated that approximately 10% of these may be oxidizable [3]. Numerous factors determine which properties of these cysteines make them available for this reaction. The range of cellular processes under redox regulation is extensive and includes both the proliferative and apoptotic pathways. However, in cancer cells, excess superoxides and hydrogen peroxide can promote cell growth and proliferation and disrupt thiol redox circuits, thus contributing to oxidative stress.

More than 127 genes and signal transducing proteins have been reported to be directly affected by redox state [27]. Transcription factors, tumor suppressors as well as members of the mitogen activated protein kinase (MAPK) family and anti-apoptotic pathways such as PI 3-K and NFκB are regulated by ROS and have roles in stimulating cell proliferation, sensitizing cancer cells to electrophilic agents and contributing to treatment resistance [28,29]. These signaling events may be further controlled by protein:protein interactions, such as through GSTP interactions with the MAPK c-jun NH2 terminal kinase (JNK). Oxidative stress can result in the reversal of GSTP regulated intrinsic JNK inhibitory activity via dissociation of the GSTP:JNK complex [30]. Under this system, GSTP serves as a sensor of intracellular changes in redox potential and has the potential to directly regulate kinase pathways, perhaps explaining the drug–resistance phenotypes of many GSTP over-expresssing cancers. Gene expression is modulated by ROS and thiol redox circuits through the interplay of extra-, intra- and even intercellular signaling pathways. In fact, ROS, in association with the mandatory presence of GSH, have been shown to reversibly inhibit gap junction inter-cellular communication (GJIC), which along with the induction of early-response genes is a hallmark of tumor promotion [31]. Furthermore, extracellular thiol/disulfide, GSH/GSSG, and overall redox potential has been linked to cell proliferation pathways mediated by epidermal growth factor (EGF) and MAPK signaling [19], two plausible targets in cancer therapy.

S-glutathionylation, which occurs when a protein cysteine forms a disulfide bond with GS•, serves as a reversible mechanism of post-translational protein regulation that has the potential to selectively regulate the function of enzymes, receptors, structural proteins, transcription factors, transport proteins, and protein-protein interactions (reviewed in [32]). As the most abundant non-protein thiol in cells, GSH plays a key role in oxidative stress. The presence of ROS/RNS directly mediates GSH/GSSG balance as well as interaction with available reactive cysteine residues. During cancer inititation, glutathionylation of the tumor suppressor p53 prevents DNA binding [33]. Furthermore, glutathionylation also has an anti-apoptotic role by preventing caspase cleavage [34]. Alternatively, glutathionylation of NF-κB influences apoptosis of hypoxic tumor cells [35]. Modulation of GSH and/or GST isozymes is an ongoing therapeutic strategy in cancer chemotherapy [30].

Both non-radical based oxidative and nitrosative species are important in regulating signaling pathways in normal and cancer cells (reviewed in [3]. However, where signaling is regulated through thiol:disulfide reactions, it should be noted that their turnover rates and consequent flux rates are quite small when compared to general cellular redox buffering. Ongoing research in redox systems biology will need to focus on the quantification of redox buffering.

Stoichiometry of competing reactions and their sub-cellular localization will control how tumor and normal cells may differ in their regulatory pathways. In particular, the mitochondrial compartment seems to be the most reduced in terms of steady state redox potential, while the endoplasmic reticulum has the most oxidized environment, a condition determinant of the function of this organelle in protein folding [36]. Specifically, ER oxidative stress is linked to increases in protein S- glutathionylation as well as to the accumulation of misfolded proteins and a cascade of transcriptional and translational events that attempt to manage this accumulation [32,37]. This phenomenon, termed the unfolded protein response (UPR), is a potential therapeutic target in some cancers [38].

The oncogene, Rac has been shown to induce ROS production and cause loss of cell-cell adhesion and ROS-mediated actin cytoskeleton reorganization eventually impacting metastasis [39]. Furthermore, ROS can induce ICAM-1 and activate matrix metalloproteinases that can act as tumor promoters [40]. Recently, ROS produced via the transcriptional activation of Nox family members have also been linked to the formation of invadapodia and to tumor cell motility/migration [41]. Cancer cells under oxidative stress exhibit decreased attachment to basal lamina as modulation of integrin function, suggesting a propensity to enter blood vessels. Additionally, constitutive ROS production in metastatic cancer cells has been linked to resistance to *anoikis*, or detachment-induced apoptosis, through persistent EGFR or Src kinase activation [42]. It has been proposed that metastasis is an oxidative stress triggered "escape program" that enables cells to avoid the oxidative stress levels associated with the primary tumor. Additionally, extracellular redox potential has been shown to influence matrix expression, mediated through TGF-β1 fibronectin expression [19]. Specific signaling pathways that are influenced by ROS have been reviewed recently [5,28].

Malignancy and cell environment:hypoxia

The ability of tumors to survive in a hypoxic state is supported by the capacity to up-regulate proteins that favor anaerobic metabolism and improve pH buffered-oxygen sensing. These include $HIF-1\alpha$, as well as glucose transporters and glycolytic enzymes for anaerobic energy production, erythropoietin and iron metabolism proteins for red blood cell production, and a number of factors that promote angiogenesis. The resulting angiogenesis-induced oxidative stress then acts in a positive feedback loop resulting in increased metastasis and aggressive tumor progression. In a recent study, Cannito et al. showed that during low oxygen tension mitochondrial produced ROS have a direct role in hypoxia-dependent epithelial-mesenchymal transition [43].

Not only does hypoxia result in glucose deprivation followed by the depletion of intracellular pyruvate and the inability to dispose of existing ROS but re-oxygenation of hypoxic tissues, such as during tumor angiogenesis, increases the concentrations of free radicals. This ROS production can further increase the production of the angiogenic factors IL-8 and VEGF as well as factors that promote vessel growth, such as MMP-1, and angiogenesis, such as iNOS. Members of the ROS producing Nox family can also contribute to pathways that lead to tumor angiogenesis and neovascularization [13]. Of recent interest is the role of tumor stem cells and the hypoxic microenvironment in activating quiescent stem cells via HIF/VEGF pathways as well as effectors such as Notch, Wnt and Oct4 and the promotion of tumorigenesis [44].

Conclusion

The role of oxidative stress in metastasis and tumor progression is complex and involves a number of factors including cell type, cellular microenvironment, and free radical type and compartmentalization. Tumor survival depends on a number of processes involving proliferation, motility, apoptosis and senescence, all of which are influenced by changes in redox metabolism. Complexity lies in the fact that individual cancers may be characterized by

different redox-based signaling mechanisms. However, as new approaches emerge, e.g. the discrete roles of extracellular vs. intracellular redox state; the importance of non-radicals in redox metabolism; the recognition of the impact of tumor microenvironment on metastasis, the utility of targeted redox-modulating therapeutics may flourish.

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Figure 1.

Accumulation of reactive oxygen species (ROS) and/or reactive nitrogen species (RNS), derived either endogenously or exogenously, results in oxidative stress. Disruption of thiol and non-radical circuits may also result in oxidative stress. The extent of this stress will either result in lethal damage and apoptosis or in cell adaptation. In cancer cells chronic oxidative stress activates redox sensitive transcription factors and signaling pathways that act to increase the expression of antioxidants, increase expression of survival factors as well inhibit the expression of pro-apoptotic pathways. ROS/RNS induced DNA injury promotes genomic instability and further provides opportunity to adapt to oxidative stress. Cancer progression occurs via the regulation of redox dependent expression of genes that play roles in proliferation, senescence evasion, metastasis, and angiogenesis. These features in association with the disruption in antioxidant profile may contribute to altered drug sensitivity and chemotherapy resistance. *Definition of abbreviations:* NOX, NADPH oxidase; nuclear factor-κB; NF-κB; Cys, cysteine; Cyss; cystine; GSH, glutathione; GSSH, glutathione disulfide, GSTP, glutathione-*S*transferase P

Table 1

