

Mini Review Article

Novel Aspects of Oxidative Stress-Associated Carcinogenesis

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ABSTRACT

Oxidative stress is associated with carcinogenesis. Reactive oxygen and nitrogen species contribute to the accumulation of mutations in the genome, presumably followed by selective processes. Recent data suggest that preferred signaling pathways exist for oxidative stress-associated carcinogenesis. Whether this completely depends on random mutations induced by reactive species or whether instead some fragile genomic loci are sensitive to oxidative damage in association with changes of transcriptional activity or other topologic or non-topologic effects remains to be explored. Reliable markers for oxidative stress as well as for oxidative stress-induced preneoplastic lesions must be established. *Antioxid. Redox Signal.* 8, 1373–1377.

OXIDATIVE STRESS AND CANCER

OXIDATIVE STRESS IS ASSOCIATED with a variety of pathological phenomena, including inflammation, ultraviolet and γ -irradiation, toxicity of transition metals and certain chemotherapeutic agents, as well as ischemia–reperfusion injury. Epidemiologic studies indicate a strong association between chronically oxidative conditions and carcinogenesis: for example, the incidence of colorectal cancer is increased in ulcerative colitis (8); chronic *Helicobacter pylori* infection is associated with a high incidence of gastric cancer (9, 37); chronic tuberculous pleuritis causes a high incidence of malignant lymphoma (20); severe burn by ultraviolet radiation is a risk factor for skin cancer (12, 26); γ -irradiation causes a high incidence of leukemia (38); and asbestosis (asbestos fibers are rich in iron) is often associated with mesothelioma and lung carcinoma (17). At least under these circumstances, and probably in other types of carcinogenesis as well, oxidative stress appears to play a major role. Here, I briefly review recently established concepts and raise unanswered questions in this area.

Cancer is one of the leading causes of death in most developed countries. It is established that multiple stepwise alterations of the original genome information are responsible for carcinogenesis (45). Excess generation of reactive oxygen and nitrogen species can cause DNA damage and modifications (6, 33, 43, 47), leading to changes in the genomic infor-

mation in spite of the robust counteractions of repair enzymes and apoptotic pathways. These changes of genetic information fall into the category of mutations. They include point mutations, deletions, insertions, or chromosomal translocations. These events may cause activation of oncogenes or inactivation of tumor-suppressor genes. Oncogene is now a classic term, meaning any gene that can be a causative factor via its activation in carcinogenesis or transformation. It is now realized that this definition is sometimes misleading, considering the fact that expression of these genes is required for tissue regeneration after injury. Tumor-suppressor genes may be classified into two broad categories: caretakers (DNA repair genes) and gatekeepers (cell-cycle inhibitors). Apoptosis-related genes are another class of cancer genes (50). After three decades of intensive search to identify the mutated genes (cancer genes) that are causally implicated in carcinogenesis, a “census” of cancer genes was recently performed. This study indicated that mutations in >1% of genes (291 cancer genes) contribute to human cancer (~80% dominant trait and ~20% recessive trait). Ninety percent of cancer genes show somatic mutations in cancer, 20% show germline mutations, and 10% show both. The most common domain that is encoded by cancer genes is the protein kinase. Several domains that are involved in DNA binding and transcriptional regulation are common in proteins that are encoded by cancer genes (10).

SIGNALING PATHWAYS AND THEIR REGULATION

Imatinib mesylate (Gleevec), a tyrosine kinase inhibitor, has recently shown success in treating chronic myelogenous leukemia in which a chimeric oncogene, *bcr-abl*, is generated via chromosomal translocation (4), and inoperable gastrointestinal stromal tumor (21). Conversely, recombinant humanized anti-HER2/c-ErbB2/Neu antibody (Herceptin) (2) is now used clinically to antagonize the receptor-type tyrosine kinase in invasive ductal carcinoma of the mammary gland (42). These exciting advancements emphasize the importance of signaling pathways in cellular proliferation. However, we have to be aware that these target signaling pathways in cancer cells have evolved by selective processes from thousands of possible mutations to establish a "robust" system (24). Unfortunately, how cells acquired those mutations is largely unknown. The general significance of oxidative stress in carcinogenesis has been established in the past decade and is summarized in Fig. 1. Importantly, mutation and persistent activation of new signaling pathways for proliferation are interrelated. Selected mutations of oncogenes generate new signaling pathways, whereas increased cellular proliferation enhances the mutation rate. In a sense, carcinogenesis may be compared with evolution, with the difference that carcinogenesis is fatally impatient with time.

Redox regulation is one of the key mechanisms for adapting to a variety of stresses, including oxidative stress (40). Recently, it was reported from several independent laboratories that an antagonizing protein for thioredoxin (thioredoxin-binding protein-2, TBP-2; also as vitamin D₃ upregulated protein-1, VDUP-1) (28) is downregulated in cancers such as human adult T-cell leukemia (1, 27), human gastric cancer (14, 19), and rat iron-induced renal cell carcinoma (7). The mode of inactivation involves methylation of the promoter region (7). Furthermore, TBP-2 is expressed at higher levels in nonmetastatic melanomas than in metastatic melanomas (11). Studies of a TBP-2-null mutant mouse (3) provided evidence that loss of TBP-2 results in enhanced sulfhydryl reduction and dysregulated carbohydrate and lipid metabolism, namely hyperinsulinemia, hypoglycemia, hypertriglyceridemia, and increased levels of ketone bodies, at least in the liver and pancreatic β -cells (18). This has been confirmed by producing TBP-2-deficient mice (35). Loss of TBP-2 appears advanta-

geous in cancer cells because it ultimately results in facilitation of the glycolytic pathway by enhancing the thioredoxin activity.

In renal tubular cells, TBP-2 is abundant in both mitochondria and nuclei (7). The mitochondrion is a key organelle that acts as a source of reactive oxygen species. The role of mitochondria in cancer was discussed in a recent forum of this journal (31). The form of superoxide dismutase present in mitochondria is manganese superoxide dismutase (MnSOD). Although some aspects of the role of MnSOD in cancer are still controversial, as discussed (15, 23, 32, 39, 52), it has been suggested that overexpression of this enzyme is a possible means of anticancer therapy (30, 36). Drugs that lead to TBP-2 and MnSOD expression would be promising as therapy for cancers that lack these pathways.

OXIDATIVE STRESS AND GENOME: OXYGENOMICS

Free radical reactions have been considered to have little specificity *in vitro*, in contrast to the extremely selective antigen-antibody interactions. For example, the second-order rate constant for the reaction of hydroxyl radical with guanine is $\sim 1.0 \times 10^{10}$ M/s (13). Thus, one might think that the genome is damaged at random and that no specific "target" genes or signaling pathways are found in oxidative stress-associated carcinogenesis. However, it may be time to revisit this doctrine. We challenged this hypothesis because ferric nitrilotriacetate (Fe-NTA)-induced renal cancers are rather homogeneous in histology (29, 47). We used a genetic strategy which revealed that *p15^{INK4B}* (*p15*) and *p16^{INK4A}* (*p16*) tumor-suppressor genes are two of the major target genes. This was the first report that showed the presence of a target gene in the free radical-induced carcinogenesis model (46). The biologic significance of this finding is enormous because *p16* is associated not only with the retinoblastoma protein pathway as a cyclin-dependent kinase 4 and 6 inhibitor, but also with the p53 pathway via p19^{ARF} and MDM2 (22). p19^{ARF} is an alternatively spliced transcript from the *p16* tumor-suppressor gene (5). Indeed, iron-mediated oxidative damage appears to attack one of the most critical sites of the genome. We later showed that allelic loss of *p16* occurs as early as 1 week after the start of the animal experiment and is gene specific (16). We believe

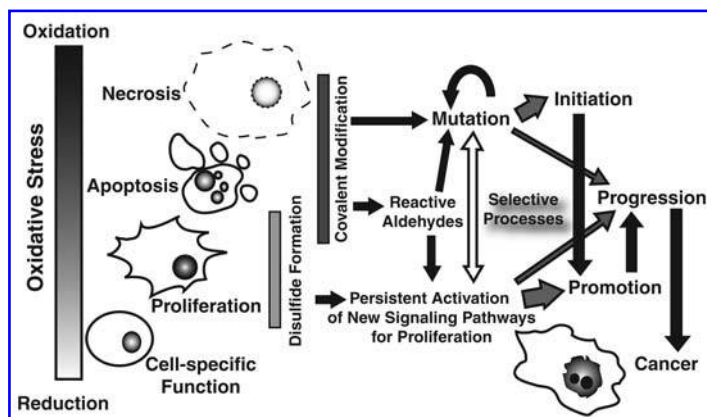


FIG. 1. Significance of oxidative stress in carcinogenesis. The left half of the figure shows the general cellular significance of oxidative stress, whereas the right half shows the significance in carcinogenesis as related to the classic concepts of initiation, promotion, and progression. The self-directed arrow at "Mutation" indicates "mutator phenotype" (25). Reactive aldehydes include 4-hydroxynonenal and other aldehydes (49). Refer to text for details.

that these results suggest the presence of fragile sites in the genome, because allelic loss of a tumor-suppressor gene does not necessarily mean loss of the signaling pathway if overriding events such as mutation or methylation of the promoter region do not occur at the remaining allele. Thus, the next question is whether carcinogenesis is a process of "random alteration of genetic information and selection" or "nonrandom alteration of genetic information and selection." The conclusion may change the chemopreventive strategy in particular cases of carcinogenesis.

Studying the localization of oxidative nucleic acid damage in comparison with genome information and cellular structure is becoming increasingly important. A plethora of data has been published on oxidative DNA damage *in vitro* by using purified DNA or cultured cells, and based on these data, it has been claimed that certain specific sequences including telomeres (34, 51) are especially vulnerable to oxidative damage. However, currently limited data are available on which part of the genome is susceptible to oxidative damage *in vivo* in individuals. The results obtained *in vitro* should be confirmed at the tissue and organ levels step by step. I believe that this is now possible, given the completion of genome projects of humans, mice, rats, and other species (48). One must be aware that nuclear genomic DNA in association with histones is integrated into the chromatin structure in the cell, and that some parts of the chromatin structure are open for transcription. It is possible that the genome areas susceptible to oxidative stress may differ depending on the kind of cell and the situation in which the cells are placed. Such difference could help to explain the different signaling pathways each type of cancer has acquired. As described earlier, tailored cancer therapy is now being developed. Cancer prevention (41, 44) is not less important than cancer therapy, considering the economic impact of current medical therapeutic costs. In the near future, tailored cancer prevention may become an important intervention. It will be essential to establish reliable markers for oxidative stress as well as for oxidative stress-induced preneoplastic lesions.

ABBREVIATIONS

Fe-NTA, ferric nitrilotriacetate; MDM, mouse double minute; MnSOD, manganese superoxide dismutase; TBP-2, thioredoxin binding protein-2.

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