

## Review Article

# Oxidants and Antioxidants in Breast Cancer

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### ABSTRACT

Although a number of risk factors have been identified for breast cancer, mechanisms by which they increase risk of the disease are not clear. Breast cancer etiology could, in part, be related to oxidative stress. Recognized risk factors for breast cancer include a family history of the disease. BRCA1 is needed for post-transcriptional repair of oxidative damage, indicating that oxidative stress may be an important risk factor for women with a family history of the disease. Reproductive and hormonal factors that result in greater exposure to circulating estrogens also increase risk, and steroid hormones are metabolized to reactive quinones and hydroquinones, which can directly damage DNA. Alcohol consumption is associated with increased risk, and the metabolism of alcohol results in production of DNA-damaging reactive oxygen species (ROS). Finally, the inverse relationship noted with consumption of fruits and vegetables could be related to their being a source of antioxidant vitamins. Endogenous factors may play an equally important role in the effects of oxidative stress on breast carcinogenesis. Genetic variability in enzymes that result in increased production of ROS and those that protect the cell from oxidative stress could also have an impact for risk of the disease. In this review, a rationale is given for linking breast cancer risk factors to oxidative stress. The possible role of genetic polymorphisms in a number of enzymes that may be important in affecting levels of ROS to which the cell is exposed, as well as those that protect the cell from oxidative stress, is discussed. *Antiox. Redox Signal.* 2, 903–917.

### EPIDEMIOLOGY OF BREAST CANCER

**D**ESPITE FOCUSED EFFORTS over the last few decades to understand further the causes of breast cancer, little new information has been gained regarding breast cancer etiology. Risk factors that are 'known' explain approximately 40% of the variability in incidence (Madigan *et al.*, 1995); the remaining risks for breast cancer remain unknown. The traditional risk factors, excepting presence of breast cancer in a first-degree relative, are primarily related to hormonal and reproductive events (Kelsey and Bernstein, 1996). Characteristics or behaviors that result in prolonged exposure to circulating estrogens, such as early age at menarche, no or few children, late first full-

term pregnancy, and late age at menopause, are all associated with increased breast cancer risk. Higher body mass index also increases risk for postmenopausal women. It is thought that the mechanism responsible for this association is the production of estrogens in peripheral adipose tissue. Regarding dietary factors, the presumed relationship between dietary fat and breast cancer risk has not been supported in epidemiologic studies (Hunter *et al.*, 1996), although there is strong support from ecologic and laboratory studies for this hypothesis. There is consistent evidence indicating that alcohol consumption, even moderate use, increases risk of breast cancer (Schatzkin and Longnecker, 1994). Finally, there are somewhat consistent data that consumption of fruits and

vegetables will decrease risk, as well as specific dietary sources of antioxidants such as ascorbic acid,  $\alpha$ -tocopherol, and carotenoids (Steinmetz and Potter, 1996).

There are primarily two paradigms proposed to link the above risk factors to breast carcinogenesis. The historically older model, which has predominated until recently, is that of two-stage carcinogenesis. Based on rodent experiments, this is a model of initiation and promotion: cells that develop mutations through DNA damage replicate and immortalize that damage. In the case of breast cancer, replication would be driven by the mitotic stimulation of circulating steroid hormones. Although we now know that there are likely multiple 'hits' that damage DNA, and multiple genetic events occurring over a number of years, this model of DNA damage and cell replication is still plausible. There are a number of factors that could initiate DNA damage, including spontaneous errors in replication, chemical carcinogens, and reactive oxygen species (ROS) that could be generated through a number of processes. The role of estrogen as a mitogen in breast carcinogenesis is clearly established, and could be sufficient and necessary breast carcinogens through this function alone.

The second paradigm of carcinogenesis in hormonally responsive tissue is that of steroid hormones as complete carcinogens, which is related to endogenously produced estrogen metabolites as well as the mitotic role of estrogens. Biosynthesis and metabolism of estrogens is mediated by a number of enzymes, many which are polymorphic. Some estrogen metabolites, namely the 4-hydroxy catechol estrogen, have been shown to bind to DNA and cause mutations (Cavalieri *et al.*, 1997; Liehr, 1997). In this scenario, estrogens would act as both the DNA damaging agent and the mitotic stimulator. The catechol estrogens also result in formation of hydroxy radicals through redox cycling. Thus, in both paradigms of carcinogenesis, ROS may play a major role.

### OXIDATIVE STRESS AND BREAST CANCER

The term "oxidative stress" is generally used to refer to the total burden of potentially harm-

ful reactive biochemical species that are present in tissue as a consequence of the routine cellular oxidative metabolism of both endogenous and exogenous compounds (Nathan and Chaudhuri, 1998). ROS, including the superoxide radical, hydrogen peroxide ( $H_2O_2$ ), and the hydroxyl radical, are continuously produced within the cell as a result of the mitochondrial electron transfer processes (Loft and Poulsen, 1996). ROS can be formed as a result of metabolism of xenobiotics by cytochrome p450 enzymes, or exposure to other environmental factors (Hayes and McLellan, 1999b), and ROS and compounds generating ROS are ubiquitous in the environment and present in inhaled smoke, polluted, air and ingested goods (Frei *et al.*, 1991; Nagashima *et al.*, 1995).

When ROS are produced as a consequence of normal metabolism and in an environment where there is sufficient antioxidant power and repair capacity, there are presumably few deleterious effects. However, when there is excessive production of ROS due to exposure to toxic agents or to pathologic processes, or there are insufficient *in vivo* defense mechanisms, oxidative stress may occur. This results in damage to DNA, including breakage, as well as lipid peroxidation, protein modification, membrane disruption, and mitochondrial damage (Halliwell and Gutteridge, 1989; Schwartz *et al.*, 1993; Cerutti, 1994; Emerit, 1994; Esterbauer and Jurgens, 1993).

Damage to DNA includes a number of oxidized purines and pyrimidines, as well as strand breaks (reviewed by Loft and Poulsen, 1996). The hydroxyl radical induces DNA modifications that include single-base deletions, base ring opening (primarily adenine and guanine), single- and double-strand breakage, and adduction of bases to form chiefly 5-OH-cytosine, 8-OH-guanine, and 8-OH-adenine (Malins, 1993; Wagner *et al.*, 1992). The most damaging ROS, the hydroxyl radical, can cause almost any DNA modification, including 8-oxodG. 8-Oxo-7,8-dihydro-2'-deoxyguanosine (8-oxodG), which is an indicator of oxidative DNA modifications that can be mutagenic (Ribeiro *et al.*, 1994; Toyokuni *et al.*, 1994), is often used in etiologic and intervention studies as a biomarker of oxidative stress, and is markedly elevated in some studies of breast cancer (Malins and Haimanot, 1991; Malins *et*

*al.*, 1993, 1996). It has also been linked to G:C to T:A transversion mutations (Ribeiro *et al.*, 1994; Toyokuni *et al.*, 1994), and transversion mutations of p53 have been observed in human breast cancers (Callahan *et al.*, 1992). In fact, Cerutti's group has shown mutagenesis in p53 directly by oxy-radicals (Hussain *et al.*, 2000).

Studies of breast cancer have found that DNA from invasive ductal carcinomas contains extensive modifications linked to oxidative stress. These include hydroxyl radical adducts of adenine, guanine, and cytosine, as well as single- and double-strand breaks (Malins and Haimanot, 1991; Malins *et al.*, 1993, 1996). Wang *et al.* (1996) identified DNA-malondialdehyde adducts, markers of oxidative stress due to lipid peroxidation, in human breast tissue. Higher levels of malondialdehyde have also been noted in urine of women with mammographic breast dysplasia (Boyd and McGuire, 1991). Damage resulting from hydroxyl radicals has also been directly linked to the progression of human breast cancer (Malins *et al.*, 1996). Oxidative damage has been reported to be higher in women with breast cancer, compared to controls, although studies to date remain small (Djuric *et al.*, 1996; Musarrat *et al.*, 1996), and these levels vary with the consumption of meats, vegetables, and fruits (Djuric *et al.*, 1998).

### LINKAGE OF BREAST CANCER RISK FACTORS TO OXIDATIVE STRESS

#### *Family history of breast cancer*

Perhaps the most consistent risk factor for breast cancer is diagnosis of the disease in a first-degree relative. A positive family history of breast cancer may or may not imply genetic susceptibility, however. It may also be due to similar environments or lifestyle habits or other less penetrant, but more prevalent, inherited factors. Among women with a family history of breast cancer, a proportion of them carry mutant alleles in *BRCA1* or *BRCA2*, which confer a high lifetime risk of breast cancer. Only a small proportion of the population of women with breast cancer carry *BRCA* mutations (<3%), but the two genes are believed to be responsible for most truly hereditary breast cancers, particularly early-onset breast cancer. Al-

though this mutation is present in families with hereditary breast cancer, it was also found in 10% of a population-based cohort of women diagnosed with breast cancer before the age of 35 (Langston *et al.*, 1996). Recently, it was found that *BRCA1* in embryonic mouse stem cells is required for the transcription-coupled repair of oxidative damage (Gowen *et al.*, 1998). Thus, poor repair due to mutations in *BRCA1*, combined with normal or higher levels of oxidative stress, could link these inherited mutations to breast cancer risk.

#### *Reproductive and hormonal factors*

Risk related to reproductive and hormonal factors could be due to the metabolism of estradiol to reactive hydroxy radicals through redox cycling of the catechol estrogens (Yager and Liehr, 1996). The semiquinone radicals have been shown to damage protein (Winter and Liehr, 1986) and to induce kidney tumors (Kirkman, 1959) in hamsters treated with estradiol. Evidence that these effects are through an oxidative stress mechanism comes from the observation that when hamsters were treated with estradiol, products of lipid peroxidation more than doubled in the kidney, and increases were noted in glutathione and glutathione peroxidase in the target tissue (Roy and Liehr, 1989). Recently, Mobley *et al.* (1999) showed that treatment of calf thymus DNA with hydroxy estradiol resulted in damage (8-oxo-2'-deoxyguanosine), and that the presence of endogenous antioxidants such as glutathione, superoxide dismutase (SOD), and catalase dramatically reduced the amount of DNA damage induced by the catechol estrogens. The authors note that extremely high levels of catechol estrogens were needed for observed DNA damage. However, Yoshie and Ohshima (1998) found that DNA strand breakage occurred when plasmid DNA was incubated with both a catechol estrogen and a nitric oxide (NO)-releasing compound, both of which are formed in the human breast. Therefore, lower amounts of catechol estrogens used by Mobley *et al.* would likely result in DNA damage in the presence of a NO-releasing compound. Estrogens have also been shown to have antioxidant capabilities (Subbiah *et al.*, 1993). The net effect (oxidant and antioxidant) may be dependent

upon levels of catechol estrogens (determined, in part, by catechol O-methyl transferase [COMT]) or other enzymatic activities.

### Diet

**Alcohol:** Alcohol consumption could increase breast cancer risk through the generation of DNA-damaging reactive species (Wright *et al.*, 1998). Ethanol can be converted to acetate through the combined activities of alcohol dehydrogenase (ADH) and xanthine oxidoreductase (XOR) and/or aldehyde oxidase (AOX). Both XOR and AOX can generate ROS. Studies of acute alcohol toxicity of the liver have noted that metabolism of alcohol produces ROS, resulting in oxidative damage to DNA, including strand breakage (Rajasinghe *et al.*, 1990). Studies from the liver and pancreas have also shown that the ROS generated are from the combined activity of XOR and AOX (Rajasinghe *et al.*, 1990; Shaw and Jayatilleke, 1992; Nordback *et al.*, 1994; Mira *et al.*, 1995). ADH and XOR are present in human breast tissue (Saleem *et al.*, 1984; Ishii *et al.*, 1995). It has been suggested that alcohol-derived ROS could have an impact on breast carcinogenesis at several stages (Wright *et al.*, 1998): they could act as initiators of tumors, or at later stages of progression and transformation. They may also affect cell proliferation.

**Dietary fat:** Dietary fat intake has long been hypothesized to be associated with breast cancer risk (Willett, 1989) on the basis of animal studies (Cave, 1994), ecologic studies (Armstrong and Doll, 1975; Carroll *et al.*, 1986), and studies of migrants from areas with low fat intake to those with high fat intake (Dunn, 1975). However, many analytic epidemiologic studies have not shown an effect of fat, including the results of a pooled analysis of seven cohort studies (Hunter *et al.*, 1996). Recently, it has been suggested that diet in childhood and at the time of puberty may be of importance (Pottischman *et al.*, 1998). Evidence from animal studies suggests that only fat intake before the first pregnancy affects risk (Ip, 1993). It is possible that the failure to identify an association of fat intake with breast cancer in epidemiologic studies may be because intake early in life, rather than recent consumption, is most important. Failure to detect an association may

also be due to fact that there is not enough variability in fat consumption within populations (*i.e.*, there are too few individuals with low intakes) (Goodwin and Boyd, 1987), or because of measurement error inherent in dietary questionnaires (Bingham *et al.*, 1994). It may also be that specific types of dietary fat are more important than total fat, and investigators have not been evaluating the proper variables.

If there is an association with dietary fat and breast cancer, it could be through a mechanism of its oxidation to ROS and stimulation of lipid peroxidation. For example, autoxidized linolenic and linoleic acids can form 8-hydroxy-2'-deoxyguanosine in DNA (Kasai and Nishimura, 1988). In fact, in an intervention study, Djuric *et al.* (1991) found that regardless of the diet arm, there was a significant linear regression relationship between total fat intake and DNA damage levels. In fact, level of oxidized DNA bases was an important marker for dietary compliance to a low-fat diet. Caloric intake, however, may be even more important in generation of oxidative stress and breast cancer risk than fat consumption (Simic and Bergtold, 1991).

**Fruits and vegetables:** Numerous nutritional epidemiologic studies have noted associations between dietary antioxidants and decreased breast cancer risk (AICR, 1997, pp. 274–276), although not all studies support such an association (Byers, 1994). The evidence for a protective effect appears to be more abundant for fruits than for vegetables (AICR, 1997, p. 281). The mechanistic relationship of these putative risk factors, however, has not been elucidated. Fruits and vegetables are sources of a number of nutrients, including antioxidant vitamins such as carotenoids, the tocopherols, vitamin C, and flavonoids, and the inverse relationships with consumption of fruits and vegetables could be tied in through their antioxidant properties. One hypothesis is that dietary antioxidants affect oxidative stress and the production of ROS by altering the balance between prooxidant cellular activity and antioxidant defenses.

**Environmental contaminants:** The interaction of xenobiotics with numerous enzyme systems has been shown to result in the metabolism of chemicals to free radical intermediates, some of which, in turn, can also activate molecular oxy-

gen via univalent reduction to superoxide (Mason, 1982; Trush and Kensler, 1991). Because of temporal and demographic trends, there has been growing interest in the role of chemical carcinogens in relation to breast cancer, and there is evidence that enzymes involved in oxidative pathways could affect these associations.

In the past several years, a number of epidemiologic studies have been conducted to evaluate possible associations between exposure to environmental factors, including organochlorines and risk of breast cancer. Results from the studies of breast cancer are inconsistent, but there have also been findings of elevated risk among specific subsets of the population. For example, Moysich, Ambrosone, and colleagues (Moysich *et al.*, 1998) found that, while there was no overall increased risk of breast cancer associated with higher serum levels of polychlorinated biphenyls (PCBs) and 1,1-dichloro-2,2-bis(*p*-chlorophenyl)ethylene (DDE), or with specific PCB congeners, risk was increased among women with higher levels who had never lactated, a major form of excretion of lipid-soluble organochlorines. We also found that in women with levels of PCBs above the median, the presence of at least one *CYP1A1* isoleucine-to-valine substitution allele increased risk almost three-fold. *CYP1A1* is an enzyme that is highly induced by organochlorines and metabolizes some of the less persistent PCBs (Moysich *et al.*, 1999). In women with lower body burden of organochlorines, no association between *CYP1A1* genotype and breast cancer risk was observed.

In addition to PCBs and DDE, other lipid-soluble organochlorines could also be associated with breast cancer risk, although they have not been studied to the same extent that PCBs and DDE have. In a Danish cohort study, Hoyer *et al.* (1998) found that higher levels of dieldrin, a highly toxic persistent pesticide, were associated with significantly increased breast cancer risk [adjusted odds ratio (OR) for fourth quartile = 2.05, 95% confidence interval (CI) = 1.17–3.57]. There was also a nonsignificant increase in risk with higher levels of  $\beta$ -hexachlorocyclohexane.

Interestingly, for both PCBs and dieldrin, a mechanism of induced oxidative stress in breast carcinogenesis has been proposed. Amaro *et al.*

(1996) have shown that PCBs can be metabolically activated to catechols and hydroquinones. These species can be further activated by peroxidases, including myeloperoxidase, to species that are capable of binding to DNA (Ariyoshi *et al.*, 1993; Oakley *et al.*, 1996b). Hydroxylated metabolites of PCBs were shown to be retained in human plasma (Bergman *et al.*, 1994), and Oakley *et al.* (1996a) investigated the hypothesis that PCBs may impact breast cancer risk by increased oxidative DNA damage due to metabolites via enzymatic and nonenzymatic mechanisms. They found that peroxidase-mediated oxidation of PCB dihydroxy metabolites results in oxidative DNA damage, using 8-oxodG as a marker.

There is also accumulating evidence that possible associations between exposure to dieldrin and cancer risk are through oxidative stress. Klaunig's group (Bachowski *et al.*, 1998) has shown that the selective toxicity of dieldrin in mouse liver, but not rat, is due to dieldrin's ability to induce oxidative stress in the liver of mice, but not in rats. Furthermore, vitamin E supplementation in mice with dieldrin-induced tumors resulted in inhibition of hepatic focal lesion growth (Kolaja *et al.*, 1998). Another chlorinated pesticide, lindane, has been shown to reduce superoxide dismutase and catalase activity in both rat and mouse liver, while increasing peroxidase and P450 activity, leading to an increased oxidative load (Junqueira *et al.*, 1986). Clearly, associations between organochlorines and breast cancer risk need to be evaluated in relation to metabolic variability in enzymes that produce and prevent oxidative stress.

## ENDOGENOUS GENERATION OF AND RESPONSE TO ROS

Variability in exposure to factors that could increase levels of ROS, through exogenous routes or by variability in endogenous processes, as well as cellular responses to ROS, will ultimately determine levels of oxidative stress in the breast. ROS are generated by numerous enzymes, *e.g.*, myeloperoxidase, or regulatory processes such as those stimulated by tumor necrosis factor- $\alpha$ . Endogenous defenses against ROS include glutathione peroxidase, catalase,

and SOD, of which there are three known forms: the cytosolic and extracellular copper/zinc SODs and the mitochondrial manganese SOD (MnSOD). These enzymes form the first line of defense against superoxide and hydrogen peroxide ( $H_2O_2$ ). The resultant secondary oxidation products may still damage DNA, proteins, and lipid, and require further detoxification. This second line of defense against ROS is provided by enzymes such as glutathione peroxidase and the glutathione S-transferases. Many of these enzymes are polymorphic and breast cancer risk related to oxidative stress could be impacted by this interindividual variability.

*Polymorphic enzymes related to oxidative stress: generation of ROS*

**Myeloperoxidase (MPO):** MPO is thought to function as an antimicrobial agent by catalyzing a reaction between hydrogen peroxide, produced by NADPH oxidase, and chloride to generate hypochlorous acid (HOCl), a toxic oxidizing agent. HOCl further reacts with other biological molecules to generate secondary radicals, including highly reactive hydroxyl ions (Klebanoff, 1980). The enzyme is present in neutrophils, which invade inflamed tissues, including the breast, to combat infection and presumably to protect breast milk during lactation (Josephy, 1996). In addition to its presence in human breast milk, detection with immunohistochemistry has demonstrated the presence of MPO in breast tissue from women with cancer (Samoszuk *et al.*, 1996), and MPO gene co-amplification was observed with *c-erbB-2* in human breast carcinomas (Coene *et al.*, 1997). A functional polymorphism has been identified that decreases expression of MPO, apparently, by destroying a binding site for the SP1 transcription factor (Piedrafita *et al.*, 1996). In a study of lung cancer, London *et al.* (1997) found that 8% of the Caucasian population in the study ( $n = 459$ ) were homozygous for the allele (A) that reduces transcription of the myeloperoxidase gene, and 31% were heterozygotes. In that study, lung cancer risk was decreased among individuals who inherited two copies of the A allele. A small study (Reynolds *et al.*, 1999) was also conducted of

the relationship between the MPO genetic polymorphism and risk for Alzheimer's disease, in which oxidizing radicals are implicated (Cross *et al.*, 1987; Multhaup *et al.*, 1997; Smith, 1998). In that study, it was found that the allele associated with higher expression of MPO increased risk of Alzheimer's disease among women, but not among men. The authors suggest that the gender difference in risk may be related to the possible effects of sex hormones on MPO gene expression. Because of the presence of MPO in the breast, and its ability to generate ROS, the polymorphism may be important in an oxidative stress pathway in human breast cancer.

**Tumor Necrosis Factor- $\alpha$  (TNF- $\alpha$ ):** The cytokine, TNF- $\alpha$  triggers receptor-mediated processes, yielding ROS and causing oxidative stress in mitochondria. TNF- $\alpha$  was discovered through its antitumor activity, but it has been implicated in the pathophysiology of diabetes and cardiovascular disease due to its physiologic involvement in oxidative stress. In fact, one of the mechanisms of TNF- $\alpha$  cytotoxicity is thought to be damage from ROS (Luster, 1999). A G-to-A transition in the gene at position 308 directly affects the regulation of TNF- $\alpha$ , and the variant allele is associated with higher constitutive and inducible levels of TNF- $\alpha$  (Wilson, 1994). In a study of TNF- $\alpha$ , genetic polymorphisms in relation to both lymphoma and breast cancer in a Tunisian population (Choucane, 1997), Chouchane found that heterozygosity for the variant allele significantly increased cancer risk. In this population, 32% of the controls were homozygous or heterozygous for the variant alleles, cited as only slightly higher than in a European population (28%). Higher levels of TNF- $\alpha$  could result in more ROS in the mitochondrion, causing oxidative stress and resultant DNA damage; conversely, low levels could be protective.

*Polymorphic enzymes related to oxidative stress: response to ROS*

Endogenous defenses against ROS include glutathione peroxidase, catalase, and SOD. There are three known forms of SOD: the cytosolic and extracellular copper/zinc SODs and the mitochondrial manganese SOD (MnSOD).

**MnSOD:** This SOD is synthesized in the cytosol and modified post-transcriptionally for transport into the mitochondrion (Wispe *et al.*, 1989; Shimoda-Matsubayashi *et al.*, 1996). In the mitochondrion, it catalyzes the dismutation of two superoxide radicals, producing  $H_2O_2$  and oxygen. MnSOD is induced with free radical challenge (Rohrdanz and Kahl, 1998a) and cigarette smoke (Gilks *et al.*, 1998). Recently, two genetic variants of the *MnSOD* gene were identified (Shimoda-Matsubayashi *et al.*, 1996). A structural mutation, a T-to-C substitution in the mitochondrial-targeting sequence, was found and changes an amino acid. The investigators who identified the polymorphism (Shimoda-Matsubayashi *et al.*, 1996) predicted that the resulting amino acid change would alter the secondary structure of the protein. Rosenblum and colleagues (Rosenblum *et al.*, 1996) suggest that the alteration might affect the cellular allocation of the enzyme and mitochondrial transport of MnSOD into the mitochondrion, where it would be biologically available. They further suggest that inefficient targeting of MnSOD could leave mitochondria without their full defense against superoxide radicals, which could lead to protein oxidation, as well as mitochondrial DNA mutations. We hypothesized that the polymorphism in the *MnSOD* gene would result in higher levels of ROS, and that in women whose diets were low in fruits and vegetables, this polymorphism would increase risk of breast cancer. Interestingly, we found this to be the case, particularly for premenopausal women (Ambrosone *et al.*, 1999a). Those who were homozygous for the variant allele had a four-fold increase in breast cancer risk in comparison to those with who were homozygous or heterozygous for the common allele (OR = 4.3, 95% CI, 1.7–10.8). Risk was most pronounced among women below the median consumption of fruits and vegetables, and of dietary ascorbic acid and  $\alpha$ -tocopherol, with little increased risk for those with diets rich in these foods. These data support the hypothesis that MnSOD and oxidative stress play a significant role in breast cancer risk, particularly in premenopausal women. Interestingly, there is a link between TNF $\alpha$  and MnSOD in the breast. When MCF-7 cells were treated with TNF, there was a five-fold in-

crease in MnSOD activity (Siemankowski *et al.*, 1999).

**Extracellular SOD (EC-SOD):** This is the principal enzymatic scavenger of superoxide in the extracellular space. Molecular genetic studies have shown that a single base substitution causing substitution of glycine for Arg213 in the heparin-binding domain of this enzyme causes the extremely high plasma level of EC-SOD (Yamada *et al.*, 1995; Marklund *et al.*, 1997). In a study of 242 healthy volunteers in Australia (Adachi and Wang, 1998), serum EC-SOD levels were found to be distributed in two discrete groups of low level (29.9–152.1  $\mu$ g/liter) and high level (940.2–1,798  $\mu$ g/liter). All of individuals within the high-level group (3.3%) carried the R213G mutation, whereas none of the low-level EC-SOD volunteers did. Similar distribution of phenotype was observed in a large cohort ( $n = 4,925$ ) in Sweden (Marklund *et al.*, 1997), where 4% had eight-fold higher plasma levels of EC-SOD. All but one of the individuals in this group carried the R213G polymorphism. It is likely that those with high EC-SOD were likely to be homozygous for the variant allele.

SOD works in conjunction with two other antioxidant proteins, catalase and glutathione peroxidase. These enzymes remove the toxic  $H_2O_2$  produced by the SODs, by converting them into water.

**Catalase (CAT):** CAT is a heme enzyme that has a predominant role in controlling  $H_2O_2$  concentration in human cells, by converting  $H_2O_2$  into  $H_2O$  and  $O_2$ . Catalase induction was elicited by  $H_2O_2$  in hamster tracheal epithelial cells (Shull *et al.*, 1991) and human retinal pigment epithelial cells (Tate *et al.*, 1995), indicating a key role for catalase in antioxidant defense. It was also found to be inducible in both primary rat hepatocytes and rat hepatoma cell lines (Rohrdanz and Kahl, 1998b). Acatalasemic mice that have blood and tissue levels of catalase that are approximately one-tenth that of normal mice (Ishii *et al.*, 1996) and females are susceptible to spontaneous mammary carcinoma. Because a preventive effect of vitamin E on human breast cancer is controversial, Ishii and colleagues used the acatalasemic mouse to test whether carcinogenesis could be prevented by vitamin E. In this study,

acatalasemic mice developed mammary tumors after 9 months after vitamin E deprivation, and 14 months after supplementation. Normal mice did not develop mammary tumors, regardless of diet. These data indicate that there could be important implications for the study of variability in CAT in relation to dietary and supplemental antioxidants and human breast cancer risk.

**Glutathione-associated metabolism** is a major mechanism for cellular protection against agents that generate oxidative stress. Glutathione participates in detoxification at several different levels, and may scavenge free radicals, reduce peroxides, or be conjugated with electrophilic compounds, providing the cell with multiple defenses against ROS and their reactive toxic products (Hayes and McLellan, 1999a).

**Glutathione peroxidases:** The glutathione peroxidases are a family of enzymes that catalyze the reduction of  $H_2O_2$  and organic hydroperoxides to water and alcohols, respectively. Se-dependent glutathione peroxidase (GPX1) is present in the cytosol and in mitochondria (Ursini *et al.*, 1986). Knockout mice studies have shown that GPX1 is of critical importance in protection against oxidative stress generated by  $H_2O_2$  (deHaan *et al.*, 1998). GPX1 is transcriptionally up-regulated as an adaptive response to oxidative stress. An amino acid substitution in the *GPX1* gene was identified by searching the human expressed sequence tags (EST) database (Forsberg *et al.*, 1999), followed by PCR and DNA sequencing. Restriction analyses of 25 individuals showed 13 homozygotes for Pro, 3 homozygotes for Leu, and 9 heterozygotes. The polymorphism in *GPX1* was evaluated in 18 populations that were endemic for malaria in relation to polymorphisms in hemoglobin  $\beta$ -chain (Destro-Bisol *et al.*, 1999). These investigators found that the erythrocytes of those heterozygous for the variant allele were more efficient in sheltering the cell membrane from irreversible oxidation and binding of hemoglobin caused by the oxidant stress exerted by the malaria parasite. An in-frame variable polyalanine (GCG) repeat polymorphism has been described, and the 6-alanine (ALA6) repeat allele also has a nucleotide substitution associated with a proline-leucine substitution (Moscow *et al.*, 1994). Measurement of 8-hy-

droxydeoxyguanosine (8OHdG), a marker of oxidative damage, in DNA from normal lung tissue revealed a trend of less 8OHdG associated with one or two copies of the ALA6 allele (Hardie *et al.*, 2000), indicating that the variant may protect DNA from ROS damage. This difference could be relevant for breast cancer associated with oxidative stress.

**Phase II enzymes:** Phase II enzymes, which include the glutathione S-transferases (GSTs), are involved in the detoxication of many reactive species and are the second line of defense after SOD, CAT, and GPX. The GSTs detoxify not only lipid peroxidation products and oxidized bases (Hayes and McLellan, 1999b), but also other endogenous oxidation products, including *o*-quinones formed from catecholamines and estrogen-3,4-quinones (Yager and Liehr, 1996; Cavalieri *et al.*, 1997). The cytosolic glutathione transferases comprise four classes, alpha, mu, pi, and theta, of which at least three are represented in both normal and breast tumor tissue (Forrester *et al.*, 1990). Although glutathione transferases appear to have a fundamental role in the detoxication of electrophilic xenobiotics by conjugation to glutathione, several enzymes possess limited glutathione-dependent peroxidase activity (Hayes and Pulford, 1995). Of these classes, the alpha class appears to possess the greatest peroxidase activity, but enzymes of this class are expressed at low levels in both normal and breast tumor tissue. Therefore, GSTM1-1, which is expressed at higher levels, may make a significant contribution to Se-independent glutathione peroxidase activity in breast (Forrester *et al.*, 1990). Of the glutathione transferases, *GSTM1* is of particular interest because it shows a null polymorphism that results in lack of the enzyme in approximately 50% of the population (Brockmoller *et al.*, 1992). As reviewed by Rebbeck (1997), studies have shown that individuals who possess the homozygous null allele are at increased risk of lung and bladder cancer, both of which are associated with exposure to chemical carcinogens. However, studies of possible associations between *GSTM1* and breast cancer risk have yielded inconsistent results (Zhong *et al.*, 1993; Kelsey *et al.*, 1997; Bailey *et al.*, 1998; Helzlsouer *et al.*, 1998). Although we did not find an association between *GSTM1* and breast

cancer in the western New York study (Ambrosone *et al.*, 1995, 1999b), Helzlsouer noted a more than two-fold increased risk with the null allele (Helzlsouer *et al.*, 1998).

#### *Oxidative stress through hormone metabolism*

The secondary metabolism of 17 $\beta$ -estradiol involves *O*-methylation by catechol *O*-methyltransferase (COMT), conjugation to glucuronides and sulfates, and clearance of reactive semiquinones and quinones, reported to involve catechol oxidation coupled to glutathione conjugation (Zhu and Conney, 1998).

*Catechol-O-methyl transferase:* COMT is one of several phase II enzymes involved in the conjugation and inactivation of the catechol estrogens (Guldborg and Marsden, 1975). Because of the potential for the catechol estrogens, particularly the 4-hydroxy catechol, to bind to DNA and result in DNA damage (Liehr, 1997; Cavalieri *et al.*, 1997), and to undergo redox cycling to damaging quinones and semiquinones, the possible role of variable activity in the enzyme in relation to breast cancer risk is important. An amino acid change (valine to methionine) at position 158/108 in the membrane-bound/cytosolic form of the protein has been linked to decreased methylation activity of COMT (Lachman *et al.*, 1996). The polymorphism is believed to be closely associated with the observed trimodal distribution of COMT enzyme activity in the human population associated with high (COMT<sup>Val/Val</sup>), intermediate (COMT<sup>Val/Met</sup>), and low (COMT<sup>Met/Met</sup>) COMT activity (Goldstein and Leiberman, 1992; Price-Evans, 1993). The role of the COMT genetic polymorphism in relation to breast cancer risk has been evaluated by three groups to date in the United States, all with conflicting results (Lavigne *et al.*, 1997; Millikan *et al.*, 1998; Thompson *et al.*, 1998). Results from a recent study in Taiwan (Huang *et al.*, 1999) indicated that COMT low-activity alleles increased breast cancer risk and that combined 'high-risk' genotypes for COMR, CYP17, and CYP1A1 inferred the greatest risk of all.

*UDP-glucuronosyltransferases (UGTs):* These are also phase II enzymes that render polarity to reactive species, making them more water soluble and more easily excreted. The UGTs are

involved not only in the metabolism of many drugs and xenobiotics, but also are important in the biotransformation of important endogenous substrates, including estradiol (deWildt *et al.*, 1999). Three human liver UGTs (UGT2B7, 1A1, 1A3) have been shown to catalyze the glucuronidation of catechol estrogens and lead to their enhanced elimination (Cheng *et al.*, 1998). UGT2B7 was shown to react with higher efficiency toward 4-hydroxyestrogenic catechols, whereas UGT1A1 showed higher activities toward 2-hydroxyestrogens (Cheng *et al.*, 1998). Both of these enzymes are polymorphic. There are variable numbers of TA repeats in the promoter TATA box of UGT1A1, and they are inversely related to levels of gene expression (Hall *et al.*, 1999). Hall *et al.* (1999) found that two UGT1A1 alleles are present in Caucasian Europeans; between 9% and 16% are homozygous for the variant allele (7) and heterozygotes range from 44 to 51% of European Caucasian populations. Variability in expression of UGT1A1 could have important effects on ultimate effects of catechol estrogens.

A polymorphism has also been identified in UGT2B7, in which a C-to-T transversion at nucleotide 802 results in a tyrosine to histidine substitution (Jin *et al.*, 1993), with allele frequencies for His268 and Tyr268 calculated at 0.52 and 0.48, respectively.

## SUMMARY

As mechanisms of carcinogenesis become more fully elucidated, the complexity of cancer etiology becomes more and more obvious, particularly for hormone-responsive diseases. Moreover, epidemiologic and laboratory studies show that the manner in which risk factors relate to disease incidence is not well understood. It is now clear that breast cancer is multifactorial, and that some relevant exposures may be those that occur before puberty. Molecular epidemiologic studies may be useful for unraveling some of that etiologic complexity. By evaluating genetic variability that contributes to ultimate effects of factors to which women are exposed, relationships may be more clearly observed. If only "sensitive" subgroups are evaluated, based upon their genetic

metabolic profiles, more precise risk estimates may be calculated. The study of variability in genes that are involved in the generation of ROS and protection from oxidative stress may elucidate pathways of carcinogenesis in the breast that are clearly linked to an imbalance between prooxidant and antioxidant forces.

## ABBREVIATIONS

8-oxo-dG, 8-Oxo-7,8-dihydro-2'-deoxyguanosine; ADH, alcohol dehydrogenase; AOX, aldehyde oxidase; CAT, catalase; COMT, catechol O-methyltransferase; CYP1A1, cytochrome P450 1A1; DDE, 1,1-dichloro-2,2-bis(p-chlorophenyl)ethylene; EC-SOD, extracellular superoxide dismutase; GST, glutathione S-transferase; GPX1, glutathione peroxidase; H<sub>2</sub>O<sub>2</sub>, hydrogen peroxide; MnSOD, manganese superoxide dismutase; MPO, myeloperoxidase; PCBs, polychlorinated biphenyls; ROS, reactive oxygen species; SOD, superoxide dismutase; TNF- $\alpha$ , tumor necrosis factor- $\alpha$ ; XOR, xanthine oxidoreductase; UGT, UDP-glucuronosyltransferase.

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