Mitochondrial DNA Repair through OGG1 Activity Attenuates Breast Cancer Progression and Metastasis

Larysa V. Yuzefovych1, Andrea G. Kahn2, Michele A. Schuler3, Lars Eide4, Ritu Arora5, Glenn L. Wilson6, Ming Tan5, and Lyudmila I. Rachek1

Abstract

Production of mitochondrial reactive oxygen species and integrity of mitochondrial DNA (mtDNA) are crucial in breast cancer progression and metastasis. Therefore, we evaluated the role of mtDNA damage in breast cancer by genetically modulating the DNA repair enzyme 8-oxoguanine DNA glycosylase (OGG1) in the PyMT transgenic mouse model of mammary tumorigenesis. We generated mice lacking OGG1 (KO), mice overexpressing human OGG1 subunit 1 in mitochondria (Tg), and mice simultaneously lacking OGG1 and overexpressing human OGG1 subunit 1 in mitochondria (KO/Tg). We found that Tg and KO/Tg mice developed significantly smaller tumors than KO and wild-type (WT) mice after 16 weeks. Histologic analysis revealed a roughly 2-fold decrease in the incidence of lung metastases in Tg mice (33.3%) compared to WT mice (62.5%). Furthermore, lungs from Tg mice exhibited nearly a 15-fold decrease in the average number of metastatic foci compared with WT mice ($P \leq 0.05$). Primary tumors isolated from Tg mice also demonstrated reduced total and mitochondrial oxidative stress, diminished mtDNA damage, and increased mitochondrial function. Targeting hOGG1 to the mitochondria protected cells from mtDNA damage, resulting in downregulation of HIF1α and attenuated phosphorylation of Akt. Collectively, we demonstrate proof of concept that mtDNA damage results in breast cancer progression and metastasis in vivo. Moreover, our findings offer new therapeutic strategies for modulating the levels of mtDNA repair enzymes to delay or stall metastatic progression. Cancer Res; 76(1); 1–5.

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Introduction

Breast cancer is the most commonly diagnosed cancer and the leading cause of cancer death among women worldwide. Despite improvements in diagnosis, treatment, and longevity, the effect on mortality has been modest. A lack of understanding about the natural history of the disease is a major contributory factor to this limitation. On a molecular level, it is still not fully understood which of the changes in breast tumors lead to invasion and metastasis. Among the potential causes are mitochondrial dysfunction, mitochondrial reactive oxygen species (mtROS) generation, and mitochondrial DNA (mtDNA) damage. Recently, mtROS production has been proposed to play an important role in breast cancer progression in both in vitro (1) and in vivo models (1, 2). Also, it has been shown that mitochondrial polymorphism and mtDNA variations modify breast cancer risk in patients (3). mtDNA variations may cause inefficient oxidative phosphorylation and affect the efficiency of electron transport chains, leading to the accumulation of ROS, mtDNA damage, and increased cancer risk. Studies using cytoplasmic hybrid technology have shown that mutations in mtDNA were associated with overproduction of ROS and can regulate tumor cell metastasis (4). Taken together, these recent findings suggest that integrity of mtDNA is crucial in cancer progression and metastasis.

The molecular mechanisms of ROS-driven tumor progression are not completely understood, but it has been shown that increased ROS generation upregulates the expression and activities of the pathways involving Akt, MAPK, hypoxia-inducible factor 1 (HIF1α), and remodeling of the extracellular matrix by metalloproteinases, which ultimately lead to tumor progression and metastasis (reviewed in 5, 6). On the other hand, ROS-induced damage to mtDNA in cancer cells causes alterations in mtDNA transcription through either base mispairing, which results in defective transcripts, or decreased transcription due to polymerase blocking. Since mammalian mtDNA encodes 13 polypeptides of the electron transport chain, 2 rRNAs, and 22 tRNAs, alterations in mitochondrial transcription could change electron transport complexes to cause decreased ATP production and also, lead to defective electron transfer, which would cause additional ROS production, thus establishing a “vicious cycle” between mtDNA damage and ROS generation, because any damage to the respiratory chain may enhance ROS production.
and thus heighten the oxidative stress to all other mitochondrial components, including mtDNA. This increased oxidative stress will exacerbate mitochondrial dysfunction, which ultimately leads to activation of signaling pathways leading to cancer progression.

Our previous data showed that the mitochondrial-targeted DNA repair enzyme, human 8-oxoguanine (8-oxoG) DNA glycosylase/AP lyase (hOGG1) enhanced mtDNA repair, increased mitochondrial function, and protected different cell types from oxidant-mediated death (7–9). In addition, we (8, 9) and others (10) have shown that targeting of hOGG1 to mitochondria decreased mtROS production, thus, supporting the vicious cycle hypothesis (8–10). The goal of this study is to investigate whether mtDNA damage controls mitochondrial dysfunction, increases mtROS production, and enhances breast cancer progression in a well-established genetic model of breast cancer, PyMT mouse.

Materials and Methods

Animals

Double transgenic female mice were generated by crossing FVB/N-Tg(MMTV-PyMT)634Mul/J male mice (The Jackson Laboratory), which are well characterized and a widely used transgenic transgenic model of metastatic breast cancer (11) laboratory (The Jackson Laboratory), which are well characterized and a widely used preclinical transgenic model of metastatic breast cancer (11) with the [OOG1<sup>−/−</sup> (KO)], mitochondrial targeted [hOGG1<sup>Tg</sup>], Tg, KO/Tg, and wild-type (WT) females on a congenic C57/BL6 background (9, 12, 13). Genotyping of mice was performed using genomic DNA derived from tails and PCR with a set of primers described for PyMT animals (Jackson Lab website) and, for OGG1 models, using previously described PCR primers (12, 13). Female double transgenic mice were maintained for 16 weeks. All procedures used in this study were approved by the Institutional Animal Care and Use Committees of the University of South Alabama and fully complied with the guidelines from the NIH.

Gross evaluation of tumor and histologic analysis

Starting at 16 weeks, mice were sacrificed, and all mammary tumors were carefully excised and weighed. Mammary tumors and lungs sections were cut into smaller portions, and fixed with 10% neutral buffered formalin for at least 24 hours before embedding in paraffin. Sections were cut at 5 μm, stained with hematoxylin and eosin, and evaluated for invasion and lung metastases in a blind fashion by an experienced histopathologist (Dr. Andrea Kahn, Pathology Department, University of South Alabama, Mobile, AL). Analyses and descriptions were in accordance with the guidelines put forth by the mouse mammary gland pathology consensus meeting in Annapolis (14) to render a diagnosis of the tumors. The grade for invasion (scored from 1 to 3) was estimated when areas of invasion other than the more expansile center of the lesion were identifiable.

Isolation of cellular fractions and 8-oxoG activity assay

Mammary tumors were dissected and homogenized in liquid nitrogen. Mitochondrial and nuclear fractions were isolated, and the purity of the preparation was checked as we previously described (10). The OGG1 activity was performed as previously described with minor modifications (7, 8).

Mitochondrial DNA damage analysis and copy number

mtDNA damage and copy number were assessed as described previously with some modifications (15). Briefly, mammary tumors were homogenized in liquid nitrogen and total DNA was isolated using a Qiagen DNAeasy kit for the DNA isolation (Qiagen). DNA was digested with EcoRI, precisely quantified, and quantitative alkaline Southern blot analysis was performed to evaluate changes in the density of mtDNA lesions using mouse mtDNA specific probe (cytochrome c oxidase, I subunit; ref. 15). The results for mtDNA damage obtained after quantitative alkaline Southern blot analysis were normalized for mtDNA copy number and presented (as arbitrary units).

Mitochondrial ATP level

Mitochondria were isolated from fresh tumor tissues and mitochondrial ATP level was analyzed as we previously described (15). Values were normalized to protein content.

Lactate dehydrogenase activity assay

Tumors were extracted for protein and then, their lactate dehydrogenase (LDH) activity was measured using an LDH assay kit (BioVision). The results were normalized to the tumor weight.

Protein isolation, Western blot analysis, and oxidative protein carbonylation

Total cellular or mitochondrial fractions from mammary tumors were isolated as described previously (15). The antibodies used were HIF1α, phospho-Akt (Ser473), total Akt (Cell Signaling Technology), Cox IV, a subunit IV component (Mitosciences), and actin (Sigma). Complexes formed were detected with horseradish peroxidase conjugated anti-mouse IgG or anti-rabbit IgG antibodies (Promega) using chemiluminescent reagents (SuperSignal; Pierce). An oxidative protein carbonylation (PCO) assay was performed as we described previously (15). Where indicated, the resultant band images were scanned and analyzed using Fujifilm Image Gauge Version 2.2 software. For HIF1α protein content, data were normalized to the density of actin bands. In addition, for PCO, a value of 1 was arbitrary assigned to the results from the PyMT/WT group, and all data were normalized to the density of bands of PyMT/WT and presented as relative units.

Statistical analysis

Data were expressed as mean ± SE. Differences between groups were assessed using one-way ANOVA (GraphPad Prism) followed by Bonferroni analysis where appropriate. Statistical significance was determined at the 0.05 level.

Results and Discussion

Targeting of hOGG1 into mitochondria in both PyMT/Tg and PyMT/KO/Tg mice suppressed tumor growth and metastases

We transgenically expressed hOGG1 in the mitochondria and generated PyMT/Tg and PyMT/KO/Tg mice. Starting at 16 weeks, mice were sacrificed, and all mammary tumors were carefully excised and weighed. As shown in Table 1, the appearance of palpable tumors in the PyMT/KO mice was about 2 weeks earlier and in PyMT/KO/TG it was delayed for 2 weeks compared with the PyMT/WT group.

Representative images of 12- to 16-week-old PyMT female mice of different OGG1 genotypes are shown in Supplementary Fig. S1. PyMT/KO mouse developed an increased number of
large and bulky tumors compared with all other genotypes. Previously, two reports demonstrated that PyMT mice on the C57BL/6 background have a longer mammary tumor latency (92 days) compared with PyMT on the FVB background (53 days) while the incidence of lung metastasis was only slightly reduced (2, 16). Our results are in line with these reports because the first tumor appearance were delayed in all genetic models (C57BL/6 background) compared with PyMT on FVB background (2, 16). Interestingly, the KO/Tg group displayed a lower (92.3%) primary tumor incidence as compared with the 100% in all other groups. By recording the total tumor weight per mouse, it was observed that both PyMT/Tg and PyMT/KO/Tg mice developed significantly smaller tumors compared with PyMT/WT. This effect was especially pronounced with PyMT/KO mice (Fig. 1A). Histopathologic analysis showed that the majority of tumors had a similar overall pattern of advanced invasive carcinoma, but there were a few (derivatives from PyMT/WT) with a more distinct morphology pattern of advanced invasive carcinoma, but there were a few (derivatives from PyMT/WT) with a more distinct morphology.

Mitochondrial expression of hOGG1 in both PyMT/Tg and PyMT/KO/Tg mice prevented lung’s metastases

As shown in Table 1, we found about a 2-fold difference ($P \leq 0.05$) in the metastatic tumor incidence in lungs between PyMT/Tg (33.3%) and PyMT/WT mice (62.5%). Remarkably, the lungs of PyMT/Tg mice showed about a 15-fold decrease in average number of metastatic foci compared to those of PyMT/WT mice [$P \leq 0.05$ (Fig. 1B; Supplementary Fig. S2)]. Therefore, based on these data, we conclude that mtDNA regulates both progression and proliferation of tumor foci at a distant site of metastasis.

### Analysis of OGG1 activity in mammary tumors from double transgenic PyMT mice

OGG1 activity was examined in mammary tumors isolated from nuclear and mitochondrial fractions from all four groups of mice. First, mitochondrial and nuclear fractions were isolated and the purity of the preparation was checked by the enrichment of mitochondrial or nuclear specific proteins as determined by Western blot (Supplementary Fig. S3A and S3C). As expected, there was no notable difference in OGG1 activity in nuclear fractions isolated from mammary tumors in the PyMT WT, Tg, or KO/Tg groups (Supplementary Fig. S3B). There was minimal OGG1 activity in nuclear fractions from PyMT/KO group (Supplementary Fig. S3B), which, most likely, indicates the involvement of some alternative nuclear enzyme/s in the repair of 8-oxoG in the nuclear fractions of KO mice. On the contrary, as shown in Supplementary Fig. S2D, OGG1 activity was elevated in mitochondria isolated from tumors both from Tg and KO/Tg animals, whereas OGG1 activity was lower in KO mice compared with WT mice.

Tumors isolated from PyMT/Tg mice showed reduced total and mitochondrial oxidative stress, diminished mtDNA damage, increased mitochondrial function, and reduced LDH activity.

First, we evaluated both total and mitochondrial oxidative stress using a common marker of oxidative stress in proteins, PCO. Whole cell extracts (Fig. 2A and B) and mitochondrial fractions (Fig. 2C and D) were analyzed by SDS-PAGE and Western blot. As shown, the expression of proteins involved in the mitochondrial and nuclear oxidative stress pathways (complex IV, ATPase, p53) were significantly increased in nuclear and mitochondrial fractions from both PyMT/Tg and PyMT/KO/Tg mice compared with WT mice (Fig. 2A and B).

Table 1. Characteristics of mice

<table>
<thead>
<tr>
<th>PyMT genotype</th>
<th>Primary tumor incidence (%)</th>
<th>Mean age in week to first palpable tumor</th>
<th>Metastatic tumor incidence (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>KO</td>
<td>100</td>
<td>9.35 ± 0.7a,b</td>
<td>82.8a,b</td>
</tr>
<tr>
<td>WT</td>
<td>100</td>
<td>11.86 ± 0.1</td>
<td>62.5</td>
</tr>
<tr>
<td>WT/Tg</td>
<td>100</td>
<td>12.89 ± 0.26</td>
<td>33.3a</td>
</tr>
<tr>
<td>KO/Tg</td>
<td>92.3</td>
<td>13.64 ± 0.3a</td>
<td>36.4a</td>
</tr>
</tbody>
</table>

NOTE: $n = 13–16$.

*aSignificance at $P < 0.05$ vs. WT group.

*p ≤ 0.05 vs. all other groups, one-way ANOVA.
fractions (Fig. 2C and D) from PyMT/Tg and KO/Tg tumors showed reduced levels of PCO compared with WT or KO groups, indicating decreased oxidative stress. Next, we evaluated mtDNA damage and copy number in mammary tumors isolated from all four groups of mice. mtDNA damage was assessed as the diminished intensity in the 14 kb major restriction band, indicating that DNA breaks have caused smaller size fragments, which migrate further down in the gel and, thus, reduced the number of full-size restriction fragments (Fig. 2E, top). Tumors from both PyMT/Tg and KO/Tg groups showed significantly greater full-size fragment band intensity, indicating that they have reduced mtDNA damage. Consistent with the reduction in mtDNA damage and reduction of the oxidative stress marker, we found that tumors overexpressing mitochondrial hOGG1 have significantly enhanced mitochondrial levels of ATP compared with both KO and WT mice (Fig. 2F). In addition, LDH activity was significantly increased in PyMT/KO tumors whereas tumors isolated from PyMT/Tg mice have reduced LDH activity (Supplementary Fig. S4).

Protection from mtDNA damage by targeting of hOGG1 into mitochondria results in downregulation of HIF1α and attenuated phosphorylation of Akt

Next, we compared the effect of mtDNA damage on the expression of HIF1α and phosphorylation of Akt (Ser473) in mammary tumors by Western blot (Fig. 3A). As shown in Fig. 3A–C, tumors isolated from PyMT/Tg and KO/Tg mice have reduced levels of both HIF1α and pAkt (Ser473) compared with PyMT/WT group.

Our study provides a proof of concept that mtDNA damage controls mitochondrial function, miROS production and thus, leads to breast cancer progression and metastases in a mouse genetic model. Until recently, mtDNA has received little attention in cancer research as prior studies have largely focused on the nuclear genome. Because most chemical carcinogens damage preferentially mtDNA rather than nuclear DNA, mtDNA is considered to be their major cellular target. Our findings are in line with a recent study that showed that targeting of mitochondrial catalase decreased mitochondrial oxidative stress and suppressed invasive breast cancer in PyMT mice (2).

Most importantly, we would like to emphasize that we believe that mtDNA damage, a prerequisite for somatic mtDNA mutations, can be detected much earlier than mtDNA mutation and thus is a better marker of cancer progression, metastasis, and treatment than mtDNA mutations. Also, as opposed to mtDNA mutations, which cannot be reversed, mtDNA damage can be repaired, and thus reversed using DNA repair enzymes, thus providing important clinical and translational significance for this potential therapeutic strategy. Interestingly, a very recent study showed that the absence of OGG1 is associated with an aggressive breast cancer phenotype in patients (17), which supports the clinical relevance of this study. However, results about the role of the hOGG1 and, particularly, mt-hOGG1 involvement in development of cancer are highly controversial (18, 19). We have used the 1α isoform (transcript variant 1a) of OGG1 as it displays DNA glycosylase activity in both the nucleus and mitochondria, as opposed to the mitochondria localized β-OGG1 (transcript variant 2a), which has been reported to lack such activity (20). Thus, our results, which confirmed that targeting of hOGG (isoform 1-α) into mitochondria protects against mtDNA damage and thus suppresses mtROS production, protects against mitochondrial dysfunction, and thereby reduces ROS-dependent tumor progression and metastasis, are of significant importance in relationship to cancer biology. Moreover, we have shown increased HIF1α and increased LDH activity in PyMT/KO tumors. Based on our results and previous reports, we propose the working model shown in Fig. 3D. The increased ROS leads to stabilization and activation of HIF1α, which in turn activates its target genes (e.g., LDH, etc.), subsequently leading to glycolysis (Warburg effect, Fig. 3D).

In addition, these results have important clinical and translational significance, as most current chemotherapeutic agents, radiotherapy, and surgical procedures all increase oxidative stress, and, therefore, will induce more damage to mtDNA, increase mtROS and, thus, can drive tumor recurrence and metastasis. Thus, this study provides the basis for novel
therapeutic approaches by which modulating the level of mitochondrial OGG1 may decrease cancer progression and metastasis.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): L.V. Yuzefovych, A.G. Kahn, R. Arora, M. Tan, L.I. Rachek
Writing, review, and/or revision of the manuscript: L.V. Yuzefovych, A.G. Kahn, M.A. Schuler, L. Eide, G.L. Wilson, M. Tan, L.I. Rachek
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