Short Communication

Increased Proliferative Background in Healthy Women with BRCA1/2 Haploinsufficiency Is Associated with High Risk for Breast Cancer

Benjamin Nisman1, Luna Kadouri1, Tanir Allweis2, Bella Maly3, Tamar Hamburger1, Simon Gronowitz4, and Tamar Peretz1

Abstract

Previous studies indicated that BRCA haploinsufficiency was associated with activation of the EGFR signaling pathway and increased proliferative activity in mammary epithelial cells of healthy women. We hypothesized that these processes might be reflected in the expression of serologic soluble EGFR (sEGFR) and thymidine kinase 1 (TK1) activity, which signal the initial and final steps of the proliferative pathway, respectively. We found that healthy carriers of BRCA1/2 mutations (n = 80) showed a significantly higher TK1 activity than age-matched controls (P = 0.0003), and TK1 activity was similar in women with BRCA1 and BRCA2 mutations (P = 0.74). The sEGFR concentration was significantly higher in women with BRCA1 than in controls and BRCA2 mutation (P = 0.013 and 0.002, respectively). During follow-up, four of 80 BRCA1/2 mutation carriers developed breast cancer. These women showed a significantly higher TK1 activity and somewhat higher sEGFR concentrations than the other 76 BRCA1/2 carriers (P = 0.04 and 0.09, respectively). All tumors were negative for ovarian hormone receptors, but showed a high EGFR expression. This study was limited by the short-term follow-up (mean, 27 months; range, 5–45), which resulted in a small sample size. Women with BRCA1 and BRCA2 mutations that had undergone risk-reducing bilateral salpingo-oophorectomy (BSO) showed significantly lower sEGFR compared with those without surgery (P = 0.007 and 0.038, respectively). Larger, prospective studies are warranted to investigate whether TK1 and sEGFR measurements may be useful for identifying healthy BRCA1/2 carriers with high risk of developing breast cancer; moreover, sEGFR measurements may serve as effective tools for assessing risk before and after BSO. Cancer Epidemiol Biomarkers Prev; 22(11); 2110–5. ©2013 AACR.

Introduction

Women with BRCA1 and BRCA2 mutations are predisposed to a high risk of breast cancer (57% and 49%, respectively) up to age of 70 years (1). However, there is great variability in the age at diagnosis, and some carriers will not develop the disease during their lifetime. At present, it is unclear how penetrance is related to different biologic factors that affect disease expression. There are no cost effective, valid, and feasible laboratory tests that might be recommended for evaluating the individual risk of breast cancer in a population of BRCA1/2 mutation carriers.

BRCA1 and BRCA2 are tumor-suppressor genes involved in the regulation of cell proliferation. Mutations in these genes were shown to influence growth-related processes. Burga and colleagues (2) studied cultivated primary mammary epithelial cells (PMEC) from healthy BRCA1 mutation carriers; they revealed a subpopulation of progenitor cells with increased capacity for clonal growth and proliferation compared with normal controls. Later, Martins and colleagues (3) reported that the number of breast epithelial cells positive for the proliferation marker, Ki67, was elevated in normal breast tissue of BRCA1 mutation carriers. Those findings suggested that in healthy women with BRCA1 haploinsufficiency, epithelial breast cells possessed enhanced proliferative potential.

Recently, we reported (4) that the proliferative background of human tissues could be assessed with high resolution by measuring the serum activity of thymidine kinase (TK) with a novel procedure (5). Thymidine kinase is a metabolic enzyme that catalyzes ATP-dependent phosphorylation of deoxothymidine to thymidine monophosphate, which is subsequently used in DNA synthesis (6). The enzyme exists in two forms: TK1 (cytoplasmic) and TK2 (mitochondrial). Because TK1 is involved in

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DNA synthesis restricted to the S- and G2-phase (7), it is considered a reliable, sensitive marker of cell proliferation. Dividing cells release TK1 during mitotic exit; this is mediated by the ubiquitin system (8). Thus, TK1 activity can be detected in serum. Recently, novel technology has facilitated the detection of serologic TK1 activity. Women with proliferative breast lesions exhibited higher TK1 activity than women with nonproliferative breast lesions and healthy controls (4).

Previous studies have suggested that deleterious BRCA1 mutations could cause malignant transformation of breast epithelium; this may be regulated by various growth factors, including EGF (9). EGF receptor (EGFR) expression was high in cultivated PMEC from healthy women with BRCA1 haploinsufficiency (2). Even a partial loss or inhibition of BRCA1 was shown to lead to the upregulation of EGF expression (9), which suggests that mutations in the BRCA1 gene may be directly or indirectly coupled with high EGFR expression and predispose PMEC to develop EGFR-positive, basal-type breast cancers. It should be emphasized that most studies until now have explored PMEC only from healthy women with BRCA1 mutation. The information on the expression of proliferation markers in healthy carriers of BRCA2 mutation is not available.

The EGFR oncogene encodes a transmembrane tyrosine kinase receptor. The extracellular binding region of this receptor can appear in a soluble form (sEGFR), either by proteolytic cleavage, which releases it from the cell surface (10, 11), or by the alternate transcription of the primary RNA (12). The sEGFR can be detected in serum. The biologic role of sEGFR is largely unknown. Some studies have suggested that it may play a role in regulating EGFR signaling in normal (13) and tumor tissues (11).

Assuming that growth factors are the main drivers of proliferation, in this study, we investigated whether two biomarkers, sEGFR and TK1, which represent the initial and final elements of the proliferative pathway, could be useful for evaluating the proliferative background in healthy carriers of BRCA1/2 mutations. The results were expected to provide new perspectives in risk assessments of breast cancer. Because bilateral salpingo-oophorectomy (BSO) is known to reduce the risk of breast cancer. Women from the second group were matched by age (± 2 years) with women in the first group. The prevalence of BRCA1/2 mutations is about 2.5% in women from an Ashkenazi Jewish population (15); therefore, two individuals were estimated to have BRCA1/2 mutations among the control group. This fraction (2/80) was not considered sufficient to influence the results. Exclusion criteria for the two groups were pregnancy and breast feeding. A third group included 35 healthy carriers of BRCA1/2 mutations; 14 had BRCA1 mutations (n = 13 with 185delAG and n = 1 with 5382insC) and 21 had BRCA2 mutations (n = 18 with 174delT, n = 2 with 1vs+1G>A, and n = 1 with G.6024dupG). This group had undergone preventive BSOs before the enrollment (mean time since surgery, 4 years; range, 1–11 years).

All participants were fully informed about the study, provided written consent, and donated a blood sample. Serum was isolated, aliquoted, stored for 20 to 30 days at −80°C, and analyzed after blind coding.

Serum TK1 activity was measured with a highly sensitive, colorimetric ELISA kit (DiviTum; Biovica International AB) as outlined previously (4). The analytic sensitivity, defined as the minimum detectable dose distinguishable from zero by 2 SDs, was ≤5 Du/L. The coefficients of variation within- and between-assays, measured at 100 Du/L, were 7.0% and 11.3%, respectively. Serum sEGFR concentrations were determined with the commercially available human EGFR immunoassay (Quantikine®, R&D systems). Results are expressed as ng/mL. The analytic sensitivity was 0.014 ng/mL. The coefficients of variation within- and between-assays, measured at 5 ng/mL, were 3.7% and 10.0%, respectively. Serum follicle-stimulating hormone (FSH) concentrations were assayed according to the manufacturer’s specifications using the Architect System (Abbott). The FSH concentrations were used to assist in determining the women’s menopausal status. The criteria used to assign postmenopausal status were: age ≥60 years, BSO, or FSH concentration >26 IU/L (reference interval for Architect System).

Statistical analysis

Measurements of markers are expressed as the mean, median, and interquartile range (IQR). The distribution of data in the DiviTum and Quantikine assays were found to be asymmetric, with high kurtosis, therefore, the nonparametric Wilcoxon signed-rank and Wilcoxon rank-sum tests were used for comparisons. The Spearman coefficient (r) was used to measure correlations between variables. Statistical calculations were conducted with SPSS, version 10 for Windows. A P value less than 0.05 was considered significant.
Results and Discussion

The group of healthy BRCA1/2 mutation carriers and the matched control group had a mean age of 37 years (range, 20–65). The group that had undergone preventive BSO had a mean age of 50 years (range, 32–66), significantly older than the other two groups (P < 0.0001 for both). TK1 activity was not correlated with age and FSH (r = 0.09, and 0.04, respectively). In accordance with previous observations (16), we found weak negative correlation of serum EGFR concentrations with age (r = −0.22) and concentrations of FSH (r = −0.23). The analysis of TK1 activity with regards to menopausal status showed that TK1 was not different in premenopausal and postmenopausal women (medians, 31 vs. 38; P = 0.25). However, sEGFR concentrations were significantly higher in premenopausal than in postmenopausal women (medians, 48.4 vs. 46.1; P = 0.004).

As may be expected, we did not find a significant association of TK1 activity with age, menopausal status, and FSH concentrations. It seems that there are some other conditions that could contribute to the variability of TK1 results. A fraction of the deviating higher TK1 levels may be due to compensatory cell division after cell destroying disease, for example, certain viral infections (17) or physical trauma, for example, surgery (18). The normalization of TK1 levels after these conditions may last for 6 to 8 weeks. In future studies, transient increases can be eliminated by establishing the stable baseline of TK1 for each individual by repeated serum sampling.

In this study, we found that BRCA1/2 haploinsufficiency in healthy women was associated with significant changes in TK1 activity and sEGFR concentration. The activity of TK1 in the serum of BRCA1/2 mutation carriers was significantly higher (Table 1 and Fig. 1A; medians, 41 vs. 20; P = 0.0003) than in that of age-matched healthy controls. In a separate analysis, both BRCA1 and BRCA2 mutation carriers showed a significantly higher TK1 activity compared with matched controls (medians, 44 vs. 18; P = 0.006 and medians, 38 vs. 21; P = 0.011).

The sEGFR concentration was not significantly different between carriers and matched controls (Table 1, Fig. 1B; medians, 48.5 vs. 48.0; P = 0.22). However, when the sEGFR distributions were analyzed by genotype, the sEGFR concentration was significantly higher in women with BRCA1 mutations compared with controls (median, 50.2 vs. 48.1; P = 0.013), with no difference between the BRCA2 and control groups (medians, 46.9 vs. 48.0; P = 0.27).

To avoid the confounding effect of age, we compared TK1 activity and sEGFR concentrations in age-matched women with BRCA1 and BRCA2 mutations. Analysis of 31 pairs showed significantly higher concentrations of sEGFR in women with BRCA1 mutation compared with those with BRCA2 mutation (medians, 49.8 vs. 46.8; P = 0.002), with no difference in the TK1 activity (medians, 42 vs. 32; P = 0.74). The age-matched carriers of BRCA1 and BRCA2 mutations did not differ in concentrations of FSH (medians, 5.4 vs. 5.0; P = 0.58).

Thus, healthy women with BRCA1 haploinsufficiency were characterized by elevated levels of two serum markers related to proliferation. These data were consistent with previous observations of high EGFR and K66 expression in PMEC obtained from healthy carriers of BRCA1 mutations (2, 3). Those cells showed a high capacity for clonal growth and proliferation. Those authors related these properties to upregulation of the EGFR pathway. We also showed that BRCA2 carriers had an elevated serum TK1 activity, but unlike BRCA1 carriers, they had low sEGFR levels. Thus, serologic sEGFR, like tissue EGFR expression, was significantly associated with BRCA1 haploinsufficiency in healthy women.

We followed 80 BRCA1/2 carriers for a mean of 27 months (range, 5–45 months). Of these, four developed breast cancer with mean time to diagnosis of 19 months (range, 13–22 months); 3 had a founder BRCA1 mutation (185delAG), and 1 had a founder BRCA2 mutation (6174delT). The TK1 activity in this small set was significantly higher compared with the other 76 women of this group (Table 1, Fig. 1A; medians, 77 vs. 39; P = 0.04). The sEGFR concentration was not significantly different between carriers and matched controls (Table 1, Fig. 1B; medians, 48.5 vs. 48.0; P = 0.22). However, when the sEGFR distributions were analyzed by genotype, the sEGFR concentration was significantly higher in women with BRCA1 mutations compared with controls (median, 50.2 vs. 48.1; P = 0.013), with no difference between the BRCA2 and control groups (medians, 46.9 vs. 48.0; P = 0.27).

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Table 1. Levels of serum TK1 and sEGFR in healthy women identified as noncarriers (control) or carriers (‘) of BRCA1/2 mutations

<table>
<thead>
<tr>
<th>Study group</th>
<th>N</th>
<th>Serum TK1 activity (Du/L)</th>
<th>sEGFR concentration (ng/mL)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Mean</td>
<td>Median</td>
</tr>
<tr>
<td>Matched healthy (control)</td>
<td>80</td>
<td>46</td>
<td>20</td>
</tr>
<tr>
<td>Matched healthy BRCA1/2+</td>
<td>80</td>
<td>47</td>
<td>23</td>
</tr>
<tr>
<td>BRCA1+</td>
<td>43</td>
<td>67</td>
<td>44</td>
</tr>
<tr>
<td>BRCA2+</td>
<td>37</td>
<td>74</td>
<td>38</td>
</tr>
<tr>
<td>BRCA1/2+ that developed breast cancer</td>
<td>4</td>
<td>90</td>
<td>77</td>
</tr>
<tr>
<td>Healthy BRCA1/2+ BSO+</td>
<td>35</td>
<td>58</td>
<td>41</td>
</tr>
<tr>
<td>BRCA1+</td>
<td>14</td>
<td>55</td>
<td>50</td>
</tr>
<tr>
<td>BRCA2+</td>
<td>21</td>
<td>61</td>
<td>37</td>
</tr>
</tbody>
</table>

*Individuals from the healthy BRCA1/2+ group.
concentration of sEGFR ng/mL was also higher in women with breast cancer compared with those without it, but the difference did not reach any statistical significance (Table 1, Fig. 1B; medians, 51.7 vs. 48.5; \( P = 0.09 \)).

Interestingly, all four cases were found to be triple-negative breast cancer (TNBC) and positive for EGFR. This confirmed results from previous studies, which showed an inverse relationship between hormone receptors and EGFR expression (19). These findings suggested a possible association between increased serologic sEGFR in women with BRCA1/2 that are at risk of breast cancer and EGFR overexpression later observed in these women with breast cancer.

Thus, the levels of two serum biomarkers, TK1 and sEGFR, in the population of healthy BRCA1/2 mutation carriers allowed the identification of individuals with increased proliferative background, who were at high risk for developing breast cancer. It should be emphasized that the short-term follow-up of this study resulted in a small sample size of breast cancer cases; this was an important limitation of this study, and it merits further investigation.

We analyzed the relationship between sEGFR and TK1 in the different subgroups, and found that they were highly correlated in carriers of BRCA2 mutations (\( n = 37; r = 0.60 \)), but not in carriers of BRCA1 mutations (\( n = 43; r = 0.09 \)). These findings may indicate that the regulation of proliferative signals may be different in women with BRCA1 and BRCA2 haploinsufficiency. We speculated that the high-serum sEGFR expression in the BRCA1 mutation group was consistent with a mechanism of constitutive EGFR activation, but in the BRCA2 group, the EGFR pathway seemed to be more responsive to external signals that led to DNA synthesis.

We also considered the possibility that TK1 and sEGFR might be associated with the observation that BSO reduced the risk of breast cancer. Analysis of the TK1 distribution in BRCA1/2 mutation carriers that underwent...
BSO did not show a normalization of TK1 activity (Table 1, Fig. 2A). Instead, TK1 activity remained increased in both BRCA1 and BRCA2 carriers compared with controls (Table 1; medians, 50 vs. 20; \( P = 0.007 \) and medians, 37 vs. 20; \( P = 0.03 \)).

The sEGFR (Table 1, Fig. 2B) concentration in women with BRCA1/2 mutations that had undergone BSO was significantly lower compared with those without preventive surgery (medians, 45.9 vs. 48.5; \( P = 0.0002 \)) and controls (medians, 45.9 vs. 48.0; \( P = 0.022 \)). Furthermore, in both the BRCA1 and BRCA2 subgroups, those that underwent BSO showed reduced sEGFR levels compared with those without BSO (Fig. 2B; medians, 46.7 vs. 50.2; \( P = 0.007 \) and medians, 44.9 vs. 46.9; \( P = 0.038 \), respectively). Among women carriers of BRCA1/2 mutation, those who had surgically induced menopause have significantly lower concentrations of sEGFR compared with those in natural menopause (medians, 46.1 vs. 49.5; \( P = 0.016 \)), with about similar concentrations of ovarian hormones mediating biologic effects (2). Nevertheless, BSO was effective in reducing the risk of breast cancer, and for whom risk-reduction interventions could be recommended.

In conclusion, our results indicated that measurements of TK1 and sEGFR may be useful for identifying women with BRCA1/2 haploinsufficiency that are at high risk of developing breast cancer, and for whom risk-reduction interventions could be recommended. Future prospective studies are warranted to explore the associations of TK1 activity and EGFR levels with other important factors associated with risk of breast cancer, such as body mass index, history of parity, breast feeding, use of hormones such as pills, hormone-replacement therapy as well as breast density to develop a model for breast cancer risk prediction in BRCA1/2 mutation carriers.

Disclosure of Potential Conflicts of Interest
S. Gronowitz is employed as Research Manager for Biovica International AB and has ownership interest (including patents) in the same. T. Peretz is a consultant/advisory board member of Biovica International AB. No potential conflicts of interest were disclosed by the other authors.

Authors’ Contributions
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Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): L. Kadouri, B. Maly, T. Hamburger, S. Gronowitz
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