AKT1 Inhibits Homologous Recombination by Inducing Cytoplasmic Retention of BRCA1 and RAD51

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Abstract

AKT1 is frequently up-regulated in sporadic breast cancer, whereas BRCA1 is frequently mutated in familial breast cancer. Because BRCA1 is involved in homologous recombination (HR), we addressed whether AKT1 also has an effect on this process. We showed that AKT1 repressed HR through cytoplasmic retention of BRCA1 and RAD51 proteins, resulting in a BRCA1-deficient–like phenotype. This process does not require direct BRCA1 phosphorylation by AKT1. The cytoplasmic retention of BRCA1 and RAD51 correlated with activated AKT1 in tumor cell lines and in biopsies from sporadic breast cancers. Under nonpathologic conditions, fibroblast growth factor, which activates AKT1 and stimulates proliferation in fibroblasts, impaired excessive HR without fully inhibiting it, promoting genome stability. Our study reveals that the regulation of BRCA1 and RAD51 is altered in a high frequency of sporadic breast cancers and highlights the role of extracellular AKT signaling-dependent regulation of HR and genome stability. [Cancer Res 2008;68(22):9404–12]

Introduction

Homologous recombination (HR), is a fundamental, evolutionarily conserved process involved in the variability/stability balance of the genome. HR is implicated in gene diversification, molecular evolution, chromosome segregation during meiosis, DNA repair, and resumption of stalled replication forks. A very precise regulation of HR is essential to maintain the equilibrium between stability and diversification of the genome. Indeed, uncontrolled excess HR can lead to genetic changes and genome rearrangements (1). On the other hand, deficiencies in HR can result in genetic instability (5–10). Cells expressing a dominant-negative form of RAD51, which poisons HR, produce more tumors when injected into nude mice (5). BRCA1 and BRCA2, two partners of RAD51 involved in HR (11–15), are frequently mutated in hereditary breast and ovarian cancers (16, 17). HR is part of the DNA damage response and most germ line mutations responsible for familial breast cancer involve genes implicated in the DNA damage response (18). However, the large majority of breast cancers are sporadic cases, and it is still not known whether the DNA damage response is also involved in these cases.

The membrane serine/threonine protein kinase Bα (AKT1), which can be regulated by extracellular factors (19, 20), is an oncogene that is either overexpressed or constitutively activated in breast, ovarian, prostate, pancreatic and thyroid tumors (21). Up-regulation of AKT1 has been reported in 38% to 54% of sporadic breast cancers and in 40% of ovarian cancers (21, 22). AKT1 also stimulates tumorigenesis of cells injected into nude mice (21). Interestingly, AKT1 can phosphorylate BRCA1 in vitro (23), but the biological significance of this phosphorylation and molecular association has not been addressed. In the current paper, we analyzed the effect of AKT1 on HR.

Materials and Methods

DNA manipulations. All DNA manipulations were performed as described (24). The constructs encoding the human hemagglutinin-tagged AKT [wild-type AKT1 (wtAKT1), membrane-targeted AKT1 (mmyAKT1), and kinase-dead [K179A] (kdAKT1)] were kindly provided by Dr. Hemmings (Friedrich Miescher Institute). PCDNA3b, containing HA-BRCA1, was a gift from Dr. Scully (Dana Farber Cancer Institute) and has been previously described (15). PRSVBRCA1 was a gift from Dr. Foray (Institut National de la Sante et de la Recherche Medicale). P-FLAGCMV2-1FPBRC1 was gift from Dr. Henderson (Westmead Millennium Institute). [T509A]BRCA1, [T590D]BRCA1 and [S615A]BRCA1, [S615D]BRCA1 were generated using the XL-Quikchange site-directed mutagenesis kit (Stratagene). The pDR-GFP plasmid and the F-Scel expression plasmid were gifts from Dr. M. Jasim (Memorial Sloan-Kettering Cancer Center).

RNA interference. The small interfering RNA (siRNA) sequence used for human BRCA1 was 5′-UCACAGUGUCCUUAGUAGA-3′ and was from Dharmacon. The siRNA sequence for AKT1 was 5′-CAAGUGUCUUAGUAGA-3′ (Eurogentec), and the nonspecific siRNA sequence was 5′-AGGUAAGUAAUCCGUUUUTTT-3′. The siRNAs were transfected into cells using Lipofectamine 2000 (Invitrogen).

Cell cultures. The generation of subline, RG37, containing a single chromosomally integrated copy of the recombination reporter plasmid, pDR-GFP, was made as described (25). All cell lines were routinely cultured in DMEM, supplemented with 10% FCS, 2 mmol/L glutamine, and 200 units/mL penicillin, in a humidified 37°C incubator with 5% CO2. The cultures were screened periodically and verified to be free of Mycoplasma infection.

Western blot analysis. Cells were washed in PBS and lysed in denaturing, loading dye buffer for 20 min at 4°C. The samples were boiled for 5 min and subjected to Western blot analysis using anti-AKT, anti-β-actin antibodies. Antibodies were visualized using the enhanced chemiluminescence detection kit (GE Healthcare).

Recombination assays in human RG37 cells. Cells were plated at 2 × 105 per well in six-well plates and transfected after 24 h with various amounts of F-Scel using JetPEI reagent. Cells were trypsinized 72 h later,
washed, and fixed in PBS/2% PAF for 15 min at room temperature. GFP+ cells were detected by flow cytometry using a FACSCalibur.

Primary breast cancer analysis. All tissues were obtained from the surgery department at Saint Louis Hospital before any treatment was given. None of the patients had a familial history of breast cancer. Biopsies from breast cancer (all ductal invasive carcinoma, stages 2–4, n = 20), normal epithelium (adjacent to tumor, n = 5), and mammoplasty (n = 1) were quick frozen after removal and kept in liquid nitrogen until cryostat sections were cut. The immunohistofluorescence on sections (4 μm) was performed after methanol-acetone fixation and staining with anti-BRCA1 antibodies (1:50, C-20, Santa Cruz or 1:40, SD118, VWR) or anti-RAD51 antibody (1:50, 8121HE, Pharmingen). Ten cryostat sections of each biopsy were used for protein extraction, and Western blot analysis was performed with an anti-[pS473]AKT1 antibody.

Statistical analysis. Results are means ± SEM of at least three independent experiments. Statistical analysis of the cell lines was performed using the Student’s t test. Statistical significance (P < 0.05) is indicated by *.

Figure 1. The role of endogenous AKT1 in endogenous BRCA1 foci inhibition in epithelial breast cancer cell lines. A, detection of phosphorylated [pS473]AKT1, AKT1, and actin, using specific antibodies, in MCF7 and MDA-MB-231 cell extracts. B, IR-induced BRCA1 foci (bottom) in MCF7 (left) and MDA-MB-231 (right) cells. Left, histograms are percentages of cells with BRCA1 nuclear foci measured after IR (6 Gy, 12 h). C, effect of siRNA (48 h, 120 nmol/L) against AKT1 on BRCA1 nuclear foci induced by IR (12 h) in MCF7 cells. Right, histograms are percentages of cells with BRCA1 nuclear foci measured after IR (6 Gy, 12 h). Magnification, 100×.
Results

AKT1 affects BRCA1 foci formation in epithelial breast cancer cell lines. We first analyzed breast cancer cell lines (MCF7 and MDA-MB-231) spontaneously exhibiting different levels of endogenous AKT1. Western blot analysis showed that AKT1 was highly expressed and constitutively phosphorylated in MCF7 cells. In contrast, AKT1 was expressed and phosphorylated at very low levels in MDA-MB-231 cells (Fig. 1A). Interestingly, the formation of endogenous BRCA1 foci, induced by IR, was strongly impaired in MCF7 cells, but not in MDA-MB-231 cells (Fig. 1B and Supplementary Fig. S1). Importantly, the silencing of endogenous AKT1 (Fig. 1A) restored the formation of IR-induced BRCA1 foci during time (Fig. 1C and Supplementary Fig. S1). These data show that high levels of endogenous AKT1 repress the assembly of endogenous BRCA1 foci in MCF-7 breast cancer cells.

Active AKT1 represses BRCA1-stimulated gene conversion.

Different mechanisms can take advantage of an intact homologous sequence for double-strand break (DSB) repair: single-strand annealing (SSA), break induce replication (BIR), synthesis-dependent strand annealing (SDSA; ref. 26). Genetic control of these different mechanisms can vary; indeed, whereas gene conversion is RAD51-dependent, SSA is RAD51-independent (27, 28). BRCA1 is a partner of RAD51, which is required in gene conversion (13).

To directly investigate the functional consequences of AKT1 overexpression, specifically on gene conversion, we used a human SV40-immortalized fibroblast cell line, RG37, because it is well characterized for HR (25). Indeed, RG37 cells contain a single chromosomally integrated copy of the pDR-GFP substrate, which specifically monitors gene conversion induced by a DSB targeted into the recombination substrate by the meganuclease.
Moreover, this cellular model allows to verify whether AKT1 can also affect BRCA1 functions in different type of cells. We first confirmed that endogenous BRCA1 was functional in HR in these cells, because the silencing of BRCA1 led to a significant reduction in gene conversion (Fig. 2A), as expected (13). RG37 cells were then cotransfected with I-SceI and different forms of AKT1: wild-type (wtAKT1), a membrane-targeted active form (myrAKT1), or a kinase-dead form (kdAKT1). Coexpression of I-SceI and active ectopic wtAKT1 or myrAKT1 led to a 5-fold to a 10-fold decrease in the frequency of I-SceI–induced GFP+ cells.

Figure 3. AKT1 affects BRCA1 and RAD51 localization. A, RG37 cells were transfected with the BRCA1 expression plasmid alone or cotransfected with different forms of AKT1 expression plasmids and were γ-irradiated. BRCA1 (red) and AKT (green) localization was visualized by immunofluorescence. Top lane, nonirradiated cells; bottom lane, irradiated (6 Gy) cells. B, percentage of cells showing nuclear, nucleo-cytoplasmic, or cytoplasmic localization of BRCA1 in the presence of different forms of AKT1. Top, nonirradiated cells; bottom, irradiated cells. C, RG37 cells were transfected with the RAD51 expression plasmid alone or cotransfected with AKT1 expression plasmids and were γ-irradiated. RAD51 (red) and AKT (green) localization was visualized by immunofluorescence. Top lane, nonirradiated cells; bottom lane, irradiated (6 Gy) cells. D, percentage of cells showing nuclear, nucleo-cytoplasmic, or cytoplasmic localization of RAD51 in the presence of AKT1. Top, nonirradiated cells; bottom, irradiated cells. Magnification, 100×.
transfection of kdAKT1 had no significant effect on the frequency of GFP⁺ cells (Fig. 2B). These results show that active AKT1 specifically inhibits gene conversion in human cells.

To more directly assess the role of BRCA1 in HR, we analyzed the effect of BRCA1 overexpression on I-SceI–induced HR in RG37 human cells. Cotransfection of I-SceI and BRCA1 led to a 6-fold to 8-fold stimulation of gene conversion (Fig. 2C). This result is in agreement with a previous work, which shows that overexpression of RAD51, a partner of BRCA1, specifically stimulates gene conversion induced by I-SceI (28). This strategy allowed us to focus specifically on BRCA1-controlled HR and, thus, the effect of AKT1 on this specific pathway. We cotransfected BRCA1 and I-SceI with different forms of AKT1 and measured the frequency of GFP⁺ cells (Fig. 2D). Both active wtAKT1 and myrAKT1 inhibited BRCA1-stimulated gene conversion. In contrast, kdAKT1 had no effect.

**Active AKT1 affects BRCA1 localization.** We then investigated the effect of AKT1 overexpression on endogenous BRCA1 foci formation induced by IR in RG37 human SV40 transformed fibroblasts. Coimmunostaining with anti-BRCA1 and anti-AKT1 antibodies showed that, in a given culture, cells expressing AKT1 failed to assemble BRCA1 foci, whereas endogenous BRCA1 assembled into foci in cells lacking AKT1 expression (Supplementary Fig. S2, left and middle and C). These data confirmed the observations made in breast cancer cell lines (see Fig. 1). Expression of kdAKT1 did not inhibit IR-induced BRCA1 foci formation (Supplementary Fig. S2B, right and C). Consistent with the above data, the presence of active wtAKT1 inhibited the formation RAD51 foci after irradiation in RG37 cell lines. The expression of kdAKT1, however, did not induce any change in RAD51 foci formation compared with the parental cells (Supplementary Fig. S2D).

The activation of AKT1 often results in the cytoplasmic sequestration of its targets, as shown for CHK1 and BAD (19, 30, 31). Therefore, it is tempting to speculate that BRCA1 is also sequestered in the cytoplasm, upon activation of AKT1. Overexpression of BRCA1 seems to be a valuable tool to unambiguously distinguish between its different subcellular localization. In addition, because AKT1 impairs the up-regulation of HR triggered by the overexpression of BRCA1 (see Fig. 2D), it should also affect the subcellular localization of overexpressed BRCA1. In human SV40-transformed fibroblasts, BRCA1 overexpression resulted in its cytoplasmic localization (Fig. 3A and B). Importantly, two different anti-BRCA1 antibodies, raised against the NH2 terminus or the COOH terminus, gave similar results. This cytoplasmic localization of BRCA1 seems to be due to the low amount of BARD1 (a partner of BRCA1 essential for its nuclear localization) in human SV40-transformed fibroblasts (data not shown).

Whereas overexpressed BRCA1 was located in the cytoplasm in untreated cells, almost all BRCA1 translocated to the nucleus (Fig. 3A and B) in few hours after radiation (Supplementary Fig. S3). The presence of active wtAKT1 or myrAKT1 impaired the nuclear localization of BRCA1 after irradiation (Fig. 3A, middle and B and Supplementary Fig. S3B), showing that the repression system is robust enough to act on the overexpressed BRCA1. Consistent with the above results, kdAKT1 did not impair IR-induced BRCA1 localization to the nucleus (Fig. 3A, right and B). These data are highly consistent with those obtained in MCF-7 breast cancer cells, in which endogenous BRCA1 and AKT1 are spontaneously highly expressed and endogenous BRCA1 is sequestered in the cytoplasm (see Fig. 1).

RAD51 behaved similarly to BRCA1; its overexpression in human fibroblast resulted in cytoplasmic localization but IR led
to the translocation of RAD51 from the cytoplasm to the nucleus (Fig. 3B and C). The nuclear translocation of RAD51 was also impaired by AKT1 (Fig. 3C and D).

To assess the effect of AKT1 on BRCA1 nuclear translocation, we transfected an YFP-tagged BRCA1, alone or with wtAKT1, and followed YFP-BRCA1 localization by video microscopy after IR. In the absence of wtAKT1, YFP-BRCA1 translocated from the cytoplasm to the nucleus 5 hours after IR. In contrast, in the presence of wtAKT1, most of the YFP-BRCA1 remained trapped in the cytoplasm (Supplementary Fig. S4). These results confirm that active AKT1 impairs the dynamic translocation of BRCA1 to the nucleus.

**AKT1 does not affect gene conversion via phosphorylation of BRCA1.** Previous studies have shown that AKT1 can phosphorylate BRCA1 in vitro (23). Interestingly, the two AKT1 phosphorylation sites are found in the two nuclear localization
signals (NLS) of BRCA1 (Fig. 4A). To investigate the role of these two BRCA1 sites in HR, we constructed single or double mutant forms of BRCA1, using site-directed mutagenesis. These mutations resulted in either nonphosphorylatable sites or phosphorylated mimetic sites, mimicking constitutive phosphorylation (Fig. 4B). Surprisingly, all of the BRCA1 mutants, including phosphorylated mimetic mutants, efficiently translocated into the nucleus after radiation and stimulated I-SceI–induced HR. Moreover, wtAKT1 inhibited nuclear translocation and the stimulatory effects of the BRCA1 mutants, to the same degree, including the nonphosphorylatable mutants (Fig. 4C and Supplementary Fig. S5). These results show that the two specific AKT1 phosphorylation sites in BRCA1 are not involved in the repression of gene conversion by AKT1. The situation is, thus, less simple than suggested, and extensive works are required to characterize the molecular mechanisms involved. Nevertheless, the present observations should have very important effects in sporadic breast cancer etiology.

**AKT1 activation correlates with BRCA1 and RAD51 cytoplasmic localization in breast cancer.** To investigate the implication of our findings in human disease, we analyzed the correlation between AKT1 activation and BRCA1 and RAD51 subcellular localization in sporadic breast cancer. Biopsies of cancer from 20 patients at diagnosis (BC) and nontumor specimens [five from normal tissue (NE) adjacent to tumors, one from reduction mammoplasty (MM)] specimens were analyzed for AKT1 activation by Western blotting (Fig. 5A).

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**Figure 6.** Impact of FGF on HR. A, cells were treated with different concentrations of bFGF, and AKT1 expression and [pS473]AKT phosphorylation were detected by Western blot analysis. B, cells were transfected with the I-SceI expression vector, and different concentrations of bFGF (indicated in the figure) were added to the medium of RG37 human fibroblasts 1 h later. Three independent experiments were performed. C, cells were irradiated at 6 Gy for 12 h and radiation-induced BRCA1 (top) or RAD51 (bottom) foci after treatment with bFGF (right) at the indicated concentration for 12 h. The histogram (left) corresponds to three independent experiments and shows the frequency of cells with more than 15 foci per cell. Magnification, 100×.
BRC1 localization was analyzed using two different anti-BRC1 antibodies. BRC1 presented three distinct localization patterns (Fig. 5B): nuclear, cytoplasmic, or nucleocyttoplasmic. The cytoplasmic localization of BRC1 was significantly correlated with high levels of AKT1 activation in breast cancer (Fig. 5B).

We then classified the breast cancer in two groups, AKT1-low (AKT1 activation lower than 2-fold) and AKT1-high (AKT1 activation higher than 2-fold, compared with normal epithelium). In AKT-high tumors, BRC1 displayed a cytoplasmic localization in 77% (with C-20 antibody; Fig. 5C) and 83% (with S118 antibody; Fig. 5D) of the tumors. Importantly, no exclusively nuclear localization of BRC1 was detected in any of the AKT-high tumors. In contrast, in AKT-low tumors, BRC1 displayed a cytoplasmic localization pattern in only 29% of the tumors (Fig. 5C and D).

Interestingly, RAD51 behaved similarly to BRC1: 77% of AKT-high tumors exhibited cytoplasmic localization of RAD51 (Supplementary Fig. S6). Immunostaining using the secondary antibody alone as a negative control did not produce any signal, confirming the specificity of the observed localization patterns (Supplementary Fig. S6).

In AKT-low breast cancers, BRC1 and RAD51 localization mainly show nuclear or nucleocyttoplasmic localization patterns. In contrast, AKT1 activation strongly favors the cytoplasmic localization of both BRC1 and RAD51 proteins. Hence, defective nuclear localization of both BRC1 and RAD51 is strongly correlated with AKT1 activation in human sporadic breast cancer.

Basic fibroblast growth factor stimulates endogenous AKT1 and reduces HR. AKT1 is an oncogene and its overexpression results in a pathology, as seen in a high frequency of sporadic breast cancers. We have shown that AKT1 overexpression leads to dysregulation of BRC1, resulting in a BRC1-like phenotype (without BRC1 mutation), and a deficiency in HR. Under physiologic conditions, AKT1, which is tightly regulated, is activated in response to extracellular growth factors via the PI-3 kinase to mediate cell proliferation (19). Because HR is essential for cell proliferation, especially for reactivation of blocked replication forks, the repression of HR by AKT1 is an apparent paradox. Two hypotheses can resolve this paradox: (a) AKT1 represses HR only under pathologic conditions (constitutive overexpression in cancer) and (b) AKT1 impairs excess HR, under physiologic conditions, without completely inhibiting it. Indeed, excess HR can be deleterious to the maintenance of genome stability; uncontrolled HR can lead to loss of heterozygosity, gene inactivation, and profound genome rearrangements (translocation, deletion, amplification). Moreover, unresolved HR intermediates are toxic (1–4).

To address these hypotheses, we treated the human fibroblast cell line, RG37, with basic fibroblast growth factor (bFGF). Activation of endogenous AKT1 was induced by the addition of bFGF to the medium (Fig. 6A). HR was decreased, in a dose-dependent manner, by the addition of bFGF to the medium (Fig. 6B). Interestingly, at the highest dose, HR was decreased by 2-fold but reached a plateau level and a robust activity was maintained. We then tested the effect of bFGF on BRC1 and RAD51 foci formation after IR (Fig. 6C). The addition of bFGF to the medium decreased the amount of BRC1 foci, as well as of RAD51 foci per cell, in a range similar to the degree of HR repression (compare Fig. 6B and C). Therefore, as proposed by the second hypothesis, bFGF both activates AKT1 and represses HR but maintains HR at a level sufficient for cell viability. These data suggest that nuclear HR can be very precisely regulated by extracellular factors.

Discussion

Because both excessive and defective HR can lead to genome instability, a very precise regulation of HR is essential to maintain the equilibrium between stability and diversification of the genome. AKT1 may influence HR under normal, physiologic circumstances and during pathologic, chronic overexpression of AKT1. Under physiologic conditions, sufficient HR activity is maintained to ensure genome stability, whereas excessive HR is repressed. In the pathologic situation, HR regulation is out of control, leading to genetic instability and predisposition to cancer.

Physiologic role of HR regulation by AKT1 for genome stability maintenance. Under physiologic conditions, AKT1 is transiently and precisely regulated to avoid uncontrolled cell proliferation; this should lead to subtle, transient, and reversible regulation of HR, as exemplified here in the bFGF experiments. In accordance with our data, serum depletion was shown to strongly stimulate HR (32).

Excessive HR is deleterious for both genome stability and cell viability. Indeed, HR between repeated sequences dispersed through the genome (which are highly frequent) can lead to genome rearrangements (deletions, amplifications, translocations). HR between hetero-alleles or with pseudogenes can lead to gene extinction or loss of heterozygosity (1, 2, 33, 34). Moreover, unprocessed HR intermediates lead to cell toxicity, which can be overcome by inhibiting HR (4). Because the preferred substrate for RAD51 is a ssDNA coated with RPA and because large amounts of this substrate are generated during the S phase, it is essential to precisely control HR during the S phase. This should prevent inappropriate HR initiation in unchallenged cells but should allow HR after DNA damage. A balance between HR initiation and repression is essential; therefore, the control of HR should be precise and, possibly, reversible. Control of HR by extracellular factors should be very adapted to these requirements. We propose that the AKT1 signaling pathway mediates such precise HR regulation.

Pathologic activation of AKT1 strongly inhibits HR and generates genetic instability. Abnormal pathologic situations are encountered in cancer cells (or in cell lines derived in the laboratory). In these extreme situations, AKT1 escapes cellular control and is constitutively activated or overexpressed. AKT1 overstimulation leads to a strong chronic repression of HR, causing genomic instability. Because AKT1 also inhibits cell death, this situation leads to a predisposition to tumors.

Germ line mutations in genes controlling the DNA damage response are responsible for familial breast cancer. However, the majority of breast cancers are sporadic cases. Our findings reveal a novel molecular mechanism underlying AKT1-associated breast cancers. Considering the high frequency of AKT1 up-regulation in sporadic breast and ovarian cancers (30–50% of cases), these findings may be of major importance. Indeed, the present data imply that BRC1 and RAD51 dysregulation (resulting in a brc1-defective phenotype, without requiring BRC1 mutation) is also important in a high frequency of sporadic breast cancers.

Because AKT1 is up-regulated in 38% to 54% of breast tumors, cytoplasmic localization of BRC1 should be frequently observed in breast tumor cells. Such frequent cytoplasmic localization of BRC1 has, indeed, been reported in sporadic breast cancer cells (35). In this study, we found cytoplasmic localization of BRC1 in 60% of the tumors analyzed, and there was a high correlation between BRC1 localization and AKT1 activity in primary breast cancer.
cancer cells. Moreover, RAD51 behaved similarly to BRCA1, strongly supporting the results obtained with BRCA1. Importantly, the correlation between AKT1 activation and BRCA1 cytoplasmic localization was observed using two different antibodies. In addition, RAD51 analysis, one BRCA1 partner, confirmed this aberrant localization, thus, with another antibody against another protein. Finally, these observations are highly consistent with the cellular models, particularly when using YFP-tagged BRCA1, which confirmed cytoplasmic localization, independent of the type of antibody used. Taken together, all the data consistently support the model of cytoplasmic retention of BRCA1 triggered by AKT1 activation.

The present data refute the logical hypothesis that the phosphorylation of BRCA1 by AKT1 might affect other functions of BRCA1, which are not involved in HR. Characterization of the molecular mechanisms involved in BRCA1 retention constitute an exciting challenge for future prospects.

Interestingly, primary breast carcinomas lacking the tumor suppressor, PTEN, show activation of AKT1, cytoplasmic sequestration of the cell cycle checkpoint protein CHK1, accumulation of DSB, and aneuploidy (31, 36). In addition, a nuclear role of PTEN, supressor, PTEN, show activation of AKT1, cytoplasmic sequestration of the cell cycle checkpoint protein CHK1, accumulation of DSB, and aneuploidy (31, 36). In addition, a nuclear role of PTEN, which are not involved in HR. Characterization of the molecular mechanisms involved in BRCA1 retention constitute an exciting challenge for future prospects.

In conclusion, our findings shed light, at a molecular level, on an important dimension of the intricate network of cellular processes that connect nuclear, plasma cell membrane, and extracellular pathways in the precise regulation of genome stability. These regulatory processes allow genetic diversity, but protect against genetic instability.

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

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