Introduction

Mutations in the tumor suppressor breast cancer–associated protein 1 (BRCA1) are associated with a high risk of breast and ovarian cancer. BRCA1 is a nuclear protein implicated in multiple processes, including genomic stability, transcription regulation, chromatin remodeling, and cell-cycle control (Starita and Parvin, 2003; for reviews see Welch and King, 2001; Deng and Wang, 2003). In normal S-phase cells, BRCA1 shows a punctate distribution with typically 10–20 prominent accumulations (foci), but upon induced DNA damage, it relocalizes to sites of DNA repair (Scully et al., 1997b; Tashiro et al., 2000; Cantor et al., 2001). Although BRCA1 does not overlap XIST RNA across the inactive X chromosome, BRCA1 foci position overwhelmingly in heterochromatic regions, particularly the nucleolar periphery where many centromeres reside. In humans and mice, including early embryonic cells, BRCA1 commonly localizes to the unpaired X and Y chromosomes in spermatocytes, implicating BRCA1 in recombination and meiotic silencing (Scully et al., 1997b; Turner et al., 2004). However, in normal somatic nuclei there is no evidence that BRCA1 spots associate with specific sites of chromatin, other than a reported association of BRCA1 with XIST RNA on the inactive X chromosome (Xi; Ganesan et al., 2002). Findings in this study demonstrate that BRCA1 foci form at particular classes of heterochromatin, linked to their replication, and suggest a novel role of BRCA1 with implications in the maintenance of genomic stability.

Results and discussion

In a fraction of cells, BRCA1 foci abut, but do not coat, the Xi

The report that BRCA1 colocalizes with XIST RNA on the inactive X chromosome (Xi) in a subset (5–10%) of cells...
(Ganesan et al., 2002) led us to further investigate the spatial relationship between XIST RNA and BRCA1. In extensive investigation of multiple cell lines, using several BRCA1 antibodies (see Materials and methods), we did not find that BRCA1 substantially overlaps XIST RNA on Xi (Pageau et al., 2006; this study). However, using methods optimized for simultaneous detection of nuclear RNA and protein (see Materials and methods), BRCA1 partially overlapped or closely abutted XIST RNA in 3–5% of hundreds of cells viewed in 2D. 3D analysis of deconvolved optical sections (Fig. 1, A and B) shows that even in cases where BRCA1 and XIST RNA appear to overlap in 2D, they largely occupy distinct spatial territories, typically with BRCA1 tightly abutting the XIST signal (Video 1, available at http://www.jcb.org/cgi/content/full/jcb.200602055/DC1). BRCA1 also did not colocalize substantially with other hallmarks of Xi-facultative heterochromatin (H3mK27 or ubiquitin; Fig. S1 A), which colocalize throughout the XIST RNA territory (Chaumeil et al., 2002; Smith et al., 2004). We also recorded a fraction of cells (∼13% in TIG1 fibroblasts, with similar results for multiple cell lines) in which a BRCA1 spot was directly adjacent to, but clearly not overlapping (even by 2D analysis), XIST RNA (Fig. 2 D and not depicted; see Materials and methods for definition of scoring terms). The significance of these more limited associations is investigated in this study. However, overall, these findings are consistent with other evidence that BRCA1 does not have a direct role in localizing XIST RNA (Pageau et al., 2006); if BRCA1 has a spatial relationship to the Xi, it is not via an association with XIST RNA.

Most BRCA1 foci localize to heterochromatic nuclear regions

To address whether the ∼10–20 prominent BRCA1 foci associate with a particular category of chromatin, we investigated whether they preferentially localize to the euchromatic or heterochromatic compartments. To delineate these compartments, we used hybridization to heterogeneous nuclear RNA (hnRNA) and labeling of splicing-factor–rich domains. Hybridization to hnRNA with a Cot-1 DNA probe delineates the inactive X chromosome (Hall et al., 2002) and heterochromatin abutting the nuclear envelope and nucleolus (Tam et al., 2004). Analysis, in two different cell lines, revealed a strong propensity for BRCA1 foci to localize in hnRNA-depleted regions; only ∼19% overlapped the Cot-1 RNA signal, which fills most of the nucleoplasm (Fig. 2 A). A surprisingly large fraction of BRCA1 foci (∼32%) localized to the Cot-1–depleted region abutting or within the nucleolus (Fig. 2 A). Another 14% localized to the peripheral heterochromatin, and 35% precisely colocalized with small discrete “holes” in the hnRNA signal (Fig. 2 A). Although not our focus in this study, an association with the centrosome (Starita et al., 2004) was not noted with cells and antibodies used here. The association of BRCA1 with the nucleolus is interesting because many centromeres localize there.

The preference for heterochromatic regions contrasted to the paucity of BRCA1 foci with SC-35 and SRM300, which are splicing components that label 20–30 large domains linked to RNA metabolism. These regions are surrounded by active genes in the euchromatic compartment (Shopland et al., 2003). These BRCA1 foci only rarely overlap (<1%) or contact (3%) SC-35 (Fig. 2 B) or SRM300 in mouse cells, suggesting they are largely excluded from these euchromatic “neighborhoods.”

BRCA1 has a substantial, but complex, relationship to mid-to-late replicating DNA

BRCA1 in normal S phase has not been thought to reflect routine DNA replication because BRCA1 distribution does not mirror that of replicating DNA (Scully et al., 1997a). We reexamined the relationship of BRCA1 foci to mid-to-late replicating DNA,
which comprises largely heterochromatic DNA. Unlike the dispersed particulate pattern of early replication, the mid-to-late pattern comprises a smaller number of larger spots (Nakayasu and Berezney, 1989; Quivy et al., 2004). Examination of whether BRCA1 foci overlapped BrdU spots confirmed the earlier conclusion that, in general, the two patterns are not the same (Scully et al., 1997a). However, close scrutiny suggested a substantial, but incomplete, relationship. Approximately 3% of the discrete BRCA1 foci overlapped a BrdU spot, but an additional 18% were abutting or adjacent to (contacting) BrdU spots. Although these mid-to-late S-phase BrdU spots occupy a much smaller area of the nucleus than SC-35 domains (Fig. 2, B and C), BRCA1 shows greater spatial association with them. Many BRCA1 spots (an additional ~27%) seemed to position consistently close (~0.3 μm) to a BrdU spot, the significance of which was initially unclear.

We also reexamined the relationship to the replicating Xi. As shown in Fig. 2 D, the subset of cells that showed BRCA1 association (either abutting or adjacent; Fig. 1 C) during replication of Xi increased two- to threefold over asynchronous cultures, which is consistent with an increased association in late S phase (Chadwick and Lane, 2005).

Many BRCA1 foci are spatially linked to components of the human interphase centromere–kinetochore complex. The aforementioned findings led us to investigate whether BRCA1 has a relationship to heterochromatin associated with centromeres. Using an antibody to centromere protein C (CENP-C), which is a constitutive component of the interphase centromere–kinetochore complex, the patterns of CENP-C and BRCA1 in human fibroblasts (TIG1) were again distinct, yet exhibited a substantial spatial association (Fig. 3 A). We categorized these associations into three types, as follows: 3% of BRCA1 spots were completely coincident with CENP-C spots, another 12% directly abutting or contacted (no separation visible by light microscopy), and an additional 24% were suggestive of a close pairing. Very similar observations (3% coincident, 14% abutting/adjacent, and 16% close) were made when we hybridized to α-satellite DNA (Fig. 3 B) or used CENP-B, which binds α-satellite, as a marker (Fig. 3 C).

We next asked whether BRCA1 foci that abut Xi reflect a relationship to centromeres. The frequency with which we found BRCA1 partially overlaps (~2%) or resides adjacent to (8%) the X centromere may largely account for BRCA1–XIST RNA association (3% partial overlap and 13% adjacent). Using the Barr body to distinguish the active and inactive X (Fig. 1 D), there was not a major difference in BRCA1 association with Xi versus active X chromosomes (Xa) centromeres (10% vs. 7%, respectively). Thus, the relationship of BRCA1 to Xi primarily reflects a relationship to centromere-associated constitutive heterochromatin, rather than specifically Xi-facultative heterochromatin. However, we do not exclude the possibility that the slightly higher association with Xi is caused by its more heterochromatic nature.
The frequency with which BRCA1 signals either overlap or directly abut interphase centromere markers indicates a substantial, albeit incomplete, association. Although the “close, but not contacting” category is less clear, this could reflect a spatial linkage to some component of the centromere–kinetochore complex (for review see Cleveland et al., 2003), which has many components that do not all completely coincide in nuclei (Sugata et al., 2000) and are not all known. Therefore, the relatively consistent gap between BRCA1 and CENP-C could contain some other component of this structure (see the following section).

**BRCA1 structurally associates with mouse chromocenters and pericentric heterochromatin**

Because BRCA1 most often “neighbors” (rather than overlaps) these centromere components, we next investigated BRCA1’s relationship to pericentric heterochromatin (PCH), which would also lie adjacent to centromeric DNA. Mouse cells have a more well-defined organization of centric and pericentric DNA than do human cells (Schueler et al., 2001); in mouse cells, centromeres cluster into 5–10 chromocenters that are easily visualized with DAPI stain. Fig. S1 B confirms a recent report (Guenatri et al., 2004) demonstrating that the DAPI-dense chromocenters comprise pericentric heterochromatin (mouse major satellite) and the centromeric DNA (minor satellite) is smaller and positions at the periphery of the larger blocks of PCH.

BRCA1 staining revealed a clear structural relationship with chromocenters (Fig. 4 A). Although not all chromocenters have associated BRCA1, and vice versa, in all of the several different lines examined (mouse 3T3, 3X mouse, mouse embryonic fibroblasts (MEFs), and mouse ES cells), 26–38% of BRCA1 spots in an asynchronous population directly associated with a chromocenter. In addition, a subpopulation of cells showed higher association; in some cells, almost all BRCA1 spots were with a chromocenter (Fig. 4 A). Typically one or two BRCA1 foci were at the immediate periphery of each chromocenter, but, not infrequently, several foci or elongated BRCA1 accumulations “hugged” the contour of the chromocenter (Fig. 4 A). Occasionally, a “paint” of nearly all the DAPI-bright PCH was apparent (Fig. 4 A, top middle). Interestingly, this association is present even in very early (1-d differentiated) embryonic stem cells (Fig. 4 A, bottom right). This is potentially important because BRCA1 knockout is early embryonic lethal (Deng and Wang, 2003).

We next examined the relationship between BRCA1 and the minor satellite (equivalent of human α satellite) of the centromere proper. When visualized together (Fig. 4 B), their relationship mirrored that seen (see previous section) between human centromeres and BRCA1, as follows: 6% coincident, 10% adjacent/abutting, and 27% close. However, when viewed with DAPI in three colors, it became apparent that, often, minor satellite and BRCA1 signals that had no direct contact were in fact associated with a common chromocenter. These observations bolster the significance of close/“paired” signals in the human; even when the BRCA1 foci are not coincident with a centromeric marker, they are spatially linked by their common association with the PCH of the chromocenter (Fig. 4 B and Video 2, available at http://www.jcb.org/cgi/content/full/jcb.200602055/DC1). The link between BRCA1 and centromeric DNA may be through the PCH, but, in either case, results indicate a connection between the discrete BRCA1 S-phase foci and centromeres, which are structures key to the proper segregation of chromosomes and maintenance of genomic integrity.

**BRCA1 association with chromocenters is temporally linked to their replication**

In both human and mouse, some cells show greater BRCA1 association with chromocenters than others, as illustrated in Fig. 4 C (middle). We addressed whether this difference might relate to replication, using proliferating cell nuclear antigen (PCNA) as a marker of the replication machinery (Bravo, 1986). Chromocenters replicate roughly synchronously in a given cell
in mid-to-late S phase (Fig. 4 C; Guenatri et al., 2004; Quivy et al., 2004). In cells in which most chromocenters had prominent PCNA label, a higher association of BRCA1 was clearly evident. Of chromocenters that label with PCNA, 55% have BRCA1 associated (15% overlap and 40% abutting), in contrast to <7% with no PCNA label (<1% overlap and 6% abutting; Fig. 2 E). Cells with the most striking BRCA1 painting of chromocenters also labeled for replication of the chromocenter. This demonstrates a temporal relationship between widespread, largely synchronous BRCA1 association and replication of PCH.

Previous work has shown that mouse chromocenters have a defined architecture such that DNA replication (and likely chromatin assembly) occurs at the periphery of the large major satellite block, and the newly replicated DNA then moves into the central region of the chromocenter (Quivy et al., 2004). This fits well with the distribution of BRCA1, which is mostly concentrated at the chromocenter periphery. Because BRCA1 did not always localize to PCNA-labeled chromocenters, it may transiently associate close to the time of replication. The fact that BRCA1 is more juxtaposed to PCNA than overlapping it is consistent with other evidence that BRCA1 may have a post-replicative role. Similar observations were made with a 15-min terminal pulse of BrdU (Fig. S1 C).

Because one recent study reports that BRCA1 regulates topoisomerase IIα (topoIIα) during routine DNA replication

Figure 4. BRCA1, mouse chromocenters, and the relationship to replication. (A) Mouse cell lines included MEFs (BRCA1, green), 3T3 (BRCA1, red), and mouse ES cells (BRCA1, green). (B) BRCA1 (red) and minor satellite DNA (green). Far right shows 3D-rendered image of BRCA1 and minor satellite on a chromocenter (blue). Middle photo shows chromosomes in black. (C) Cells were labeled for replication with PCNA (red) and BRCA1 (green). In top panel, the upper nucleus has more BRCA1 and PCNA on chromocenters. (D and E) topoIIα (green) on mouse chromocenters (blue) is seen in many S-phase cells (PCNA, red).
(Lou et al., 2005), we briefly addressed whether topoIIα associates with mouse chromocenters. Although topoIIα is enriched at mitotic centromeres, and there is one report of its association with late S-phase BrdU (Agostinho et al., 2004), it is not known to be enriched at chromocenters/centromeres during S phase. As shown in Fig. 4 D, we found topoIIα commonly enriched on mouse chromocenters; in ∼40% of interphase cells, topoIIα concentrates on essentially all chromocenters. Many of these cells are in S phase, with PCNA on their chromocenters (Fig. 4 E).

Initial characterization of BRCA1 mutant cells is suggestive of mitotic defects

Our findings suggest that BRCA1 may have a role in replication-linked maintenance of peri/centromeric heterochromatin. As the study of X inactivation has demonstrated, the epigenetic state of heterochromatin is controlled at numerous levels that work synergistically and provide redundancy; for example, heterochromatic features of the Xi are compromised only very slightly over the long term if XIST RNA is lost from somatic cells (Csankovszki, 2001). Similarly, reintroduction of XIST RNA in somatic cells would not simply correct a deficit in heterochromatin (Wutz and Jaenisch, 2000; Hall et al., 2002). Thus, short-term loss or gain of BRCA1 could have no immediate effect on heterochromatin but still be important for its long-term maintenance and stability in an organism. We found that short-term acute loss of BRCA1 by RNAi in HeLa cells impacts proliferation and reduces mitotic figures by >60% (Fig. S2, available at http://www.jcb.org/cgi/content/full/jcb.200602055/DC1), which is consistent with other reports. Although this could reflect an impact on the complex epigenetic state or repair of pericentric heterochromatin, it could also reflect other short-term effects of BRCA1 loss on centromere function (Starita et al., 2004), DNA decatenation (Lou et al., 2005), or cell-cycle checkpoints (Cao et al., 2003; Deng and Wang, 2003).

Breast tumor cells such as HCC1937 are exposed to longer-term BRCA1 loss. As an initial effort to investigate some properties of centric heterochromatin, we examined CENP-A, a constitutive interphase kinetochore component directly linked to specifying a centromeric property, and CENP-F, the first transient kinetochore protein bound in G2 (Maiato et al., 2004). Localization of these centromeric components appeared normal in these BRCA1 mutant cells (Fig. 5 A). However, given the essential role of CENP-A in kinetochore assembly, this may not be surprising.

Lou et al. (2005) reported that a high fraction (∼10%) of HCC1937 cells had lagging chromosomes or DNA bridges after mitosis. We attempted to confirm these findings, but extended our analysis to MCF7 (BRCA1+) breast cancer cells and normal diploid fibroblasts. It was obvious in DAPI-stained slides of HCC1937 that many early G1 daughter pairs contain a “bridge” of DNA extending between them (Fig. 5 B); in contrast, this was almost never seen in BRCA1+ MCF7 or in normal fibroblasts. Many mitotic figures showed lagging chromosomes, and early G1 pairs showed thin bridges of DNA. For example, in 100 G1 daughter pairs, visible DNA bridges were seen 31 times in HCC1937 cells, in contrast to 3 times in diploid fibroblasts (TIG1) and 4 times in MCF7 cells. Most mitotic figures with

Figure 5. Centromeric markers and DNA bridges in BRCA1−/− HCC1937 cells. (A) TIG1 (left) and HCC1937 cells (right) stained for CENP-A and -F. (B) In HCC1937 early G1 daughter cells, DAPI staining shows thin DNA bridges. (C) Centromeric DNA (green) in DNA bridges (left and right) and lagging chromosomes (middle) in HCC1937 cells.
These results are consistent with the possibility that a defect in BRCA1 may contribute to a generalized failure of heterochromatin maintenance.

Materials and methods

Ceils and cell culture

Human diploid fibroblast lines WI38 (CC-75) and IMR-90 (CC-186) were obtained from the American Type Culture Collection, and TIG-1 (AG06173) were obtained from Coriell Cell Repositories. In addition, 3X mouse cells (Smith et al., 2004) and MCF7 cells were used. WI38, TIG-1, MCF7, and 3X mouse cells were grown in MEM supplemented with 10% FBS, 2 mM L-glutamine, 1% penicillin/streptomycin, NIH 3T3 cells, and MEFs were grown in DME supplemented with 10% FBS, 2 mM L-glutamine, and 1% penicillin/streptomycin. HCC1937 cells were obtained from the American Type Culture Collection (CRL-2334) and were grown in RPMI with Hepes medium supplemented with 10% FBS, 2 mM L-glutamine, and 1% penicillin/streptomycin. For BrdU labeling, cells were plated for 48 h, followed by a 15-min treatment with 30 μM BrdU just before fixation. HCC1937 cells reconstituted with BRCA1 were obtained from J. Chen (Mayo Clinic, Rochester, MN; Lou et al., 2005).

Antibodies

Monoclonal antibodies to mouse [HH118] and human (M5110) BRCA1 were a gift from D. Livingston and S. Ganesan (The Dana Farber Cancer Institute, Boston, MA; Ganesan et al., 2002). A monoclonal antibody to polyubiquitinated proteins (UBF/Z) was obtained from Affiniti BioReagents. Polyclonal antibodies to BRCA1 (KAPST0201) were obtained from Assay Designs and C. Deng (National Institutes of Health, Bethesda, MD). Antibodies to BrdU (rat monoclonal) were obtained from Harlan. Polyclonal antibodies to CENP-C (rabbit) were obtained from W. Earnshaw (University of Edinburgh, Edinburgh, UK), and CENP-B antibodies (rabbit; H-65) were obtained from Santa Cruz Biotechnology, Inc. An antibody to CENP-A was obtained from M. Valdovis (Universidad de Cadiz, Cadiz, Spain), and an antibody to CENP-F was obtained from D. Cleveland (University of California, San Diego, La Jolla, CA). Antibodies to PCNA were obtained from Immunovision (Human). An antibody to topoisomerase Ii was obtained from Lab Vision (rabbit).

Immunofluorescence

Initial studies involved testing two fixation methods; paraformaldehyde fixation followed by Triton X-100 extraction, as described by Ganesan et al. (2002), or brief Triton X-100 extraction before fixation, as described previously (Clemson et al., 1996; Tam et al., 2004). For extraction, cells were extracted in CSK buffer with 0.5% Triton X-100 and 2 mM vanadyl adenosine phosphatase for 5 min. Cells were then fixed in 4% paraformaldehyde in 1×PBS for 10 min, incubated with primary antibodies in 1×PBS/1% BSA for 1 h at 37°C, and rinsed successively in 1×PBS, 1×PBS + 0.1% Triton X-100, and 1×PBS for 10 min. Detection was carried out with secondary antibodies tagged with fluorescein, rhodamine, or Texas red (Jackson Immunoresearch Laboratories).

DNA and RNA FISH

RNA FISH used previously established protocols (Clemson et al., 1996; for review see Tam et al., 2004). XIST RNA was detected with a 104-kb probe.
plasmid (pG1A) spanning intron 4 to the 3′ end of XIST, or with plasmid (pXISTh-B) containing intron 1 (Clemson et al., 1994). Probes were nick translated using biotin-11-dUTP or digoxigenin-6-dUTP (Boehringer Mannheim). Hybridization was detected with either antidigoxigenin antibody (Boehringer Mannheim) coupled with rhodamine or fluorescein or, for biotin detection, avidin conjugated to Alexa Fluor–strepavidin 594 (red) or fluorescein (Boehringer Mannheim). RNA in situ was added for simultaneous RNA FISH and antibody staining. After detection and washing, cells were re-fixed in 4% paraformaldehyde in PBS for 10 min at 25°C and processed for RNA FISH as described in this section.

For combined BRCA1 staining and DNA FISH, cells were stained first for BRCA1 and fixed in 4% paraformaldehyde for 10 min. Cells were then denatured in 0.2 N NaOH for 5 min at room temperature (rather than 70% formamide with heat) because this better preserved BRCA1 staining. A probe directed against all human centromers (Open Biosystems Human Pancentromere Paint BIOTIN) was obtained from Cambio and hybridized overnight at 37°C as directed by the manufacturer and detected with Alexa red streptavidin diluted 1:500 in 4×SSC/1% BSA. Oligos (5′-GAAACGT-GTATATCAAGTAGGTTTCC-3′) and 5′-CCACACTGTAACGATATGAG-3′) to the mouse minor satellite were used at 5 pmol in 10% formamide. The X centromere was labeled with a Spectrum Orange X centromere paint (Vysis) according to the manufacturer’s directions and rinsed as described in the previous paragraph.

Microscopy and image analysis

Digital imaging analysis was performed using an Axiovert 200 or an Axiohot microscope [Carl Zeiss Microimaging, Inc.] equipped with a 100× Plan-Neofluar objective (NA 1.4; Carl Zeiss Microimaging, Inc.) and 800× multibandpass dichroic and emission filter sets (Chroma Technology Corp.) set up in a wheel to prevent optical shift. Images were captured with a camera (OrcoER; Hamamatsu) or a cooled charge-coupled device camera (200 series; Photometrics). Where rhodamine was used for detection in red, a narrow band-pass fluorescein filter was inserted to correct for any bleed through of rhodamine fluorescence into the fluorescein channel. Optical sections and 3D images were created using Axiovision 4.4 (Carl Zeiss Microimaging, Inc.). Images were captured at 0.1-μm intervals, and stacks were deconvolved with a constrained iterative algorithm. Rendered images are maximum value projections.

Definition of molecular cytology scoring terms

For scoring purposes, the following definitions are used for scoring terms: (1) Nonoverlap indicates any relationship that appears to involve “contact” (no physical separation visible by 2D light microscopy). These were further divided into three categories of association. (1) Painting, which typically indicates almost complete overlap of two signals, but in this analysis any overlap >50% would have been included. (2) Abutting/partial overlap, which indicates a signal which very closely pressed against another, such that when viewed in two dimensions there appears a slight overlap of the two signals. 3D analysis may show the two signals are actually not overlapping. (3) Adjacent, which indicates two signals that are juxtaposed and appear in contact, but for which even 2D analysis indicates no overlap. “Closely paired” signals are distinct in that this category indicates two signals that do not contact, but are separated by ~0.2–0.4 μm.

Online supplemental material

Fig. S1 shows hallmarks of X inactivation on the Xi, localization of major and minor satellite DNA relative to chromocenters, and localization of BRCA1 and BrdU to mouse chromocenters. Fig. S2 shows decreased proliferation in BRCA1 siRNA-treated versus control siRNA-treated cells and contains RNAi methods. Video 1 is a 3D movie of BRCA1 and XIST. Video 2 is a 3D movie of BRCA1 and a mouse centromere. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200602055/DC1.

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