

PROSPECT

Breast Cancer Gene 1 (BRCA1): Role in Cell Cycle Regulation and DNA Repair—Perhaps Through Transcription

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Abstract Mutations of BRCA1 gene are associated with more than half the cases of hereditary breast cancer. Breast cancer formation in BRCA1 mutation carriers is generally accompanied by loss of the wild-type allele, suggesting that BRCA1 protein may function as a tumor suppressor. The human BRCA1 gene encodes a nuclear protein of 1863 amino acids. Although several lines of evidences suggest that BRCA1 protein may have a role to play in cell cycle regulation, DNA repair, and other processes, the exact mechanism of functioning by BRCA1 protein is not clear. Recent evidences from several laboratories suggest that BRCA1 may regulate the expression of many genes like p21^{WAF1/CIP1}, Gadd45, Cyclin B1, DBB2, XPC, 14-3-3 σ and others at the level of transcription. These BRCA1-regulated gene products have been implicated directly or indirectly in cell cycle regulation and DNA repair. Thus a plausible model is proposed in which BRCA1 protein may bring its effects on cell cycle and DNA repair through its ability to modulate gene expression at the level of transcription. *J. Cell. Biochem.* 88: 1084–1091, 2003. © 2003 Wiley-Liss, Inc.

Key words: breast cancer; BRCA1; transcription; DNA repair; cell cycle regulation

Breast cancer is one of the most common cancers affecting women worldwide. It is estimated that approximately one in eight to ten women living in western countries will develop breast cancer during their lifetime [Casey, 1997]. Most of the breast cancers are sporadic. About 5–10% of breast cancers are considered to be familial. Of the breast cancer susceptibility gene identified so far, BRCA1 and BRCA2 are the most important “high risk” genes accounting for majority of families with multiple cases of breast and ovarian cancer [Antoniou et al., 2002]. Women who inherit a mutant allele of either of these two tumor suppressors genes have a significantly increased lifetime breast cancer risk compared to the general population. Increased risk to develop breast cancer is due to

the inheritance of mutant copy of the gene and the cancer occurs when the second copy of the gene is lost or mutated [Smith et al., 1992; Nauhausen and Marshal, 1994]. Surprisingly, even though the inherited mutations of BRCA1 and BRCA2 are responsible for most of the familial breast cancer cases, neither gene is clearly involved in the development of sporadic breast cancer. Even though the majority of breast cancers are of sporadic type, the study of hereditary breast cancer has provided valuable information about breast cancer in general.

Several lines of approach have been attempted by different laboratories to define the biochemical function of BRCA1 protein. BRCA1 has thus far implicated in regulation of cell cycle checkpoints, apoptosis, DNA-damage repair, transcription-coupled repair and ubiquitin ligase activity. Although the participation of BRCA1 in these functions has been clearly demonstrated, the exact mechanism of BRCA1 function remains unclear. The presence of functional motifs on BRCA1 protein and the identification of many BRCA1 interacting cellular proteins linked to those functions shed some light about the possible mode of function by BRCA1. Involvement in DNA repair and cell cycle regulation by far seem to be the two most

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important well-studied functions of BRCA1. After the initial report on the identification of transcription activation domain in the C-terminus of BRCA1 [Chapman and Verma, 1996; Monterio et al., 1996], several transcriptional targets of BRCA1 have been identified. The functions carried out by the many of the genes isolated as BRCA1-transcriptional targets, either induced or repressed, adequately explain a possible mechanism in which BRCA1 would participate in DNA repair and cell cycle regulation through its ability to regulate gene expression at the level of transcription. The main focus of this review will be the various BRCA1 transcriptional targets so far identified and how BRCA1 could be linked to its functions, particularly to DNA repair and cell cycle regulation, through these targets.

STRUCTURE OF BRCA1 PROTEIN

The first breast cancer susceptibility gene (BRCA1) was found on chromosome 17q12–21 in humans and encodes an 1863 amino acid polypeptide (Fig. 1) [Miki et al., 1994]. BRCA1 is a large and complex gene about 100 kb long with a transcript size of 7.8 kb. The N-terminal end of BRCA1 contains a zinc-finger domain with a conserved pattern of cysteine and histidine residues, which are found in variety of proteins that interact with DNA either directly or indirectly [Miki et al., 1994]. The N-terminus of BRCA1 also interacts with BARD1 [Wu et al., 1996], BAP-1 [Jensen et al., 1998], E2F-1 [Wang et al., 1997]. Exon 11 of BRCA1 is the

largest exon, encoding over 60% of the protein, and contains two nuclear localization signals [Thakur et al., 1997]. Cellular proteins that interact with exon 11 of BRCA1 either directly or indirectly are RAD51 [Scully et al., 1997c], RAD50 [Zhong et al., 1999], p53 [Zhang et al., 1998], RB [Aprelikova et al., 1999], c-Myc [Wang et al., 1998]. The C-terminus of BRCA1, which contains transcription activation domain [Chapman and Verma, 1996; Monterio et al., 1996] and two BRCT (BRCA1 C-Terminal domain) domains [Koonin et al., 1996], interacts with RNA Polymerase II [Scully et al., 1997a], p300/CBP [Cui et al., 1998; Neish et al., 1998], BRCA2 [Chen et al., 1998], RNA helicase [Anderson et al., 1998], and CtIP [Yu et al., 1998; Li et al., 1999].

TRANSCRIPTIONAL REGULATION BY BRCA1

The first line of evidence implicating BRCA1 in transcription control came from an observation that the C-terminus of BRCA1 (amino acids 1528–1863), when fused to the GAL4 DNA-binding domain and transfected into cells, activates transcription of GAL4-dependent promoters [Chapman and Verma, 1996; Monterio et al., 1996]. Furthermore, some of the BRCA1 mutations found in BRCA1-associated tumors abolish transcriptional activity in this assay, implying that the loss of transcriptional activation by BRCA1 may be involved in tumorigenesis. Subsequent to this observation, many BRCA1 targets genes have been identified. Induction of

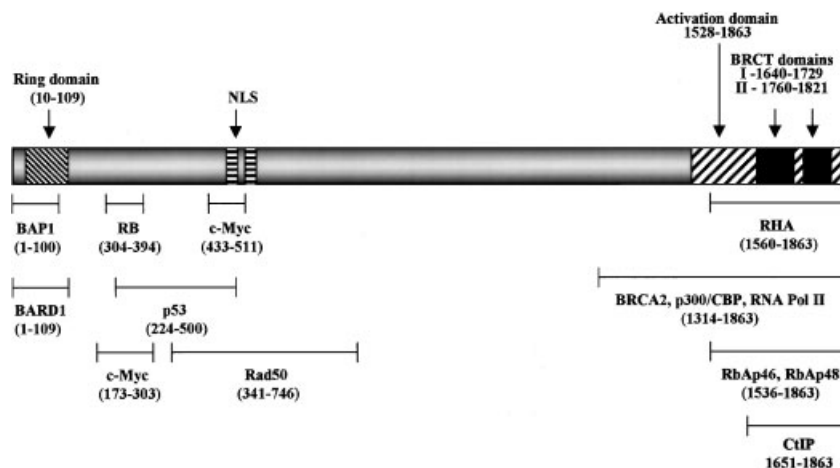


Fig. 1. A schematic diagram of BRCA1 protein is shown in the middle. Shown below are names and the interacting regions (with BRCA1 protein) of BRCA1 interacting proteins. Various functional domains of BRCA1 are shown above the BRCA1 protein.

p21^{WAF1/CIP1} either dependent or independent of p53 by BRCA1 has been shown by several groups [Somasundaram et al., 1997, 1999; Ouchi et al., 1998; Zhang et al., 1998; Li et al., 1999; Maclachlan et al., 2000; Welsh et al., 2002]. Similarly transcriptional activation of Gadd45 [Harkin et al., 1999; Maclachlan et al., 2000; Mullan et al., 2001; Fan et al., 2002; Hartman and Ford, 2002], 14-3-3 β [Aprelikova et al., 2001], p27(Kip1) [Williamson et al., 2002], DDB2 [Takimoto et al., 2002; El-Deiry, 2002; Hartman and Ford, 2002], XPC [Hartman and Ford, 2002] and TNF- α [Houvras et al., 2000] has been shown. BRCA1 has also been shown to repress the expression of certain genes at the level of transcription. Cyclin B1 [Maclachlan et al., 2000], estrogen receptor α (ER α)-responsive genes [Fan et al., 1999] and insulin growth factor 1 (IGF1) [Maor et al., 2000] are repressed by BRCA1.

Although the transcriptional regulation by BRCA1 has been shown to be specific, many in the field have questioned the physiological relevance of the transcriptional activity of BRCA1. DNA damage induced phosphorylation of BRCA1 protein is well documented [Scully et al., 1997b; Thomas et al., 1997]. So far three kinases—ATM [Cortez et al., 1999], ATM-related kinase (ATR) [Tibbetts et al., 2000], and hCds1 (CHK2) [Lee et al., 2000] have been shown to phosphorylate BRCA1 after DNA damage. The link between transcriptional regulation by BRCA1 and DNA damage was provided by the following observation. The activation potential of BRCA1 is partially suppressed by the CtIP-CtBP complex, which binds to the BRCT domain of BRCA1 [Li et al., 1999, 2000]. The association between BRCA1 with CtIP is abrogated by DNA damage induced ATM-dependent phosphorylation of CtIP, thus relieving the repression of transactivation by BRCA1. Thus the DNA damage mediated activation of BRCA1 transcription function suggests that transcriptional activation BRCA1 is indeed physiological.

Another lacuna is that there is no evidence that BRCA1 is able to bind to promoter regions of the target genes. BRCA1 binds to DNA without any sequence specificity, which may be an important part of its role in DNA repair transcription [Paull et al., 2001]. Mondal and Parvin [1999] have proposed that BRCA1 functionally links certain upstream enhancer-binding factors to the basal transcription

machinery in the holoenzyme and that BRCA1 may act as a transcriptional coactivator. In fact, a number of observations, as listed below, confirm the above hypothesis. BRCA1 protein is a component of the RNA polymerase II holoenzyme, and a deletion of the C-terminal 11 amino acids of BRCA1 reduces its association with the RNA polymerase II holoenzyme [Scully et al., 1997a; Neish et al., 1998]. BRCA1 also interacts with RNA polymerase II via a linkage with RNA helicase [Anderson et al., 1998]. Thus it is possible that BRCA1 interact with DNA-bound transcription factors to mediate signal to RNA polymerase II. In fact, transcriptional activation by BRCA1 has been shown to occur in many examples by its ability to associate with sequence-specific DNA-binding transcription factors. BRCA1 binds to p53 resulting in the activation of p21^{WAF1/CIP1} [Ouchi et al., 1998; Zhang et al., 1998], 14-3-3 β [Aprelikova et al., 2001], and DDB2 [Takimoto et al., 2002]. Interaction between ATF1 and BRCA1 results in the activation of TNF- α [Houvras et al., 2000]. BRCA1 interacts with Oct-1 and NF-YA, which results in the activation of Gadd45 [Fan et al., 2002]. BRCA1 also binds to ZBRK1, which is a transcription factor binding specifically to a DNA sequence, GGGxxxCAGxxxTTT [Zheng et al., 2000]. ZBRK1 binding sequence motif is present in the promoter regions of many transcriptional targets of BRCA1 like p21^{WAF1/CIP1} (3 sites), Gadd45, and EGR1. Coexpression of ZBRK1 and BRCA1 were found to actually repress the Gadd45 promoter, contrary to what one would expect given previous findings of activation of Gadd45 expression by BRCA1. Thus far, it is hypothesized that overexpression of BRCA1 may titrate ZBRK1 away from the promoter, allowing transcription to occur. In addition, DNA damage induced phosphorylation of BRCA1 and binding of BRCA1 to other repressors like CtIP etc. may actually modify this regulation [Maclachlan and El-Deiry, 2000]. Thus it appears that BRCA1 may regulate transcription as a coactivator by binding to sequence-specific DNA-binding transcription factors.

LINK BETWEEN TRANSCRIPTIONAL REGULATION BY BRCA1 AND ITS FUNCTIONS

Although, BRCA1 has been implicated in a variety of functions, its role in cell cycle regulation and DNA repair has been very well

documented [MacLachlan and El-Deiry, 2002; Venkitaraman, 2002]. An attempt is made below to link the developments with regard to BRCA1-mediated transcriptional regulation to its functions, particularly cell cycle regulation and DNA repair (Fig. 2).

Cell Cycle Regulation by BRCA1

The regulation of cell cycle by BRCA1 has been demonstrated by several observations. The initial findings, which include the expression pattern of BRCA1 mRNA and protein and the association of BRCA1 with cell cycle regulatory proteins, suggested the possible role of BRCA1 in cell cycle regulation. The expression of BRCA1 mRNA and protein during different stages of cell cycle is highly specific, occurring late in the G1 phase and peaking in the S-phase [Chen et al., 1996; Gudas et al., 1996; Vaughn

et al., 1996]. Western blot analysis of BRCA1 interacting protein (BIP) complex revealed binding of antibodies specific for cdc2, cdk2, cdk4, cyclin A, cyclin B1, cyclin D1, cyclin E, and E2F-4, suggesting an association between BRCA1 with these proteins [Wang et al., 1997]. BRCA1 is phosphorylated by kinases associated with cyclin D and cyclin A as well as by CDK2 in vitro [Chen et al., 1996]. The phosphorylation of BRCA1 continued throughout S and onto the G2/M phases, after which it was progressively dephosphorylated. It is likely that phosphorylation of BRCA1 may have some functional significance as it occurs in a cycle dependent manner.

The direct link between BRCA1 and its role in the cell cycle checkpoints came from the following observations. Overexpression of BRCA1 activated p21^{WAF1/CIP1} in a p53-independent manner and inhibited cell cycle progression into

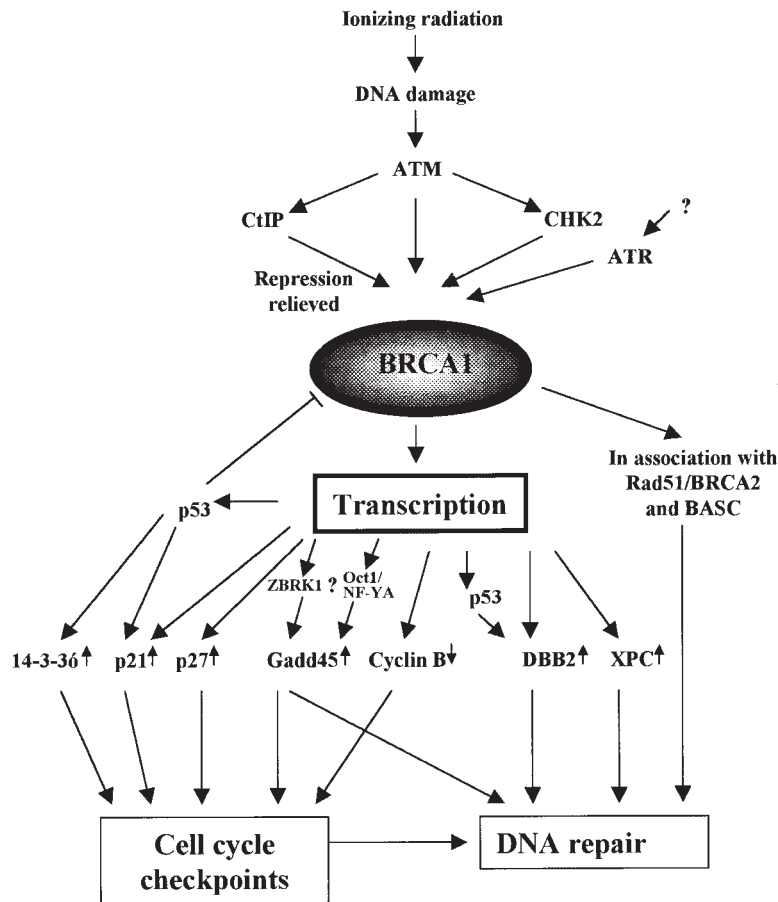


Fig. 2. Connection between BRCA1-mediated transcriptional regulation and its role in DNA repair and cell cycle regulation. The ability of BRCA1 to activate (shown by ↑) or repress (shown by ↓) transcription of certain genes specifically provides another mechanism by which BRCA1 carries out DNA repair functions either directly or indirectly by inducing cell cycle arrest.

S-phase [Somasundaram et al., 1997]. Moreover, this arrest in G1 phase is dependent on the presence of p21^{WAF1/CIP1}, as expression of BRCA1 in isogenic cell lines lacking p21^{WAF1/CIP1} does not lead to G1 arrest [Maclachlan et al., 2000]. In another study, exogenous overexpression of BRCA1 has been shown to cause Rb-dependent cell cycle arrest in some cell lines [Aprelikova et al., 1999]. Exogenous overexpression of BRCA1 also activated p27(Kip1), which may also contribute to its ability to induce G1 arrest [Williamson et al., 2002]. BRCA1 overexpression also resulted in the transcriptional activation of Gadd45 [Harkin et al., 1999; Maclachlan et al., 2000]. Introduction of BRCA1 through a recombinant adenovirus in a variety of cell lines resulted in the increase of cells with G2/M phase DNA content [Maclachlan et al., 2000]. Gadd45 has been implicated in G2/M checkpoint, as Gadd45-knockout mice possess a defective G2/M checkpoint [Hollander et al., 1999]. A role for BRCA1 in G2-M checkpoint has been demonstrated by using mouse embryo fibroblasts carrying a homozygous deletion of BRCA1 exon 11 [Xu et al., 1999]. Therefore, it is possible that BRCA1 may in part induce the Gadd45 protein to activate G2/M checkpoint. BRCA1 also has been shown to transcriptionally activate 14-3-3 δ in a p53-dependent manner [Aprelikova et al., 2001]. As 14-3-3 δ has previously been shown to be a major G2/M checkpoint control gene, 14-3-3 δ induction may also play an important role in the BRCA1-mediated G2/M checkpoint. Another target gene of BRCA1 identified was cyclin B1, which was actually repressed by exogenous expression of BRCA1 [Maclachlan et al., 2000]. Repression of cyclin B1 can easily be linked to BRCA1 regulated G2/M checkpoint because depletion of cyclin B1 would lead to inactivation of mitotic kinase cdc2. Indeed, the same study showed that exogenous expression of cyclin B1 abrogated the G2/M arrest induced by BRCA1 overexpression.

BRCA1 and DNA Repair

Studies from many laboratories suggested that BRCA1 is involved in DNA-damage repair. One set of evidences came from the findings that BRCA1 protein interacts with other cellular proteins involved in DNA repair and recombination. The DNA repair proteins with which BRCA1 has been shown to interact are Rad51 [Scully et al., 1997c], BRCA2 [Chen et al.,

1998], hRad50-Hmre11-p95 complex [Zhong et al., 1999]. Immunoprecipitation studies also revealed that BRCA1 protein is associated with a large complex (>2 Mda), called BRCA1-associated genome surveillance complex (BASC) [Wang et al., 2000]. BASC is composed of many proteins involved with DNA repair either directly or indirectly like Mut S homologue (MSH2), Mut S homologue 6 (MSH6), Mut L homologue 1 (MLH1), ATM kinase, Bloom (BLM), and the hRad50-hMRE11-p95 complex [Wang et al., 2000].

The second set of evidences from the analysis of stem cells derived from BRCA1-deficient embryo. Mouse embryonic stem cells carrying homozygous deletion of BRCA1 are defective in their ability to carry out transcription-coupled repair and hypersensitive to ionization radiation and hydrogen peroxide [Gowen et al., 1998]. Another report showed that Brca1-deficient mouse embryonic stem cells have impaired the repair of chromosomal DNA double-strand breaks (DSBs) by homologous recombination [Moynahan et al., 1999]. Mouse embryo with a BRCA1-deficiency was not only hypersensitive to γ -irradiation but also displayed numerical and structural chromosomal aberrations [Shen et al., 1998]. Consistent with this view, Abbott et al. [1999] showed that a human cancer cell line carrying a mutated BRCA1 allele is hypersensitive to ionizing radiation. More importantly, exogenous expression of certain regions of BRCA1 reversed the radiation sensitive phenotype.

Above studies involving BRCA1-interacting proteins and *BRCA1* knockout mice clearly demonstrate that BRCA1 has an important role to play in the DNA repair. The possible mechanism of action by BRCA1 could be that BRCA1 may influence the DNA repair process through its association the proteins involved in DNA repair. On the other hand, there is enough evidence to functionally link the transcriptional regulation by BRCA1 to its DNA repair functions. For example, proteins encoded by many of the transcriptional targets of BRCA1 participate, either directly or indirectly, in the DNA damage response, including DNA repair. BRCA1 collaborates with p53 to induce DDB2 following UV- and cisplatin-induced damage via a p53 responsive element present in the human DDB2 promoter [Takimoto et al., 2002; El-Deiry, 2002]. Furthermore, the DNA repair activity is significantly increased by the

introduction of BRCA1 into WT as compared to DDB2-deficient cells. DDB2 is the smaller subunit of the DDB heterodimer, which binds to DNA damaged by UV or cisplatin and is mutated in a subset of patients with cancer-prone syndrome Xeroderma pigmentosum complementation group E [Chu and Chang, 1988]. Recent evidence suggests a role for DDB in enhancing global genomic repair (GGR) of cyclobutane pyrimidine dimers [Tang et al., 2000]. In another observation, Hartman and Ford [2002] showed that BRCA1 enhances GGR pathway by transcriptional induction of nucleotide excision repair (NER) genes XPC, DDB2 and GADD45 in a p53-independent manner. The important role played by GADD45, DDB2 and XPC gene products in NER pathway has been demonstrated previously [Tang et al., 2000; Emmert et al., 2000; Tran et al., 2002]. Thus the DNA repair functions of BRCA1 may also be attributed to its ability to induce NER genes.

Cell cycle checkpoints represent integral components of DNA repair that coordinate cooperation between the machinery of the cell cycle and several biochemical pathways that respond to damage and restore DNA structure. By delaying progression through the cell cycle, checkpoints provide more time for repair before the critical phases of DNA replication, when the genome is replicated, and of mitosis, when the genome is segregated. Loss or attenuation of checkpoint function may increase spontaneous and induced gene mutations and chromosomal aberrations by reducing the efficiency of DNA repair. In fact many BRCA1 target genes like p21^{WAF1/CIP1} and Gadd45 would induce a robust cell cycle arrest thus allowing cells enough time to repair the damaged DNA. As discussed early, overexpression of BRCA1 can cause both G1/S and G2/M arrest. Several BRCA1 target genes, whose activation or repression by BRCA1 can bring about a clear G1/S or G2/M arrest. The details are given above in the previous sections. The ability of BRCA1 to induce G1/S arrest could be linked to BRCA1 targets p21^{WAF1/CIP1} [Somasundaram et al., 1997; Ouchi et al., 1998; Zhang et al., 1998; Li et al., 1999; Maclachlan et al., 2000; Welcsh et al., 2002] and p27(Kip1) [Williamson et al., 2002]. BRCA1 induced G2/M arrest could be attributed to BRCA1 targets Gadd45 [Harkin et al., 1999; Maclachlan et al., 2000; Mullan et al., 2001; Fan et al., 2002], 14-3-3 σ [Aprelikova et al., 2001], and Cyclin B1 [Maclachlan et al., 2000].

CONCLUSIONS

Involvement of BRCA1 in the development of hereditary breast cancer is very well established. Development of breast cancer among BRCA1 mutation carriers is accompanied by the loss of remaining WT BRCA1 allele, which suggests the importance of BRCA1 protein in the etiology of the disease. It is now becoming apparent that BRCA1 is a protein with complex and diverse set of functions. Several lines evidence implicates that BRCA1 is a protein with DNA repair function. Isolation of many BRCA1 interacting proteins, implicated in DNA repair processes, suggests that BRCA1 protein may be directly involved in the repair process. However, the identification of a handful of BRCA1 target genes, many of which either directly or indirectly by inducing cell cycle arrest involved in DNA repair process, suggest an additional model by which BRCA1 would participate in the DNA repair. That means a more elaborate study of transcriptional control by BRCA1 is required to understand better its role in DNA repair processes.

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