

NBS1 is regulated by two kind of mechanisms: ATM-dependent complex formation with MRE11 and RAD50, and cell cycle-dependent degradation of protein

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ABSTRACT

Nijmegen breakage syndrome (NBS), a condition similar to Ataxia-Telangiectasia (A-T), is a radiation-hypersensitive genetic disorder showing chromosomal instability, radio-resistant DNA synthesis, immunodeficiency, and predisposition to malignances. The product of the responsible gene, *NBS1*, forms a complex with MRE11 and RAD50 (MRN complex). The MRN complex is necessary for the DNA damage-induced activation of ATM. However, the regulation of MRN complex formation is still unclear. Here, we investigated the regulatory mechanisms of MRN complex formation. We used an immunoprecipitation assay to determine whether levels of the MRN complex were increased by radiation-induced DNA damage and found that the levels of these proteins and their mRNAs did not increase. ATM-dependent phosphorylation of NBS1 contributed to the DNA damage-induced MRN complex formation. However, pre-treatment of cells with an ATM-specific inhibitor did not affect homologous recombination (HR) and non-homologous end-joining (NHEJ) repair. G0 phase cells, decreasing NBS1 and HR activity but not NHEJ, gained HR-related chromatin association of RAD51 by overexpression of NBS1, suggesting that the amount of NBS1 may be important for repressing accidental activation of HR. These evidences suggest that NBS1 is regulated by two kind of mechanisms: complex formation dependent on ATM, and protein degradation mediated by an unknown MG132-resistant pathway. Such regulation of NBS1 may contribute to cellular responses to double-strand breaks.

KEYWORDS: DNA damage, NBS1, ATM, cell cycle checkpoint, homologous recombination

INTRODUCTION

DNA double-strand breaks (DSBs) often occur in genomic DNA after exposure to ionizing radiation (IR). Unrepaired DSBs can have severe consequences, such as the induction of genome instability and subsequent tumorigenesis, or the promotion of apoptosis. Therefore, cells are able to activate DNA damage responses (DDRs)

immediately after the detection of DSBs in genomic DNA, such as cell cycle checkpoint and DNA repair mechanisms. DSBs are repaired mainly through non-homologous end-joining (NHEJ) and homologous recombination (HR). NHEJ directly rejoins two DSB ends, but sometimes requires end-resection, particularly for radiation-induced DSB ends. Hence NHEJ is known to be an error-prone DSB

repair mechanism, leading to nucleotide loss. In contrast, during HR repair, the non-damaged homologous DNA region is used as a template for the repair of DSB regions, which is why HR is an error-free DSB repair mechanism [1].

Radiation-hypersensitive genetic disorders, such as Ataxia-Telangiectasia (A-T) and Nijmegen breakage syndrome (NBS) have been studied in order to elucidate the underlying mechanisms of DSB-induced cellular responses [2, 3]. Their cellular phenotypes are similar as well, showing radiation hypersensitivity, chromosome instability, and radiation-resistant DNA synthesis, and it was suggested that the genes responsible for these diseases (*ATM* in A-T and *NBS1* in NBS) play physical or functional roles during the DSB-induced response. The product of *ATM* is a protein kinase, while the product of *NBS1* is an adaptor protein that regulates DDRs through the formation of a protein complex [1, 2]. *ATM* kinase is activated in response to DSBs and has a fundamental role in the regulation of cell cycle checkpoints through the phosphorylation of DDR proteins, including p53, Chk2 and *NBS1* [4]. Bakkenist and Kastan [5] showed that the generation of radiation-induced DSBs results in an intermolecular modification within *ATM* dimers that leads to their activation through autophosphorylation at serine 1981. This phosphorylation triggers dimer dissociation and the free monomers subsequently phosphorylate several nuclear targets that recruit DDR proteins [5].

The product of human *NBS1* is a 754-amino acid (a.a.) protein that contains several functional domains, mainly located in the N- and C-termini. The N-terminus includes a forkhead-associated (FHA) domain and two BRCA1 C-terminus (BRCT) domains, which contribute to the binding of several phosphorylated proteins [1]. The C-terminus of *NBS1* protein interacts with several functional proteins as well, including *ATM* and *MRE11*, and these interactions are vital for various DNA damage responses [6, 7]. *MRE11* is a mutated gene responsible for another radiation-hypersensitive disorder (Ataxia-Telangiectasia-like disorder; AT-LD), which codes for a 708-a.a. protein that possesses DNA nuclease activity [8]. *NBS1* forms a complex with *MRE11* and *RAD50* through its C-terminal region (a.a. 682–693), and this interaction facilitates the localization of the complex to the nucleus [6]. Since HR activity is considerably reduced in *NBS1*- or *MRE11*-defective chicken DT40 cells and in patient cells, this indicates that the formation of this complex and its nuclear localization are crucial for activation of the HR pathway [9]. Another conserved motif (a.a. 734–754) in the C-terminus of *NBS1* directly interacts with *ATM* [7]. The cells of NBS patients less efficiently recruit *ATM* to DSB sites following IR, and show an insufficient activation of *ATM* kinase, suggesting an important role for the interaction between *NBS1* and *ATM* via this motif during *ATM* activation [7]. Additionally, *NBS1* interacts with *RNF20* (histone modification enzyme) for HR repair, and with *Rad18* for translesion DNA synthesis, through the C-terminal conserved motifs [10, 11]. Therefore, *NBS1* represents a multifunctional protein involved in several DDR pathways.

Formation of the *MRE11/NBS1/RAD50* (MRN) complex was discovered >15 years ago. It is believed that this complex is stable under most cellular conditions, and *NBS1* may be regulated through formation of the MRN complex. Therefore, we investigated the regulatory mechanisms of MRN complex formation, and its role in

DNA damage responses. We showed that the rate of *NBS1* interactions with *MRE11* and *RAD50* increased following the generation of DSBs by gamma irradiation. We discuss the relationship between this complex formation and DDRs.

MATERIALS AND METHODS

Cell culture

HeLa, U2OS, hTERT-immortalized human fibroblast (48BR), SV40-transformed normal fibroblast (MRC5SV), SV40-transformed AT patient-derived fibroblast (AT5BIVA), SV40-transformed AT-LD patient-derived fibroblast (ATLD2) and SV40-transformed NBS patient-derived fibroblast (GM7166SV) cells [12, 13] were cultured in Dulbecco's Modified Eagle Medium (DMEM; Sigma-Aldrich) supplemented with 10% fetal bovine serum (FBS; Invitrogen) and antibiotics. NBS cells, expressing wild-type (WT) or mutated *NBS1* (serine substituted with alanine at a.a. 278 and 343) were prepared as reported previously [14]. Growth arrest occurred at G0 in 48BR or U2OS-DRGFP and U2OS-pEJ by exchanging serum-rich media for the serum-free media. Generally, 3 days after the exchange, these cells were considered as G0 cells [15].

Antibodies

The following antibodies were used for western blot analysis: phospho-*ATM* (S1981), γ -H2A histone family X (H2AX) mouse monoclonal and H2B rabbit polyclonal antibodies (Millipore Co.); *MDC1*, and phospho-*KAP1* rabbit polyclonal antibodies (Bethyl Laboratories Inc.); *Chk2*, phospho-*Chk2* (T68), phospho-*Chk1* (S317), and phospho-*Rad17* rabbit polyclonal antibodies (Cell Signaling Technology); human meiotic recombination 11 (*MRE11*), *RAD50*, and *NBS1* rabbit polyclonal antibodies (Novus Biologicals); *RPA32*, *RPA70* mouse monoclonal and *ATM* rabbit polyclonal antibodies (Merk Millipore); *NBS1*, *MRE11*, and *RAD50* mouse monoclonal antibodies (GeneTex); *RAD51* rabbit polyclonal antibody (Bioacademia); beta-actin mouse monoclonal antibody (Sigma-Aldrich); c-myc mouse monoclonal antibody (Covance).

Irradiation with γ -ray

Irradiation of cells with gamma rays was carried out with Gammacell 40Ex (MDS Nordion; Dose rate 0.9 Gy/min) at room temperature.

myc-His-*NBS1* transfection

Plasmids expressing WT and two different types of mutated *NBS1* gene (serine substitution with alanine at a.a. 278 and 343, or *MRE11*-binding domain deletion) were prepared as reported previously [14]. Subconfluent MRC5SV or AT5BIVA cells, seeded in the culture dishes a day before the transfection, were transfected with these plasmids using Fugene HD (Promega). Two days later, these cells were re-seeded, and they were used for immunoprecipitation assays the following day.

Immunoprecipitation assays

Immunoprecipitation was performed as reported previously [12]. Immunoprecipitation was performed by incubating the samples with anti-*MRE11* rabbit polyclonal antibody (Novus Biologicals) or anti-*NBS1* mouse monoclonal antibody (GeneTex). Co-immunoprecipitates were detected by western blot analysis.

Western blot analysis

Western blot analyses were carried out as described previously [12]. Target proteins were detected with the primary antibodies listed above and horseradish peroxidase (HRP)-conjugated anti-rabbit IgG or anti-mouse IgG antibodies (GE Healthcare). The bands of target proteins were visualized using the ECL plus chemiluminescence system (GE Healthcare). Quantification of the visualized bands was carried out by ImageJ software, and the ratios to quantities in unirradiated samples were calculated.

Analysis of complex formation using cross-linking with formalin

The protein extracts were prepared with lysis buffer (10 mM Tris/HCl pH7.8, 1% NP-40, 150 mM NaCl, 1 mM EDTA). After centrifugation, formalin (final concentration 4%) was added to the supernatants and they were incubated at 37°C for 5 min. Then, cross-linking complexes were detected with western blot analysis using anti-NBS1 or MRE11 rabbit polyclonal antibodies.

Quantitative PCR analysis

Total RNA was isolated from HeLa, U2OS, 48BR and GM7166SV (NBS) cells by the RNAqueous Total RNA Isolation Kit (Ambion). cDNA molecules were synthesized with the SuperScript III First-Strand Synthesis System (Invitrogen), and quantitative PCR analysis was performed with the 7500 Real time PCR system (Applied

Biosystems) using the Power SYBR Green PCR Master Mix (Applied Biosystems), NBS1 primers (Qiagen #249900) and GAPDH primers (forward primer, 5'-TCTCCCCACACACATGCACTT; reverse primer, 5'-CCTAGTCCCAGGGCTTTGATT).

HR and NHEJ activity analyses

HR and NHEJ analyses were performed as previously reported [16, 17]. Briefly, in order to measure the HR or NHEJ repair of I-SceI-generated DSBs, 50 µg of the I-SceI expression vector (pCBASce) was introduced to 1×10^6 U2OS-DRGFP (for HR) or U2OS-pEJ (for NHEJ) cells by electroporation (GenePulser; BIO-RAD). To determine the level of HR or NHEJ activity, the percentage of GFP-positive cells were quantified at Day 3 after electroporation using FACSCalibur (Becton Dickinson).

RESULTS

The rate of MRN complex formation increased in response to DSB generation

First, we examined whether the formation of MRN complex increases after gamma-ray IR using immunoprecipitation with anti-MRE11 antibody (Fig. 1). Anti-MRE11 antibody co-precipitates NBS1 and RAD50, forming the MRN complex with MRE11, and the amount of co-precipitated NBS1 increased in HeLa cells following IR (Fig. 1A and B), but the levels of co-precipitated RAD50 were unchanged after IR. In U2OS cells, a similar increase in the

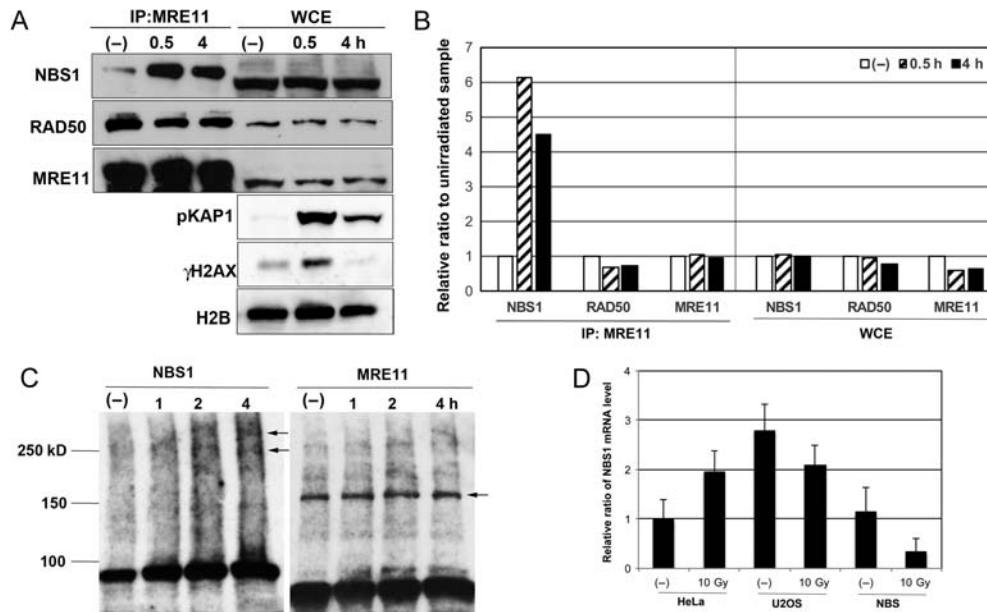


Fig. 1. Immunoprecipitation with anti-MRE11 antibody detected increases of MRN complex in response to DSB damages. (A) Extracts from HeLa cells without (-) or with 10 Gy of IR were immunoprecipitated with anti-MRE11 antibody, and then the immuno-complexes were detected by Western blot analysis using the indicated antibodies. WCE = whole cell extract. Quantification was carried out by ImageJ software, and the ratios to unirradiated samples were calculated as shown in (B). (C) Detection of MRN complex by cross-linking with formalin. Whole cell extracts from irradiated (10 Gy) or unirradiated cells were treated with formalin, and then cross-linked MRN complex (arrows) was detected by Western blot analysis using the indicated antibodies. (D) The levels of NBS1 mRNA were quantified as shown in *Materials and Methods* using unirradiated and irradiated cells (10 Gy).

amount of MRN complex components was observed following the IR (Fig. S1A). However, the amount of NBS1 in whole cell extracts (WCEs) was unchanged (Fig. 1A and B). Anti-NBS1 antibody is also able to detect the increase in MRN complex formation (Fig. S1B). When we treated cell extract with formalin to stabilize complex formation through cross-linking, we observed the appearance of two bands at >250 kD after IR using the anti-NBS1 antibody (Fig. 1C), suggesting an increase in the MRN complex following IR. On the other hand, anti-MRE11 detected 150 kD bands with and without IR, suggesting that MRE11 might always form the stable homodimer. In the case of mRNA expression, we did not observe a remarkable increase in NBS1 at the same level to that of immunoprecipitated NBS1, as shown in Fig. 1A and B (Fig. 1D). These results suggest that the number of MRN complexes might increase upon IR-induced DSB formation, but this increase may not depend on increase in the amounts of protein or mRNA of the individual components of this complex.

DSB-induced increase in the MRN complex was independent of the stabilization of each component

Previously, it was reported that in some DNA damage-related complexes, such as the XRCC4/ligase IV complex, the formation of the complex can lead to the stabilization of their components [18]. In order to investigate this, we used proteasome inhibitor, MG132. When 48BR cells were pre-treated with MG132, we did not observe any increase in NBS1, MRE11 or RAD50 levels in WCEs, or any disturbance in MRN complex formation following the IR (Fig. 2A). The same treatment of cells with MG132 stabilized cyclin A (G0+MG132; Fig. 4B), which is known to be degraded by a proteasome-dependent mechanism [19]. This pre-treatment did not influence ATM-dependent phosphorylation of KAP1 and Chk2 (Fig. 2B). It has been reported that MRE11-deficient AT-LD cells have not only less MRE11 protein, but also less NBS1 and RAD50 protein due to a decrease MRN complex formation [20]. We also investigated whether such instability in ATLD2 was overcome by MG132 treatment; however, the treatment did not increase the levels of the proteins (Fig. 2C). Taken together, each component of the MRN complex and the complex formation might be regulated independently of the proteasome pathway.

ATM was necessary for DSB-dependent formation of the MRN complex

NBS1 is indispensable for the DSB-dependent activation of ATM [7], and since NBS1 is a substrate of ATM kinase, this phosphorylation could lead to intra-S phase checkpoint, namely inhibition of DNA synthesis [21, 22]. We investigated whether this phosphorylation might contribute to DSB-dependent formation of the MRN complex. Pre-treatment of U2OS cells with an ATM-specific inhibitor, KU55933, inhibited the phosphorylation of KAP1 and Chk2, known to be ATM-dependent (Fig. 3A), and also repressed an IR-dependent increase in the levels of co-immunoprecipitated NBS1 (IP:MRE11; Fig. 3A). ATM-defective A-T patient fibroblasts (AT5BIVA) also showed a similar tendency to immunoprecipitate NBS1 (Fig. S2A). These results suggest that the kinase activity of ATM is necessary for DSB-dependent formation of the MRN complex.

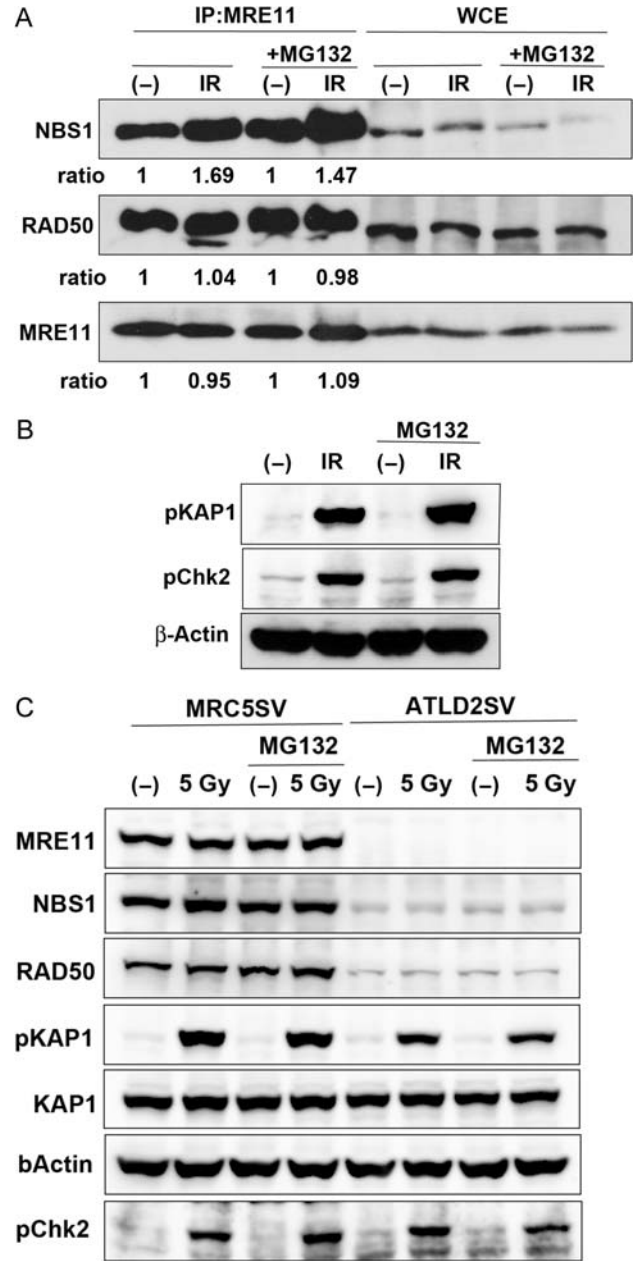


Fig. 2. Treatment of MG132 did not disturb DSB damage-dependent increase in MRN complex. (A) 48BR cells were treated with MG132 (10 μ M) 1 h before 10 Gy of IR. The extracts were immunoprecipitated with anti-MRE11 antibody, and then the immuno-complexes were detected by Western blot analysis using the indicated antibodies. (B) U2OS cells were treated with MG132 (10 μ M) 1 h before 10 Gy of IR (0.5 h of post-irradiation). Then, ATM-dependent phosphorylation was confirmed by Western blot analysis using the indicated antibodies. (C) MRC5SV and MRE11-defective ATLD2SV cells were treated with MG132 (10 μ M) 1 h before 5 Gy of IR (0.5 h of post-irradiation), and analyzed using the indicated antibodies.

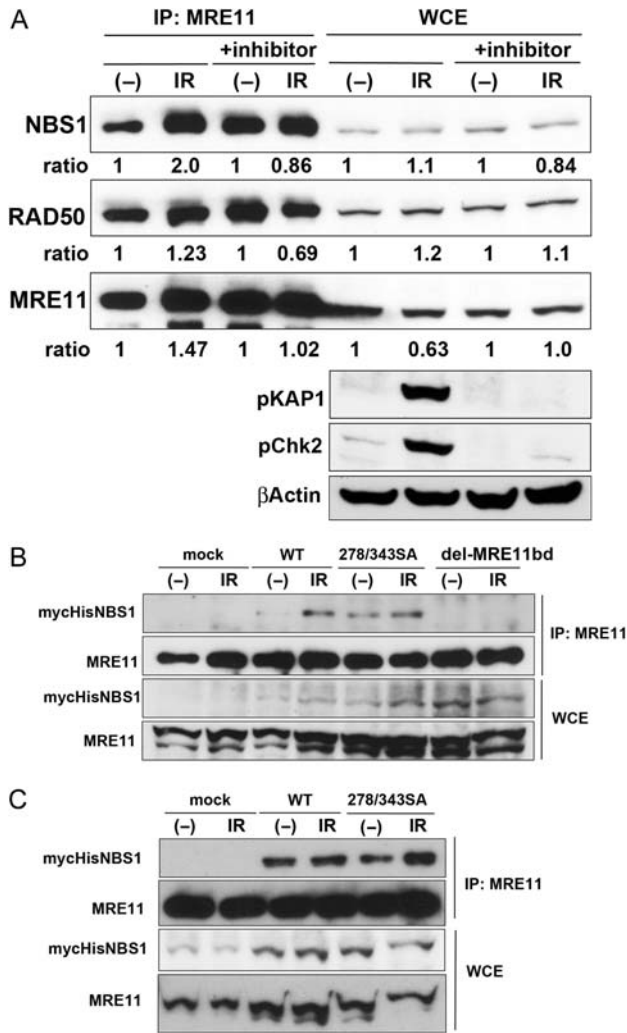


Fig. 3. ATM was indispensable for DSB damage-dependent complex formation of MRN. (A) U2OS cells were treated with KU55933 (10 μ M; +inhibitor) 1 h before 10 Gy of IR (1 h of post-irradiation). The extracts were immunoprecipitated with anti-MRE11 antibody, and then the immuno-complexes were detected by Western blot analysis using the indicated antibodies. The intensity of the bands was quantified by ImageJ software and the ratio was calculated as shown for the lower positions of each band. (B)(C) NBS1-WT or mutated NBS1 (278/343SA or del-MRE11bd) were transfected to MRC5SSC (B) or AT5BIVA (C). After 2 days, their cells were irradiated with 10 Gy of IR (1 h of post-irradiation), and then extracts were prepared from them. Their extracts were immunoprecipitated with anti-MRE11 antibody and then the immuno-complexes were detected by Western blot analysis using anti-c-myc (for mycHisNBS1) and anti-MRE11 mouse monoclonal antibodies.

As serine residues 278 and 343 in NBS1 are phosphorylated by ATM, leading to regulation of the intra-S phase checkpoint [21, 22], we examined the relationships between the phosphorylation of these

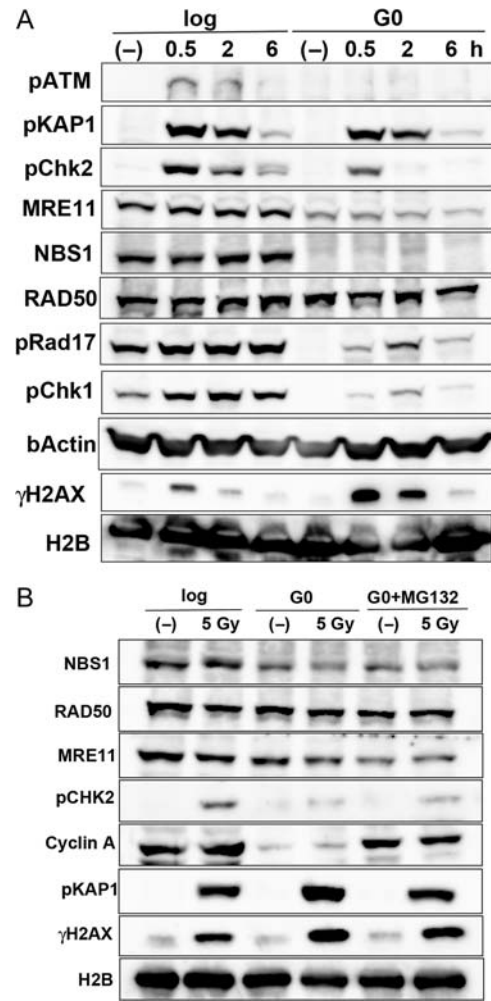


Fig. 4. Regulation of MRN components in G0 phase. (A) Extracts from growing (log) and growth-arrested serum-starved (G0) cells (48BR cells) were analyzed by Western blot using the indicated antibodies. (B) MG132 treatment did not recover NBS1 expression. G0 cells were pre-treated with MG132 (10 μ M), and then irradiated with 10 Gy of IR (1 h of post-irradiation). Western blot analysis was performed using extracts from the cells and the indicated antibodies.

sites and DSB-dependent formation of MRN complex, using an NBS1 mutant in which both serine 278 and 343 were replaced by alanine. When we transfected MRC5SSV cells with WT or mutant NBS1, anti-MRE11 antibody was able to co-precipitate WT-NBS1 following the IR, but one of the mutated NBS1 genes (del-MRE11bd), lacking the MRE11-binding domain [6], could not be co-immunoprecipitated using the anti-MRE11 antibody (Fig. 3B). The other NBS1 mutant, 278/343SA-NBS1, was co-immunoprecipitated with the antibody used, but the levels of this molecule did not increase after IR. In the case of AT cells (Fig. 3C) we were not able to observe any increase in the levels of either WT or mutated NBS1 between unirradiated and irradiated cells. MDC1 is another component of the MRN

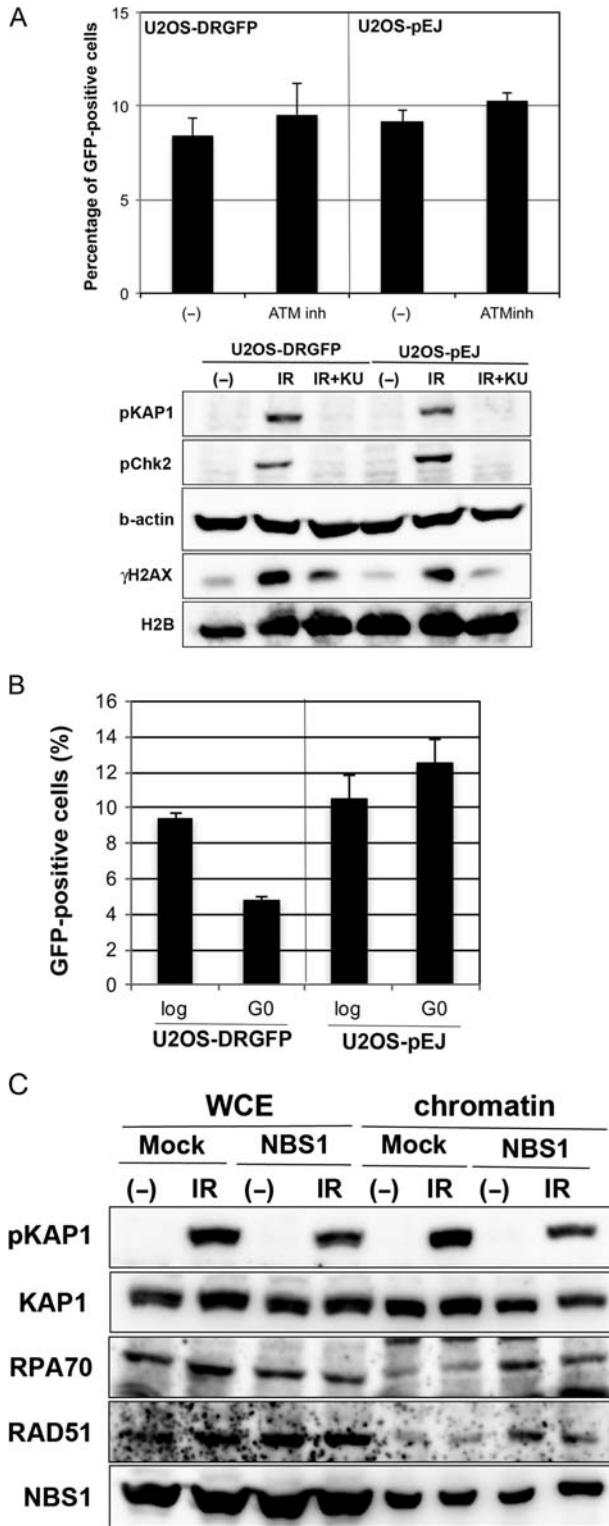


Fig. 5. DSB damage-dependent complex formation of MRN was important for sufficient activation of the ATM-related pathway. (A) NHEJ and HR activity in ATM inhibitor-treated cells. U2OS-DRGFP or U2OS-pEJ cells were treated with KU55933 (10 μM; ATM inh) for 1 h before

complex, which directly binds NBS1 [23]. MDC1-depleted U2OS cells by siRNA showed reduced DSB-dependent increase in MRN complex formation, suggesting that MDC1 may be important for the formation of this complex (Fig. S2B).

Regulation of MRN components in the G0 phase

The expression of many molecules involved in HR, such as RAD51 and BRCA, is induced in S phase, because HR is activated by DSBs in late S and G2 phases [24]. As the MRN complex is important for HR as well [9], we investigated the cell cycle-dependent role of MRN using G0 (growth-arrest phase) cells. When we maintained hTERT-immortalized human fibroblasts (48BR cells) in serum-free media, cyclin A (S/G2 phase marker protein) levels decreased at 2 and 3 days after medium change (Fig. S3A) and were arrested at G0 phase [15]. Cell cycle analysis by flow cytometry showed that the cells after 3 days of serum starvation arrested at G0 phase (G0/G1: 87.5%; Fig. S3B). NBS1 levels also decreased at these time-points as well, but the levels of other components, MRE11 and RAD50, were unchanged. We also verified that NBS1 mRNA levels were unchanged after serum starvation (Fig. S3C). The phosphorylation of ATM substrates (KAP1, Chk2 and ATM itself) was induced in the cells in the growth (log) phase, but their phosphorylation levels were considerably reduced in G0 phase (Fig. 4A), while the growth arrest at G0 phase did not reduce the expression of ATM or that of the substrates, KAP1 and Chk2 (Fig. S3A; right panel). Figure 4A also showed that γH2AX levels increased in G0 phase after irradiation, suggesting that the reduction in NBS1 levels may lead to DSB repair defects. Additionally, we examined whether the decrease in NBS1 levels in G0 phase was due to the changes in stability, caused by the components of the proteasome pathway. Although the pre-treatment of MG132 was able to recover cyclin A levels in the G0 phase, NBS1 levels were unchanged by this treatment (Fig. 4B), suggesting that the decrease in NBS1 may be regulated by an MG132-resistant pathway at the protein level. We also measured MRN complex formation in the G0 phase. As expected, the co-immunoprecipitated NBS1 levels completely decreased with and without the induction of DNA damage [IR and camptothecin

transfection. Then, I-SceI expression plasmids were transfected to these cells by electroporation and analyzed by flowcytometer. Each result represents an average value and standard deviation from three experiments. Lower panel: The cells were treated with KU55933 (10 μM; KU) 1 h before 5 Gy of IR (0.5 h of post-irradiation). Then, ATM-dependent phosphorylation was confirmed by Western blot analysis using the indicated antibodies. (B) Serum-starved (for 3 days) or growing U2OS-DRGFP or U2OS-pEJ cells were electroporated with I-SceI expression plasmids and analyzed by flow cytometer. Each result represents an average value and standard deviation from three experiments. (C) Chromatin-associated proteins such as RAD51 and RPA were prepared from precipitates after RIPA buffer extraction and were then detected by Western blot analysis using the indicated antibodies.

(CPT)] in G0 cells, possibly due to a decrease in NBS1 protein levels (Fig. S3D).

DSB-dependent formation of the MRN complex was important for ATM-related pathway activation

Since MRN complex formation increases in response to DSBs, and is ATM-dependent, we investigated the role of the ATM kinase activity in HR and NHEJ repair using the GFP-reporter assay (U2OS-DRGFP for HR; U2OS-pEJ for NHEJ). When their cells were pre-treated with ATM inhibitor, the percentage of GFP-positive cells remained unchanged (Fig. 5A, upper), but this pre-treatment reduced the levels of ATM-dependent phosphorylation of KAP1 and Chk2 (Fig. 5A, lower). ATM kinase activity might be dispensable for HR and NHEJ pathways, which is agreement with an earlier report by Kass *et al.* [25]. We next investigated the effect of NBS1 reduction on HR repair and NHEJ repair by serum starvation (G0): HR activity almost 50% decreased in U2OS-DRGFP, but NHEJ did not in U2OS-pEJ cells (Fig. 5B). Furthermore, overexpression of NBS1 in G0 phase increased the chromatin association of HR factors RAD51 and RPA (Fig. 5C), suggesting that the reduction in NBS1 protein in G0 phase may be important for repressing HR activity.

We next investigated the relationship between DSB-dependent phosphorylation, which is related to stabilization of the MRN complex, and the ATM-related pathway. We investigated the cell cycle distribution after unirradiated and irradiated cells, using propidium iodide (PI) staining (Fig. S4A). At 6 h after irradiation, the percentage of WT-NBS1-expressing cells in G2 phase considerably increased, due to the activation of the G2 checkpoint, but an increased number of cells in S phase was not observed. After 12 h, some of these cells were released from G2 checkpoint arrest, and these cells were able to progress to G1 phase. Both NBS cells and 278/343A-NBS1-expressing cells showed S phase arrest at 6 h after IR, and the percentage of the cells in G1 phase was low at 12 h. We also confirmed the induction of apoptosis by PI staining (Fig. S4B). Camptothecin treatment was able to induce the death of >10% of NBS cells, but the rates of apoptosis were reduced in WT- and 278A/343A-mutated NBS1-expressing cells (Fig. S4B). Taken together, ATM-dependent phosphorylation of NBS1, and subsequent amplification of the MRN complex may be important for cell cycle checkpoints, but not for the apoptosis pathway.

DISCUSSION

So far, the MRN complex has been believed to stably exist independently of DNA damage responses, but we here clarify that the complex increases in response to the generation of DSB damage. DSB-induced MRN complex formation could be dependent on ATM-dependent phosphorylation of NBS1 (Fig. 3), and this phosphorylation may be indispensable for regulation of the ATM-dependent cell cycle checkpoint, but not for HR repair (Fig. 5A and S4A). On the other hand, the level of NBS1 proteins may be important for HR repair, but not for NHEJ (Fig. 5B and C). We conclude that the two types of regulation of NBS1 have distinct roles in DNA damage responses, namely NBS1 phosphorylation

plays a role in regulating the ATM-dependent checkpoints, and the NBS1 protein level plays a role in HR repair.

Growth-arrest in G0 phase by serum starvation caused a considerable decrease in NBS1 levels, but the levels of MRE11 and RAD50 remained unchanged (Fig. 4). The levels of cell cycle regulators, cyclins, are known to be reduced in the G0 phase; we confirmed that the levels of cyclin A were reduced in the G0 phase and that a treatment with proteasome inhibitor, MG132, abolished this reduction (Fig. 4). However, MG132 treatment did not stabilize NBS1 in G0 phase (Fig. 4). The formation of several DNA repair complexes is known to stabilize each component of the complex. XRCC4 and ligase IV form a complex necessary in the final step of NHEJ. The levels of ligase IV in XRCC4-defective CHO cells was shown to be reduced, but the introduction of XRCC4-expression plasmids to these cells successfully recovered the levels of ligase IV [18], suggesting that complex formation is important for XRCC4 stability. NBS1 is dependent on other components of the MRN complex as well. MRE11 expression, but also the expression of NBS1 and RAD50 proteins, is reduced in MRE11-defective AT-LD patient cells [20]. However, MG132 treatment could not recover NBS1 or RAD50 in MRE11-defective ATLD2 cells (Fig. 2C). It is likely that the MG132-resistant system might degrade NBS1 protein in G0 phase, and the system may be important for avoiding accidental activation of HR.

HR activity in G0 phase cells was reduced; this finding, together with reduction in the ATM cell cycle checkpoint, suggested that these cells may show an increase in radiosensitivity compared with cells in the growth phase. Since A-T or NBS1-defective patient cells are radiation hypersensitive, the repression of NBS1 may effectively enhance radiosensitivity. The G0 phase is positively regulated by both p53 and RB, which are the products of tumor suppressor genes, and these genes are inactivated in many types of tumors. It is possible that, in p53 and RB-active tumors, the repression of NBS1 by activation of G0 phase may contribute to the enhancement of radiotherapy effects. However, in many tumors where p53 and RB are inactivated, different methods of NBS1 inhibition are necessary. Therefore, clarification of the NBS1 degradation mechanism in further studies is expected to develop radiotherapy.

SUPPLEMENTARY DATA

Supplementary data are available at the *Journal of Radiation Research* online.

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CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest.

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