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애기장대로부터 DNA 수선 단백질인 XRCC1 을 암호화하는 유전자의 클로닝과 분석

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Cloning and Analysis of the Gene Encoding a DNA Repair Protein XRCC1 from *Arabidopsis thaliana*

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ABSTRACT : X-Ray Cross-Complementing group 1 (XRCC1) is a DNA repair protein that responds to DNA damage. A cDNA clone, *XRCC1*, from *Arabidopsis thaliana* was isolated, sequenced, and, through combined analysis of the cDNA and genomic DNA, found to contain seven introns. It was determined that the XRCC1 coding sequence is 1062 bp in length and encodes a 353 amino acid, 40 kDa protein. The predicted amino acid sequence of XRCC1 contains a consensus BRCT domain and is similar to, but significantly shorter than, the XRCC1 counterparts from animals. XRCC1 was shown to increase resistance to methylmethane sulfonate (MMS) in wild type yeasts, whereas mutant yeast cells deficient in RAD51 or RAD52 were not rescued by overexpression of XRCC1.

INTRODUCTION

Damaged DNA created from exposure to radiation can lead to the disruption of cellular processes, such as DNA replication and recombination. To counteract this damage, the cell has evolved tolerance mechanisms in which damaged DNA is rapidly repaired through the precise and concerted activities of a variety of proteins. DNA repair mechanisms also maintain genetic stability and suppress the formation of aberrant aging events that can cripple the cell. XRCC1 (X-Ray Cross-Complementing group 1) is a DNA repair protein needed to repair DNA damage caused by ionizing radiation or DNA methylating agents. XRCC1 has been primarily characterized in *Homo sapiens* (Thompson et al., 1990), *Cricetulus griseus* (Shen et al., 1998), and *Drosophila melanogaster* (Taylor et al., 2000). Human XRCC1 consists of three distinct domains, including the N-terminal domain (NTD), which can interact with DNA polymerase (Marintchev et al., 2000), and two other domains known generally as breast cancer carboxy-terminals (BRCT), which are thought to serve as modules for protein- protein interactions (Zhang et al., 1998). BRCT-I

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and BRCT-II motifs may interact with poly (ADP-Ribose) polymerase (PARP; Pleschke et al., 2000) and DNA ligase III, respectively.

As part of a long-term investigation on the process of DNA repair mechanisms in plants, we have initially identified genes involved in DNA repair processes from *Arabidopsis thaliana*. This genome, which has been completely sequenced (The Arabidopsis Genome Initiative, 2000), provides fertile ground for isolating important genes that can participate in or regulate repair events. The partial gene structure of XRCC1 was recently reported (Theologis et al., 2000) from *A. thaliana* and contains a coding sequence with significant homology to animal XRCC1 (Taylor et al., 2002). But, functional information about this gene was not described; thus, we characterized the gene encoding XRCC1 with the immediate goal of elucidating the function of the XRCC1 protein. Here, we report the cloning of the *Arabidopsis* gene encoding a DNA repair protein, XRCC1, but also extend the study to an examination of its activity in yeast strains deficient in a variety of DNA repair activities.

MATERIALS and METHODS

Plant materials

Arabidopsis thaliana ecotype Columbia (Col) was raised in a 23C growth chamber with a light intensity of 100 $uE.m^{-1}.s^{-1}$ and a photo-period of 14 hours light followed by 10 hours darkness.

DNA sequence analysis

An EST clone (GenBank Acc. No. N37375, cDNA ID 210J9T7) was obtained from the Arabidopsis Biological Resource Center (ABRC, Ohio State University). The clone was derived from *A. thaliana* (Col) cDNA library (D'Alessio et al. 1992) prepared in Zip-Lox (GibcoBRL, Inc.) containing plasmid pZL1. DNA sequencing was performed by the dideoxynucleotide chain termination method with an automatic sequencer (AlFexpress DNA sequencer, Pharmacia Biotech, Inc.). Nucleotide sequences and amino acid sequences were compared with sequences present in the GenBank and EMBL databases and analyzed using BLAST and PILEUP of the GCG Wisconsin Package or Biology WorkBench 3.2 (http://workbench.sdsc.edu; San Diego Supercomputer Center; University of California San Diego). Comparison of sequences with published animal XRCC1 sequences was performed at the nucleotide and amino acid level.

Overexpression of XRCC1 *in yeasts and MMS resistance test*

To investigate the function of At XRCC1, the cDNA was subcloned into the yeast expression vector pYES2/CT (Invitrogen Corp., Carlsbad, CA) by *KpnI* and *XbaI* sites to generate plasmid pYES-*XRCC1*; expression of XRCC1 is under the control of the inducible GAL1 promoter. pYES-*XRCC1* or pYES2/CT (as a negative control) were transformed into a wild-type yeast strain (LSY678; Liu et al. 2001) or strains lacking *RAD51* (LSY402) or *RAD52* (LSY386), respectively. Transformants were selected and maintained on agar containing SD supplemented media without Ura (SD-Ura, Invitrogen Corp.; Liu et al. 2002).

The resistance to DNA damage of yeast strains conferred by plasmid pYES-*XRCC1* was

assessed using a traditional radiomimetic drug-sensitivity assay as follows: A single yeast colony was inoculated and grown in SD-Ura liquid media to OD_{600}=0.7. XRCC1 was then induced by replacing the SD-Ura media with a second SD-Ura media containing 2% galactose, which induces the GAL1 promoter in the plasmid. The culture was grown to OD_{600}=0.5-0.9 over a period of 9 to 24 hours. The culture was diluted $1/10^{-5}$, and plated on SD-Ura+Gal media containing various concentrations of the mutagen methylmethane sulfonate (MMS) ranging from 0-0.05%. The highest concentration of MMS (0.05%) is sufficient to kill the entire wild-type population.

RESULTS

Identification of XRCC1 cDNA and sequence analysis

DNA repair genes typically exhibit sequence similarity, even among widely differing species. To identify genomic sequences from *Arabidopsis* plants based on sequence similarity to known DNA repair genes, we performed a database search with various gene fragments known to encode conserved regions of DNA repair proteins. Queries to the GenBank database using human XRCC1 protein sequences (GenBank Acc. No. M36089) by TBLASTN revealed an *Arabidopsis* gene with similar sequence (GenBank Acc. No. AC018849), and we identified it as a putative *XRCC1* gene. Queries to the *Arabidopsis* EST database with the genomic sequence identified an EST 210J9T7 (GenBank Acc. No. N37375) as another putative XRCC1 coding region. The EST clone (210J9T7) was obtained directly from the Arabidopsis Biological Resource Center (ABRC) and was processed for DNA sequence analyses.

Sequence analysis revealed that the 210J9T7 clone contains a full length cDNA of the *Arabidopsis XRCC1* gene, and that its sequence was identical to the genomic sequence (GenBank Acc. No. AC018849) derived from BAC clone T21F11 in Chromosome 1. The 1390bp cDNA contains an open reading frame (ORF) of 1062bp, and a 141bp 3′-untranslated region ending with a 30 nucleotide polyA-tail (Fig 1). But full, unimpeded extension from first start codon to the 5′ end of the cDNA clone was viewed as likely, due to the presence of three stop codons existing in frame with the coding sequence.

The ORF, however, did encode a 353 amino acid polypeptide with a calculated molecular weight of 39.8kDa and a theoretical isoelectric point of 6.2. Inspection revealed that amino acids 58-146 are highly homologous to the BRCT-I motif (Fig 2A) present in XRCC1 homologs from *H. sapiens*, *R. norvegicus*, *C. griseus*, and *D. melanogaster* (Fig 2B), and typical for this subfamily of poly(ADP-ribose) polymerase (PARP)-interacting proteins (Masson et al., 1998). The deduced amino acid sequence of XRCC1 (353 amino acids) is similar to but shorter than the mammalian counterparts (Table 1). At XRCC1 possesses a BRCT domain associated with PARP binding, but appears to lack the N-terminal domain for interacting with DNA polymerase . The C-terminal BRCT-II motif is not totally conserved in the plant gene, but some partial motifs are located in downstream from the BRCT-I domain.

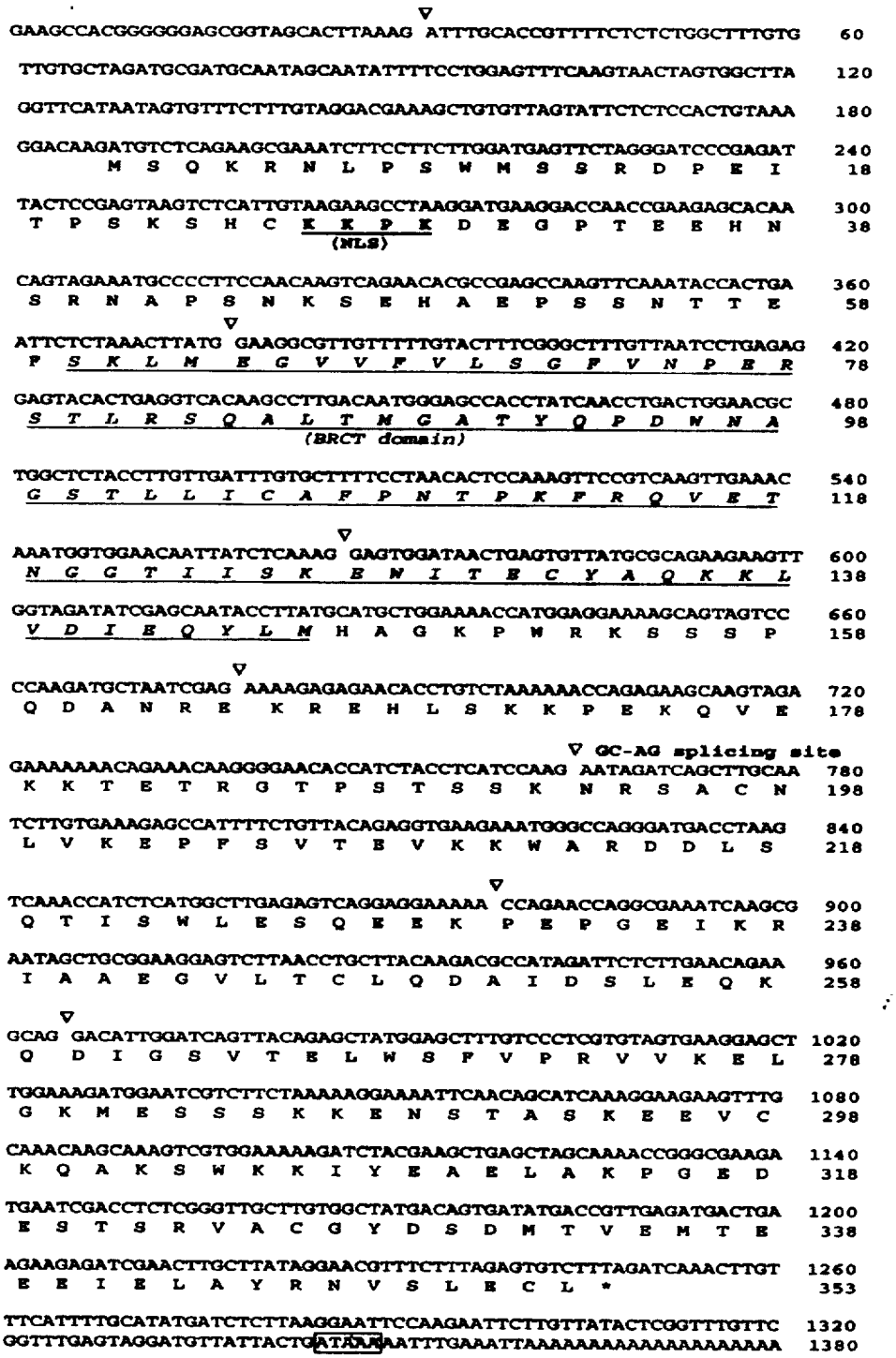
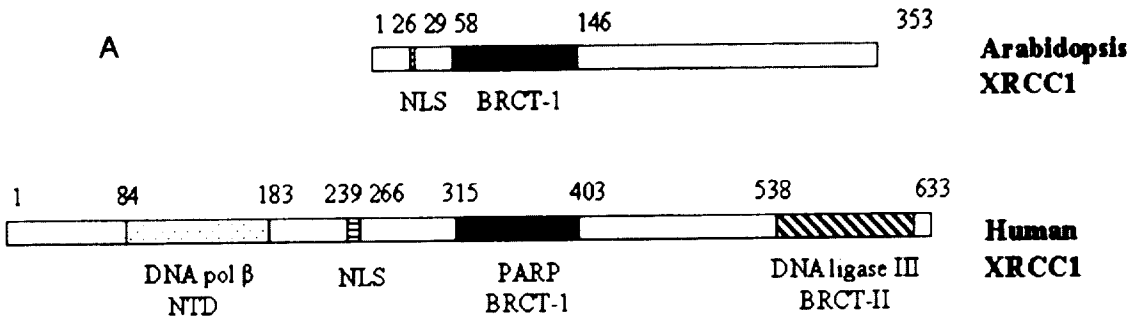


Fig 1. *XRCC1* cDNA sequence.

Features of a *XRCC1* cDNA sequence was presented. Mark represents the junction of intron and exon in splicing site and the GC-AG site is written followed by mark. Nucleus localization signal (NLS) and conserved BRCT domain were underlined with bold-type or italics, respectively. The stop codons and a poly(A) signal is indicated by an asterisk and a box, respectively.



B

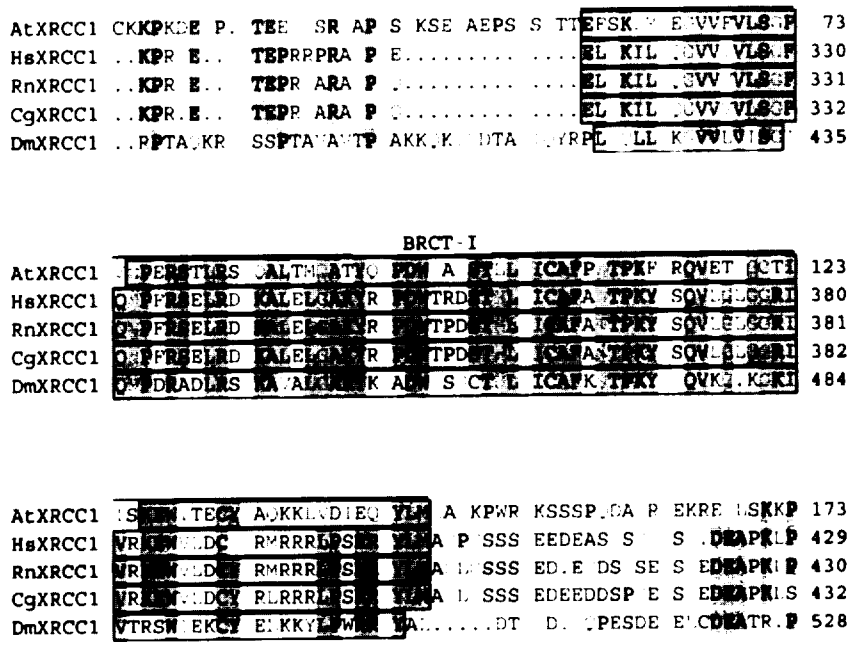


Fig 2. Amino acid sequence homology in XRCC1.

A: Schematic diagram of XRCC1 domains in Arabidopsis and human. B: The GCG program PILEUP (blosum62.cmp program) was used to generate the alignment. Dashes indicate gaps introduced to optimize the alignment. The identical amino acids among 4 out of 5 were shadowed and the conserved BRCT-I domain was boxed. The GenBank accession numbers for each sequence are as follows: *Arabidopsis thaliana* (AtXRCC1), AF324348, this study; *Cricetulus griseus* (CgXRCC1), AF034203; *Rattus norvegicus* (RnXRCC1), AF290895; *Homo sapiens* (HsXRCC1), M36089; *Drosophila melanogaster* (DmXRCC1), AF132142.

Table 1. Amino acid sequence homology among *XRCC1* from *Arabidopsis* and other organisms.

Species	Numbers of Amino acids	Sequence identity to AtXRCC1	Sequence similarity to AtXRCC1	Conserved domains
Arabidopsis thaliana	353	-	-	NLS, BRCT-I
Drosophila melanogaster	614	28%	36%	NTD, NLS, BRCT-I
Homo sapiens	633	34%	43%	NTD, NLS, BRCT-I, BRCT-II
Rattus norvegicus	631	30%	39%	NTD, NLS, BRCT-I, BRCT-II
Cricetulus griseus	633	29%	38%	NTD, NLS, BRCT-I, BRCT-II

NTD: N-terminal domain
NLS: Nuclear localization signal
BRCT-I: Breast cancer carboxy-terminal domain I
BRCT-II: Breast cancer carboxy-terminal domain II

Nuclear localization signal

The N-terminal sequence of XRCC1 contains a putative nuclear localization signal (NLS) consisting of KKPK in amino acids 26-29, as predicted by the PSORT program (http://psort.nibb.ac.jp/, mainly developed by K. Nakai, University of Tokyo). These residues were classified as a four-residue pattern (pat4) composed of four basic amino acids (K or R), or composed of three basic amino acids (K or R) and either H or P (Hicks et al., 1995).

XRCC1 genomic DNA

Cloning of *XRCC1* genomic DNA from *A. thaliana* (Col) revealed an identical sequence to the genomic sequence previously reported by Arabidopsis Genome Project (GenBank Acc. No. AC018849). Combined analysis by The Genetics Computer Group (GCG) software with the cDNA and genomic sequences revealed that the *XRCC1* gene consists of eight exons, which is clearly different from the gene organization (four exons) suggested by using several softwares at The Institute for Genomic Research (TIGR). The softwares for gene prediction used by TIGR are Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (Mihaela Pertea, http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org).

Through careful combined analysis of the cDNA and genomic DNA in *A. thaliana*, a minor GC-AG splicing site was detected among seven introns (Fig 3). By using this splicing site, the predicted molecular weight of XRCC1 is increased to 39.8kDa (with the minor splicing site) from 26.2kDa (without the site).

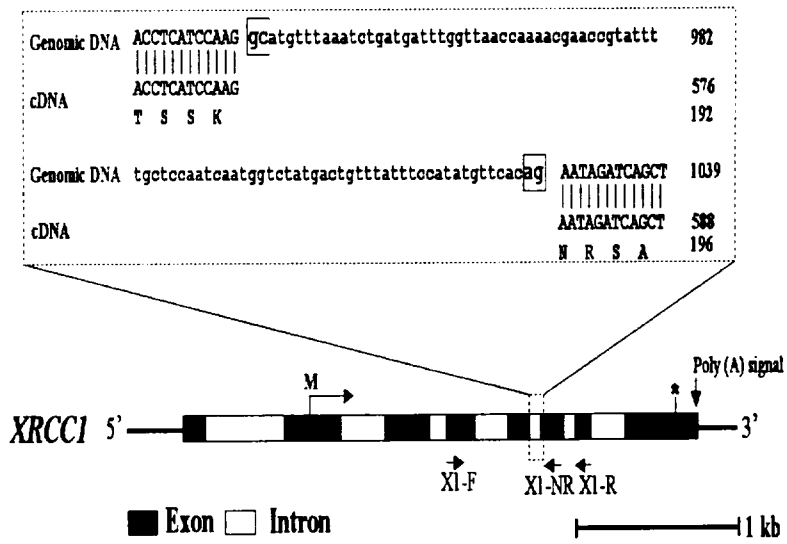


Fig 3. Genomic structure of *XRCC1*.
The start and stop codons are indicated by M or *, respectively. The numbers in Genomic and cDNA sequences are beginning from start codon.

MMS resistance

Methylmethane sulfonate (MMS) induces DNA damage through double strand breaks. Cells do not survive if the damage is not properly or efficiently repaired. We can, therefore, predict that overexpression of DNA repair proteins, such as XRCC1, would result in an increased resistance to DNA damaging agents, such as MMS. The effect of expressing the *XRCC1* gene on the resistance to DNA damage was investigated in a wild-type yeast strain (LSY678) bearing a fully-active set of DNA repair genes. The results, shown in Fig 4A, indicated that the wild-type yeast strains containing pYES-*XRCC1* exhibit enhanced resistance to MMS relative to yeast cells containing the control plasmid pYES2/CT. In complementary experiments, overexpression of pYES-*XRCC1* strains deficient in RAD51 or RAD52 function reveal that XRCC1 cannot provide protection against MMS toxicity.

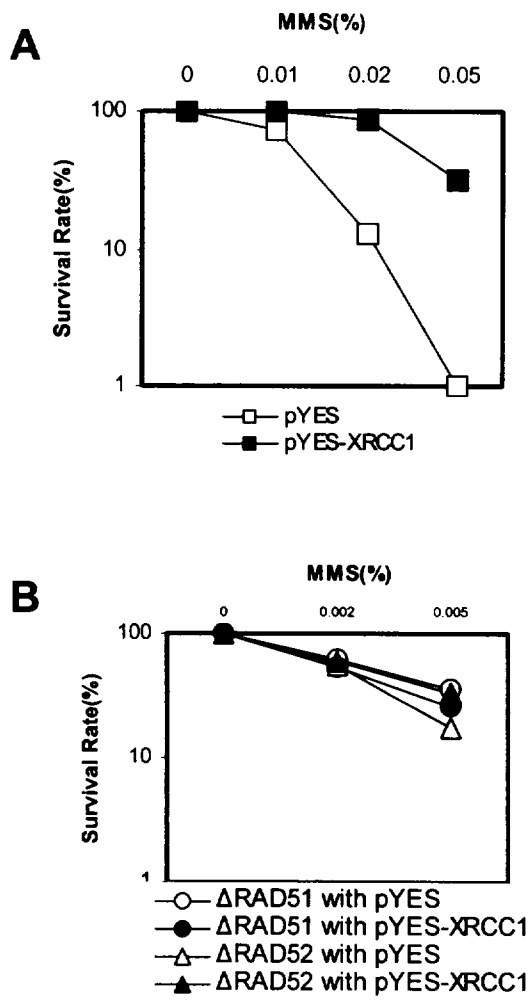


Fig 4. MMS resistance test after overexpression of XRCC1 in yeasts.

Each transformants with pYES-*XRCC1* in wild-type (A) and mutant yeasts (B) were measured MMS resistance by survival tests in log scale of Y-axis.

DISCUSSION

We have sequenced and characterized cDNA and genomic clones encoding the *XRCC1* gene from *A. thaliana*, a flowering plant. The *XRCC1* sequence displays significant homology with other *XRCC1* sequences from several animals, including *H. sapiens*, *R. norvegicus*, *C. griseus*, and *D. melanogaster* with a particularly high homology in the BRCT domain. The genomic sequence of *XRCC1* is identical to a previously reported sequence by Arabidopsis Genome Project (Theologis et al., 2000). The results reported here, therefore, confirm and extend the first identification of the *XRCC1* gene from *A. thaliana* (Theologis et al., 2000).

The *XRCC1* gene encodes a protein with several important protein domains, including a nuclear localization signal (NLS) and BRCT. The existence of NLS suggests a potential role of XRCC1 in the nucleus or least for nuclear transport (Schmidt-Zachmann and Nigg, 1993). Although it is possible that a protein without an NLS can enter the nucleus via cotransport with a protein that has NLS, most nuclear proteins such as ribosomal proteins or transcription factors have their own NLSs (Schmidt et al., 1995). Presently, NLSs are classified into two categories (reviewed in Hicks and Raikhel, 1995). The classical type of NLSs, e.g. SV40 large T antigen, is sub-divided into two rules. One rule in this type is a four-residue pattern (pat4) composed of four basic amino acids (K or R), or composed of three basic amino acids (K or R) and either H or P (Hicks et al., 1995). Another rule in this type is a pattern (pat7) starts with P, followed within three residues by a basic segment containing three K/R residues out of 4 residues. And the signature sequence (KKPK) for NLS of At XRCC1 falls into pat4 type in the classical category. Another type of NLS is the type of *Xenopus* nucleoplasmin proposed by Robbins et al. (Robbins et al., 1991). The pattern is: 2 basic residues, 10

residue spacer, and another basic region consisting of at least 3 basic residues out of 5 residues. Many nuclear proteins are generally rich in basic residues: If the sum of K and R compositions are higher than 20%, then the protein is considered to have higher possibility of being nuclear than cytoplasmic (Makkerh et al., 1996).

The highly-conserved BRCT domain is known as a site for protein-protein interaction with such proteins as poly(ADP-ribose) polymerase (PARP) (Caldecott et al., 1996; Masson et al., 1998; Pleschke et al., 2000; Taylor et al., 2002). The deduced amino acid sequence of XRCC1 (353 amino acids) is similar to, but shorter than, other XRCC1 proteins. But, the absence of the N-terminal domain (NTD) and C-terminal BRCT-II motif in At XRCC1 suggest a limited role in DNA repair by interaction with DNA polymerase or DNA ligase III. Wild-type yeast strains containing pYES-*XRCC1* exhibit enhanced resistance to MMS relative to wild-type cells bearing only the control plasmid pYES2/CT. Furthermore, expression of XRCC1 in mutant strains deficient in *RAD51* or *RAD52* genes indicates that XRCC1 fails to complement MMS sensitivity in those yeast strains. At present, no yeast homolog for XRCC1 has been found, and our homology-based searches did not reveal any candidate genes. It is assumed that XRCC1 functions in signaling to recruit DNA repair proteins to DNA damage sites, such as mismatch or single-strand break regions (Caldecott et al., 1996; Pleschke et al., 2000)

XRCC1 functions on the pathway in single-strand break repair in animals. The damaged DNA sites mostly on sugar, detected by XRCC1, are repaired firstly by PARP and the damaged termini are converted to 3′-OH or 5′-P residue by DNA polymerase or polynucleotide kinase. Lastly, the gap is filled by DNA ligase. The function recruiting the key enzymes such as PARP, DNA polymerase, or DNA ligase greatly enhances efficiency in single-strand break repair. AtXRCC1 has only one conserved domain of BRCT-I for interacting PARP which suggest a limited role on DNA repair and existence of additional pathways for single-strand break repair to survive cells in plants.

Sequence date from this article have been deposited with the Gen Bank data libraries under accession number AF324348.

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요 약

X선 상호보상군1 (XRCC1) 은 DNA 손상에 반응하는 DNA 수선 단백질이다. 애기장대로부터 XRCC1 을 암호화하는 cDNA 클론이 분리되고 염기서열분석을 한 후 cDNA 와 genomic DNA 의 종합 분석의 결과 7개의 인트론으로 구성되어 있음을 발견했다. 또한 XRCC1를 암호화하는 서열은 1062 염기쌍의 길이를 가지며 353 개의 아미노산과 40 kDa 단백질을 암호화한다는 것이 결정되었다. XRCC1 의 예상 아미노산 서

열은 잘 보존된 BRCT 도메인을 함유하고 있고 동물로부터 온 XRCC1 과 유사하나 동물에 비해 특이적으로 작았다. XRCC1 은 야생형 효모에서 MMS에 저항성을 증가시키는 것을 보였으나 RAD51 이나 RAD52 가 결여된 돌연변이 효모들은 XRCC1 의 과발현에 의해 회복되지 않았다.

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