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CDNA ENCODING A RECA HOMOLOG IN EUKARYOTES

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United States Patent [19]

[11] **Patent Number:** **5,674,992**

Jagendorf et al.

[45] **Date of Patent:** **Oct. 7, 1997**

[54] **CDNA ENCODING A RECA HOMOLOG IN EUKARYOTES**

4,774,180	9/1988	Toth et al.	435/69.7
4,849,335	7/1989	Hofnung et al.	435/6
4,963,487	10/1990	Schimmel	435/172.3
5,087,564	2/1992	Mai et al.	435/69.7

[75] **Inventors:** **Andre Jagendorf, Ithaca, N.Y.; Heriberto Cerutti, Durham, N.C.**

[73] **Assignee:** **Cornell Research Foundation, Inc., Ithaca, N.Y.**

FOREIGN PATENT DOCUMENTS

0 063 522	10/1982	European Pat. Off.
WO 87/00203	1/1987	WIPO
WO 91/17267	11/1991	WIPO

[21] **Appl. No.:** **261,110**

OTHER PUBLICATIONS

[22] **Filed:** **Jun. 16, 1994**

Murphy, R.C. et al., *Journal of Bacteriology* 172(2): 967-976 (1990).

Related U.S. Application Data

[63] **Continuation of Ser. No. 938,332, Aug. 28, 1992, abandoned.**

Primary Examiner—Mindy Fleisher
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[51] **Int. Cl.⁶** **C12N 15/29**

[52] **U.S. Cl.** **536/23.6**

[58] **Field of Search** 536/23.6; 530/370; 435/240.1, 240.2, 240.4, 243, 320.1

[57] **ABSTRACT**

A nucleotide and deduced amino acid sequence of a cDNA encoding the *Arabidopsis thaliana* RecA protein is disclosed.

[56] **References Cited**

U.S. PATENT DOCUMENTS

4,713,337 12/1987 Jasin et al. 435/172.3

2 Claims, 2 Drawing Sheets

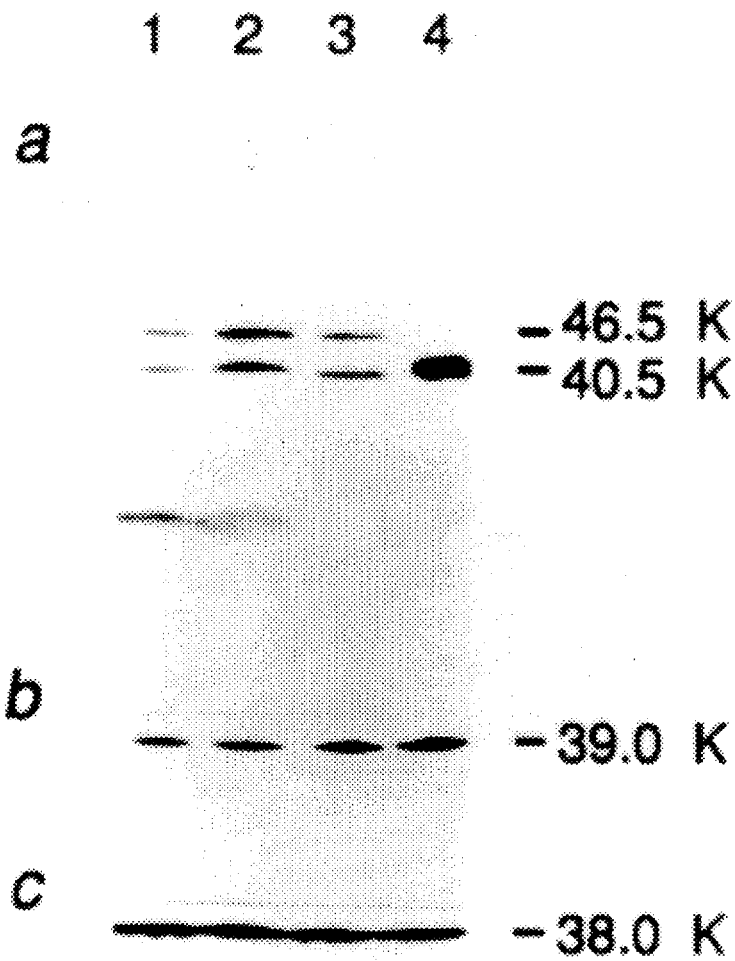


FIG. 1

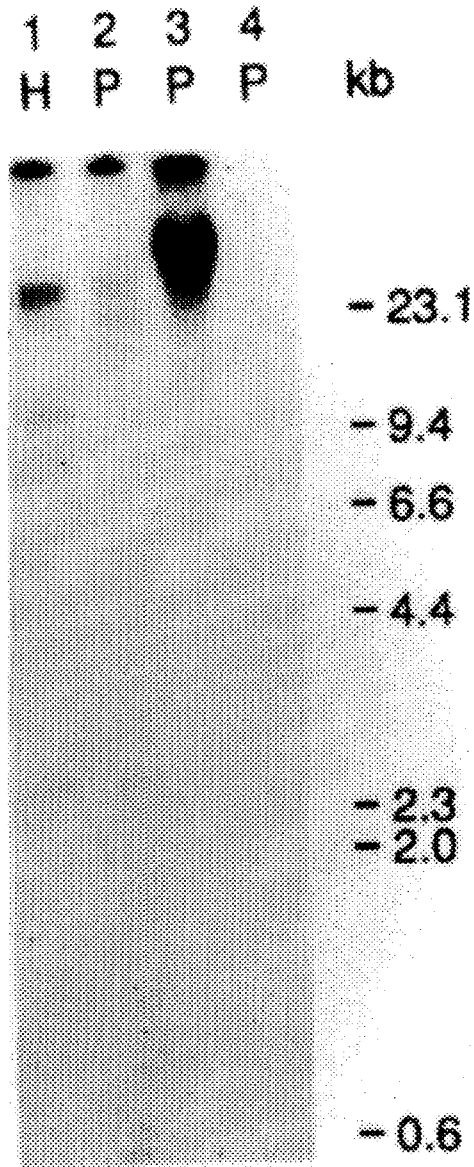


FIG. 2

CDNA ENCODING A RECA HOMOLOG IN EUKARYOTES

CROSS REFERENCES TO RELATED APPLICATIONS

This application is a continuation of U.S. application Ser. No. 07/938,332, filed Aug. 28, 1992, now abandoned.

The observation of chloroplast DNA recombinants in somatic hybrids of higher plants [see *Proc. Natl. Acad. Sci., USA* 82:6960 (1985)], genetic studies of the inheritance of chloroplast markers in several crosses of *Chlamydomonas* [see Boynton, J. E., Gillham, N. W., Newman, S. M., & Harris, E. H. (1991) in *Cell Organelles. Advances in Plant Gene Research*, ed. Herrmann, R. (Springer-Verlag, Vienna) Vol 6, pp. 1-48], the integration of donor DNA by homologous recombination in chloroplasts of transformed *Chlamydomonas* [see *Proc. Natl. Acad. Sci., USA* 88:1721 (1991)], and extensive comparative analyses of chloroplast genome structure [see *Curr. Genet.* 13:343 (1988); *Annu. Rev. Genet.* 19:325 (1985); *TIGS* 6:115 (1990)] all indicate that DNA recombination occurs in chloroplasts of both higher plants and green algae. The biochemistry of any recombinational mechanism in chloroplasts is completely unknown, however.

It has been argued that the primary biological role of recombination is the repair of DNA damage [see *Science* 229:1277 (1985)]. Exposure of *E. coli* to DNA damaging agents induces the SOS response, resulting in derepression of approximately 20 genes (including *recA*). The *RecA* protein is involved in multiple aspects of this response, namely, regulation of gene induction by promoting cleavage of the LexA repressor [See *Ann Rev. Biochem.* 54:425 (1985); *Cell* 29:11 (1982)], recombinational repair, SOS mutagenesis, DNA replication [see *Proc Natl. Acad. Sci. USA* 84:6805 (1987)] and duplication mutagenesis. In other organisms, genes involved in DNA repair/recombination are also induced in response to DNA damage [see *BioEssays* 12:295 (1991)].

It is generally accepted that plastids originated from cyanobacterial progenitors, acquired by an ancestral eukaryotic cell through an endosymbiotic event [see *J. Mol. Evol.* 28:98 (1988); *EMBOJ.* 10:3073 (1991)]. Therefore we believed that any chloroplast recombination system should be related to an eubacterial counterpart.

In *E. coli*, and many other prokaryotes, the *RecA* protein, a 38 KDa protein essential for homologous DNA recombination and a variety of SOS responses to DNA damage [see *Biochimie* 73:289 (1991); *J. Mol. Biol.* 212:79 (1990); *Mutat. Res.* 236:301 (1990); *Crit Rev. Biochem. Mol. Biol.* 25:415 (1990); *J Bacteriol* 171:2415 (1989)]. It is the pairing reaction between homologous DNA sequences that ultimately leads to homologous recombinations which makes *RecA* protein useful for DNA diagnostics and therapeutic applications.

In addition to the preceding journal articles, a number of patents have recently issued which make reference to the *recA* gene or *RecA* protein. However, these patents are not relevant to the *recA* gene or *Rec* protein of higher plants as is the present invention.

U.S. Pat. No. 5,087,564, for example, describes a method to create fusion proteins in bacteria using the endogenous *RecA*, on the end of which oligopeptides or polypeptides are fused; collecting the expressed fusion protein; and removing the unwanted endogenous protein following making a split between them by a specific endopeptidase. However, this teaching has nothing to do with a higher plant *recA* gene, or nuclear DNA transformation in higher plants.

U.S. Pat. No. 4,849,335 deals with mutagen damage to DNA. In bacteria, damage to its DNA evokes an "SOS" response leading to the induction of enzymes that help repair damaged DNA. One of the crucial enzymes in this response, and one that is induced, is *RecA*. The goal of this patent is to enhance bacteria for production of increased amounts of either *RecA* or one of the other SOS proteins, following exposure to potentially mutagenic agents. However, this teaching has nothing to do with a higher plant *recA* gene, or nuclear DNA transformation in higher plants.

U.S. Pat. No. 4,774,180 describes a teaching aimed at constructing fusion proteins of several enzymes in a row, hoping that these might be more efficient for some industrial uses than having individual enzymes. Such a technique would certainly aid in the purification of the expressed enzymes since all of them could be isolated as a single package. As described, in order to achieve this goal, inactivation of the endogenous *recA* gene was necessary. However, this teaching has nothing to do with a higher plant *recA* gene, or nuclear DNA transformation in higher plants.

U.S. Pat. Nos. 4,713,337 and 4,963,487 describe a method to inactivate any desired gene in the bacterial chromosome, and requires the *RecA* protein to be present in the initial step, and then absent (either inactivated or deleted) for the second step. However, this teaching has nothing to do with a higher plant *recA* gene, or nuclear DNA transformation in higher plants.

European Published Patent Application 0 063 522 appears to describe a signal which inhibits cell division if DNA replication is prevented or if the DNA is damaged. The inventors postulate that this signal activates the *RecA* protein to a form which aids LexA autodigest. Digestion of LexA leads to derepression of the genes involved in the SOS response, including massive synthesis of *RecA* itself. This technique is irrelevant to higher plant *RecA* protein since there is no evidence of any SOS response in higher plants similar to that found in bacteria; even if there were one, it cannot be initiated with the *RecA* protein according to the present invention interacting with a repressor of nuclear genes because the *RecA* protein of the present invention is found only inside of chloroplasts, far removed from the nucleus. Thus, this teaching has nothing to do with a higher plant *recA* gene, or nuclear DNA transformation in higher plants.

International Published Patent Application WO 87/00203 describes a technique for the overproduction of desired proteins in bacteria. This is accomplished by substituting the gene for the desired protein into the same place on a plasmid now occupied by the toxin, colicin. To be effective, the production of the desired protein needs to be induced by some environmental change, and it is suggested to use a strain of *E. coli* in which the *recA* gene protease function is inducible by high temperature. This teaching has nothing to do with a higher plant *recA* gene, or nuclear DNA transformation in higher plants.

International Published Patent Application WO 91/17267 describes a method for in vitro hybridization and amplification of DNA which utilizes the *RecA* protein from bacteria. While this is a defined use of bacterial *RecA*, it has nothing to do with a higher plant *recA* gene, or nuclear DNA transformation in higher plants.

In searching for a possible higher plant *recA* gene, in making the present invention, we used a cyanobacterial *recA* as a probe, and found homologous sequences in nuclear DNA from pea and *Arabidopsis thaliano*. With the same probe we have cloned an *Arabidopsis thaliana* cDNA that

encodes a protein highly homologous to eubacterial RecA, except for a predicted chloroplast transit peptide at its amino terminus. The likely expressed protein was detected in chloroplast stromal extracts by cross-reaction with polyclonal antibodies to *E. coli* RecA protein.

Chloroplast DNA recombination has been studied extensively, particularly in *Chlamydomonas* by genetic analysis [see *Theor. Appl. Genet.* 79:17 (1990)]. There has been much work suggesting the involvement of certain sequence elements in plastid DNA recombination. However, up until the making of the present invention, very little was known at the enzymatic level. The finding of a plastid localized recA homolog, according to the teachings of the present invention, provides the first biochemical evidence for a chloroplast recombination system and strongly supports its relationship to the eubacterial counterpart. The present invention also provides the first observation of a recA homolog in any eukaryote. While recombination/repair enzymes have been identified in various other eukaryotes [see *J. Biol. Chem.* 65:11108 (1990); *Cell* 29:367 (1982); *Proc. Natl. Acad. Sci. US* 85:5560 (1987); *Proc. Natl. Acad. Sci. US* 85:3683 (1988); *J. Biol. Chem.* 264:20568 (1989)], they have structures and enzymatic characteristics that differ from the bacterial RecA protein.

A more thorough understanding of the present invention will be achieved after consideration of the following figures and examples. These figures and examples are provided to allow for a more complete understanding of the present invention, and are in no way intended to limit or otherwise define the exact terms of the present invention to the exclusion of equivalent or modified embodiments of the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 depicts the detection of proteins immunologically related to *E. coli* RecA in *Arabidopsis thaliana*; and

FIG. 2 depicts the southern blot showing sequences related to *Synechococcus recA* in genomic DNA from *Arabidopsis* and pea.

More specifically, and as will be more thoroughly discussed in the following examples and discussion, FIG. 1 shows a gel composite of three separate separations in which lane 1 contains a protoplast fraction; lane 2 contains a chloroplast fraction; lane 3 contains a chloroplast stromal fraction (half the amount of protein as loaded in lanes 1 and 2); and lane 4 contains a purified *E. coli* RecA protein. Separation "b" depicts mitomycin C induction in the steady state level of the chloroplast protein similar to *E. coli* RecA. This protein is slightly smaller in pea (38 kDa) than in *Arabidopsis*. In this separation, pea protoplasts were incubated for 12 hours in the presence of 0, 6, 15 or 30 μ M mitomycin C (lanes 1 to 4, respectively), before protein isolation. Separation "c" depicts the same blot shown in "b" which was reprobbed with antiserum to the γ subunit of the chloroplast ATP synthetase, a nuclear encoded chloroplast protein similar in size to RecA. This protein was not induced by DNA damaging agents and served as a control for the proper loading of the lanes. In FIG. 2, lanes 1 and 2 contained total *Arabidopsis* DNA (1 μ g); lane 3 contained total pea DNA (8 μ g); lane 4 contained pea chloroplast DNA (1 μ g). Restriction enzymes used included Hind ("H") and PstI ("P"). A further explanation and importance of these gels are described in the discussion of the data obtained from the following examples.

The following example I depicts the isolation of stroma from intact chloroplasts and the immunodetection of a RecA protein in accordance with the present invention:

EXAMPLE I

Protoplasts were prepared from leaves of *Arabidopsis* or pea by digestion with 3% (w/v) Cellulysin (Calbiochem) and 0.5% (w/v) Macerace (Calbiochem) according to the following protocol:

Pea seedlings (cv. Progress No. 9) were grown on a 12 hr day in growth chambers, in vermiculite, for 9 to 12 days. Unfolded, but not fully expanded leaves (1 g fresh weight) were surface sterilized with NaOCl, cut into strips, and placed into 9 cm Petri dishes with 10 ml of buffer A (20 mM MES, pH 5.8; 350 mM sorbitol; 1 mM KH_2PO_4 ; 5 mM MgCl_2 ; 30 mM CaCl_2 ; 1 mM DTT; 1% BSA) containing 3% Cellulysin and 0.5% Macerace. The dishes were incubated for 4-5 hr at room temperature, in the dark, with shaking at 40 rpm for the final hour.

Protoplasts were isolated by filtration through 100 μ m nylon mesh followed by centrifugation (5 min, 75 g). The pellet was resuspended in buffer B (50 mM Tricine; pH 7.0; 380 mM sucrose; 20 mM CaCl_2 ; 0.5% BSA; 25% Percoll), and overlaid with buffer C (buffer B without Percoll) and buffer D (buffer C with 380 mM sorbitol in lieu of sucrose). After centrifugation (12 min, 370 g), intact protoplasts were collected at the interface between buffers C and D, and washed once (5 min, 75 g) with either chloroplast isolation buffer [see *Methods in Enzymology* 118:282 (1986)], for cell fractionation, or culture medium [see *In Vitro Cell Dev Biol* 25:571 (1989)], for treatment with DNA damaging agents. Finally, protoplasts were resuspended in the same solutions, counted, and adjusted to the desired density.

Chloroplasts were broken by osmotic lysis in which intact chloroplasts (300 μ l) were sedimented in an Eppendorf microcentrifuge for 2 minutes. The supernatant was discarded, and the chloroplasts resuspended by vortex mixing with 10 mM Na-pyrophosphate to cause osmotic breakage; thylakoid membranes removed by centrifugation.

The supernatant from the osmotic lysis was concentrated by acetone precipitation to give the chloroplast stromal fraction according to the following procedure:

A supernatant solution (as after centrifuging the osmotic lysate) was put into a fresh tube, and to it was added 4 volumes of -20°C . acetone. The tubes were vortexed, and kept on ice for 20 or more minutes. The tubes were then centrifuged for 7 min in an Eppendorf centrifuge (10,000 \times g); the supernatant removed, and the proteins redissolved in buffer containing 2% sodium dodecyl sulfate, 50 mM Tris pH 8.5, 50 mM dithiothreitol, 2% lithium dodecyl sulfate and 12% (w/v) sucrose. These were then ready for analysis by electrophoresis on acrylamide gels.

Potential bacterial contamination was tested by plating aliquots of isolated protoplasts or chloroplasts on LB medium [see Sambrook, J., Fritsch, E. F. & Maniatis, T. (1989) *Molecular Cloning: A Laboratory Manual*]. Proteins from different fractions were separated by 12% SDS-polyacrylamide gel electrophoresis, and electroblotted onto nitrocellulose [see *Proc. Natl. Acad. Sci. USA* 76:4350 (1979)] and probed with two polyclonal rabbit antisera to RecA protein from *E. coli* strain K12. The efficiency of transfer was determined by staining the filters with Ponceau S. The filter was treated with 5% non-fat dry milk in TBS (50 mM TRIS-HCl, pH 7.4; 200 mM NaCl) for 1 hr at room temperature, to fill up any spot on the filter without any protein on it with casein. RecA antiserum was added in the same solution as above at 1:2000 dilution and incubated overnight. After three 15 min washes with TBS (at least one containing Tween 20), the filters were blocked as before and incubated with a 1:2000 dilution of commercially available

goat antibodies against rabbit IgG. The goat anti-rabbit IgG antibodies had been covalently bound to horseradish peroxidase. These were incubated with the nitrocellulose sheet for 2-3 hr at room temperature.

The nitrocellulose sheets were then washed three times with 5% non-fat dry milk in TBS, and three times with TBS (at least once with TBS containing 0.1% Tween 20). A chemiluminescent substrate (Amersham) was used for the autoradiographic detection. The nitrocellulose sheets, with horseradish peroxidase bound only where the original rabbit antibody, then the goat antibody had been bound, were mixed with the 2 components of the peroxidase detection kit for 1 minute, as in the manufacturer's directions. The action of peroxidase on the peroxidase + peroxidase substrate combination leads to a chemical reaction so energetic that it releases light for about 2 hrs. The nitrocellulose filter, with a few glowing spots, was placed next to a piece of X-ray film in the dark. After variable lengths of time, the X-ray film was removed from the filter and developed. Relative protein amounts were determined by densitometric scanning (Universal Imaging, Inc.) of the film images.

In some cases, the enzyme was inactivated by incubation in H₂O₂ and the blot reprobed with an antibody against the γ subunit of CFI.

The techniques for probing with polyclonal antisera are further described in *Proc. Natl. Acad. Sci. USA* 76:4350 (1979) and Harlow, E. and D. Lane, *Antibodies—A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring, N.Y. (1988).

The results from Example 1 were used to study the detection of a protein in chloroplast stroma immunologically related to *E. coli* RecA. An immunoblotting technique was used to detect *Arabidopsis* proteins related to RecA (see FIG. 1, "a"). Although the data is not depicted in the figures, preimmune serum did not reveal any bands, however, two polyclonal antibodies raised against *E. coli* RecA cross reacted with three protoplast proteins. Two of them are soluble chloroplast proteins detected in the stromal fraction (see FIG. 1, "a"). The apparent molecular mass (Mr) of the faster moving stromal protein as 40.5 kDa, almost identical with that of *E. coli* RecA. Similar proteins were also identified in pea chloroplasts (see FIG. 1, "b"). Consistent with the presence of RecA in chloroplasts, DNA strand exchange, an essential activity of *E. coli* RecA, in crude stromal extracts from pea was also detected.

The following example II depicts the isolation of DNA and probing with a cyanobacterial recA gene fragment in accordance with the present invention.

EXAMPLE II

Total DNA was isolated from *Arabidopsis* leaves by a miniprep procedure. Isopycnic CsCl centrifugation was used for the purification of total DNA from pea leaves, and of chloroplast DNA from intact pea chloroplasts. Standard procedures were used for digestion, electrophoretic separation, and transfer of the DNA to nylon membranes. The filters were probed with a [³²P] labelled Bst EII fragment, comprising the 5' half of the coding sequence [see *J. Bacteriol.* 172:967 (1990)]. Prehybridization was at 70° C. for 6 hours and hybridization overnight at 60° C. [see *Proc. Natl. Acad. Sci. USA* 81:1991 (1984)]. Filters were washed 3 times for 1.5 hours with 2×SSC/0.1% SDS at room temperature, then 3 times in 0.2×SSC/0.1% SDS at 50° C. for another 1.5 hours. The membranes were exposed to Kodak XAR-5 film with an intensifying screen.

The following example III depicts the cDNA cloning and sequencing in accordance with the present invention.

EXAMPLE III

A cDNA was isolated by screening approximately 300,000 members of an *Arabidopsis* library in the "lambda-YES" vector [see *Proc. Natl. Acad. Sci. USA* 88:1731(1991)], using as probe the *Synechococcus recA* gene. The bacteriophages were plated [see *Molecular Cloning—A Laboratory Manual* (2nd ed), Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. (1989)] on an *E. coli* strain deleted for recA in order to avoid confusion with the inserted plant recA gene (since both would have been detected by the labeled probe) [see *Genetics* 93:321 (1979)]. Standard procedures were used for library screening. After sub-cloning into Bluescript (Stratagene), nested deletions were generated and the DNA sequenced on both strands by the dideoxy chain termination method using T7 DNA polymerase. The sequences were analyzed with the Genetics Computer Group software package [see *Nucleic Acids Res.* 12:387 (1984)].

Genomic hybridization revealed sequences homologous to the *Synechococcus recA* gene in pea and *Arabidopsis* (see FIG. 2). However, any hybridization to purified chloroplast (see FIG. 2) or mitochondrial DNA was unable to be detected. Homology to recA has not been found in the completely sequenced chloroplast genomes of tobacco [see *EMBOJ* 5:2043 (1986)], *Marchantia* [see *Nature* 322:572 (1986)], or rice [see *Mol. Gen. Genet.* 217:185 (1989)]. Moreover, induction of the stromal protein was prevented by protein synthesis inhibitors acting on cytosolic (80 S) ribosomes, also suggesting a nuclear localization for this gene.

Using the *Synechococcus recA* gene as a probe, an *Arabidopsis* cDNA library was screened in accordance with the present invention utilizing conventional techniques. A gene showing extensive homology to eubacterial recA was cloned in accordance with the present invention. The cloned cDNA was sequenced by standard techniques. Polymerase chain reaction analysis showed that this was the longest cDNA in the library encoding the RecA protein. This was accomplished with the aid of PCR methodology which can amplify DNA sequences based upon recognition of 2 separate sites by specific primers. For the right (3') end primer, a primer was selected which was homologous to an internal stretch of the gene, not too far from the 5' (left) end. The primer for the 3' end of the piece to be amplified was chosen to be homologous to a part of the vector which was carrying the gene. The formation of new DNA, homologous to this template, would thus include the 5' end of the gene itself.

This procedure was applied to the entire cDNA library as a template. A fairly large number of amplification products were selected and electrophoresed. By using radioactive nucleotides, the amplified clones could be detected by autoradiography. If there had been a cDNA in the library more complete at the 5' end than the one originally discovered, it should have appeared as a longer fragment of DNA. Sequencing of the longest one located showed it to be identical to the only originally isolated; there was no detectable clone any longer.

Although the cDNA is truncated at its 5' end, it is long enough to reveal the features of the encoded protein.

The following are the nucleotide and deduced amino acid sequences of a cDNA encoding the *Arabidopsis thaliana* RecA protein in accordance with the present invention. The nucleotide sequence is SEQ ID NO:1:

GAT	TCA	CAG	CIA	GTC	TTG	TCT	CTG	AAG	CTG	AAT	CCA	AGC	39
TTC	ACT	CCT	CTT	TCT	CCT	CTC	TTC	CCT	TTC	ACT	CCA	IGT	78
TCT	TCT	TTT	TCG	CCG	TCG	CTC	CGG	TTT	TCT	ICT	TGC	IAC	117
TCC	CGC	CGC	CTC	TAT	TCT	CCG	GTT	ACC	GTC	TAC	GCC	GCG	156
AAG	AAA	CIC	TCC	CAC	AAA	ATC	AGT	ICT	GAA	TTC	GAT	GAC	195
AGA	ATC	AAC	GGC	GCT	CTC	TCT	CCC	GAC	GCT	GAT	TCC	CGC	234
TTC	CTC	GAC	CGC	CAA	AAG	GCT	TTA	GAG	GCA	GCT	ATG	AAT	273
GAC	AIT	AAC	AGT	TCA	TTT	GGT	AAA	GGA	AGT	GTA	ACA	AGA	312
TTG	GGG	AGT	GCT	GGT	GGA	GCA	TIA	GTG	GAG	ACC	TTT	TCG	351
AGT	GGT	AIT	TTG	ACT	CTT	GAT	CTT	GCT	TTA	GGT	GGA	GGC	390
CTA	CCA	AAG	GGT	CGG	GTA	GTC	GAA	ATA	TAT	GGA	CCA	GAA	429
AGT	AGT	GGC	AAG	ACC	ACG	CTA	GCA	CTC	CAT	GCT	ATT	GCT	468
GAA	GTG	CAG	AAG	CTT	GGA	GGC	AAT	GCA	ATG	CTT	GTT	GAT	507
GCA	GAG	CAT	GCC	TTT	GAT	CCA	GCG	TAT	TCT	AAA	GCA	TTA	546
GGT	GTT	GAT	GTA	GAA	AAT	TTG	ATA	GTG	TGC	CAG	CCA	GAT	585
AAT	GGC	GAG	ATG	GCT	TTA	GAA	ACT	GCA	GAC	CGT	ATG	TGT	624
CGC	TCA	GGT	GCG	GTT	GAC	CTT	AIA	TGT	GTT	GAT	TCT	GTT	663
TCA	GCA	CTT	ACT	CCA	CGA	GCT	GAG	AIT	GAA	GGT	GAG	AIT	702
GGA	ATG	CAG	CAA	ATG	GGT	TTG	CAA	GCT	CGT	CTT	ATG	AGT	741
CAA	GCT	CTT	CGT	AAA	ATG	TCA	GGA	AAC	GCC	TCT	AAA	GCT	780
GGG	TGT	ACT	CTT	AIT	TTC	CTA	AAC	CAA	ATA	AGA	TAC	AAG	819
AIT	GGT	GTG	TAC	TAT	GGG	AAT	CCA	GAG	GTG	ACT	AGC	GGA	858
GGA	AIT	GCG	TIA	AAG	TTC	TTC	CGG	TCG	GTC	CGT	CTA	GAA	897
AIT	CGT	TCT	GCT	GGG	AAG	ATC	AAA	TCT	TGC	AAA	GGG	GAT	936
GAA	GAT	AIT	GGT	CTT	CGG	GCT	CGT	GTA	AGA	GTG	CAG	AAG	975
AGC	AAG	GTT	TCA	AGA	CCG	TAT	AAG	CAA	GCA	GAG	TTT	GAG	1014
AIT	ATG	TTT	GGG	GAA	GGA	GTC	AGT	AAA	CTG	GGA	TGC	GTT	1053
CTT	GAT	TGT	GCT	GAA	AIT	ATG	GAA	GTT	GTG	GTC	AAG	AAA	1092
GGT	TCC	TGG	TAC	AGC	TAC	GAA	GAC	CAA	AGG	CTC	GGG	CAA	1131
GGA	AGA	GAG	AAA	GCA	CTG	CAG	CAC	TTA	AGG	GAA	AAC	CCT	1170
GCT	CTT	CAA	GAC	GAA	AIT	GAG	AAG	AAA	GTG	AGA	TTG	TTG	1209
ATG	TIA	GAT	GGA	GAA	GTT	CAT	CGA	TCA	ACT	CCT	TTG	ATG	1248
AGC	AGC	AGC	TCT	TCC	TCG	GCT	TCA	CAT	CGC	GAA	GAA	GAA	1287
GAA	GAA	GAC	TCG	CTT	GAC	GAT	TTC	CAA	TGA	1317			
CATAACACTT AAGCTTGAGA CTTTCGGATC TAATGGATGTA 1357													
CAACACTTGA TTTTCTCTCA TCATGTTTCAC CTCTTGTTTC 1397													
AAGTTTC 1404													

This sequence depicts a truncated cDNA containing a continuous open reading frame starting at its 5' end. The stop codon (TGA at 1315-1317) is followed by sequences with 75 to 80% homology to elements implicated in efficient polyadenylation of plant mRNAs [see Mogen, B. D., MacDonald, M. H., Graybosch, R., & Hurt, A. G. (1990) *The Plant Cell* 2:1261-1272].

The deduced areinc acid sequence for this peptide is as follows: SEQ ID NO:2:

Asp Ser Gln Leu Val Leu Ser Leu Lys Leu Asn Pro Ser Phe Thr	5	10	15
Pro Leu Ser Pro Leu Phe Pro Phe Thr Pro Cys Ser Ser Phe Ser	20	25	30
Pro Ser Leu Arg Phe Ser Ser Cys Tyr Ser Arg Arg Leu Tyr Ser	35	40	45
Pro Val Thr Val Tyr Ala Ala Lys Lys Leu Ser His Lys Ile Ser	50	55	60
Ser Glu Phe Asp Asp Arg Ile Asn Gly Ala Leu Ser Pro Asp Ala	65	70	75
Asp Ser Arg Phe Leu Asp Arg Gln Lys Ala Leu Glu Ala Ala Met	80	85	90
Asn Asp Ile Asn Ser Ser Phe Gly Lys Gly Ser Val Thr Arg Leu	95	100	105
Gly Ser Ala Gly Gly Ala Leu Val Glu Thr Phe Ser Ser Gly Ile	110	115	120
Leu Thr Leu Asp Leu Ala Leu Gly Gly Gly Leu Pro Lys Gly Arg	125	130	135

-continued

Val Val Glu Ile Tyr Gly Pro Glu Ser Ser Gly Lys Thr Thr Leu	140	145	150
Ala Leu His Ala Ile Ala Glu Val Gln Lys Leu Gly Gly Asn Ala	155	160	165
Met Leu Val Asp Ala Glu His Ala Phe Asp Pro Ala Tyr Ser Lys	170	175	180
Ala Leu Gly Val Asp Val Glu Asn Leu Ile Val Cys Gln Pro Asp	185	190	195
Asn Gly Glu Met Ala Leu Glu Thr Ala Asp Arg Met Cys Arg Ser	200	205	210
Gly Ala Val Asp Leu Ile Cys Val Asp Ser Val Ser Ala Leu Thr	215	220	225
Pro Arg Ala Glu Ile Glu Gly Glu Ile Gly Met Gln Gln Met Gly	230	235	240
Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg Lys Met Ser Gly	245	250	255
Asn Ala Ser Lys Ala Gly Cys Thr Leu Ile Phe Leu Asn Gln Ile	260	265	270
Arg Tyr Lys Ile Gly Val Tyr Tyr Gly Asn Pro Glu Val Thr Ser	275	280	285
Gly Gly Ile Ala Leu Lys Phe Phe Ala Ser Val Arg Leu Glu Ile	290	295	300
Arg Ser Ala Gly Lys Ile Lys Ser Ser Lys Gly Asp Glu Asp Ile	305	310	315
Gly Leu Arg Ala Arg Val Arg Val Gln Lys Ser Lys Val Ser Arg	320	325	330

-continued

Pro	Tyr	Lys	Gln	Ala	Glu	Phe	Glu	Ile	Met	Phe	Gly	Glu	Gly	Val
			335						340					345
Ser	Lys	Leu	Gly	Cys	Val	Leu	Asp	Cys	Ala	Glu	Ile	Met	Glu	Val
			350						355					360
Val	Val	Lys	Lys	Gly	Ser	Trp	Tyr	Ser	Tyr	Glu	Asp	Gln	Arg	Leu
				365					370					375
Gly	Gln	Gly	Arg	Glu	Lys	Ala	Leu	Gln	His	Leu	Arg	Glu	Asn	Pro
				380					385					390
Ala	Leu	Gln	Asp	Glu	Ile	Glu	Lys	Lys	Val	Arg	Leu	Leu	Met	Leu
				395					400					405
Asp	Gly	Glu	Val	His	Arg	Ser	Thr	Pro	Leu	Met	Ser	Ser	Ser	Ser
				410					415					420
Ser	Ser	Ala	Ser	His	Arg	Glu	Glu	Glu	Glu	Glu	Asp	Ser	Leu	Asp
				425					430					435

Asp Phe Gln

The areinc acid sequence contains a putative chloroplast transit peptide (residues 1 to 51, inclusive of SEQ ID NO:2; the transit peptide has a nucleotide sequence as shown in SEQ ID NO:5 and an amino acid sequence as shown in SEQ ID NO:6) with a perfect consensus cleavage site (Val Tyr Ala Ala) located at residues 49 to 52, inclusive of SEQ ID NO:2. The predicted start of the mature protein begins with the alanine residue at position 51 of SEQ ID NO:2.

The amino terminus showing no similarity to bacterial RecA sequences is, as stated above, believed to be a chloroplast transit peptide. Chloroplast transit peptides are not highly homologous, except for a loosely conserved motif at the cleavage site for the stromal processing protease [see *Eur. J. Biochem* 180:535 (1989); *FEBS Lett.* 261:455 (1990)]. The deduced amino acid sequence contains a perfect match to this consensus cleavage site. When such a match is found, it is predicted to specify the correct cleavage site with 90% probability. The sequence upstream of the putative cleavage site is enriched for serine and threonine (29.5%), and is almost devoid of acidic residues (2.0%). It also lacks predicted secondary structures except for two relatively small regions, one of them an amphiphilic β -strand next to the cleavage site. These are typical features of chloroplast transit peptides [see *FEBS Lett.* 278:1 (1991)], and strongly support that identity for the first 51 amino acids of the truncated sequence.

The mature protein is predicted to be 387 amine acids long, with an amino acid sequence as shown in SEQ ID NO:4 and being encoded by the nucleotide sequence as shown in SEQ ID NO: 3 (residue 51 to residue 438 of SEQ ID NO:2 represent the amino acid sequence of the mature protein), with a calculated molecular mass of 41.8 kDa. This is close to the Mr of the faster moving protein identified in the chromoplast stromal fraction. The amine acid sequence of the peptide according to the present invention, specifically for *Arabidopsis thaliana* shows a 60.7% overall identity with the *Synechococcus* sp. protein, and 52–57% identity with 20 other prokaryotic RecA proteins, 10 of which are shown in the following table:

TABLE 1

Comparison Of The Amino Acid Sequences of Arabidopsis RecA and Several Eubacterial Homologs	
organism	percentage homology
<i>Arabidopsis thaliana</i>	100.0
<i>Synechococcus</i> sp	60.7
<i>Anabaena variabilis</i>	55.1
<i>Bacteroides fragilis</i>	57.0
<i>Bacillus subtilis</i>	54.3
<i>Aquaspirillum magnetotacticum</i>	56.5
<i>Neisseria gonorrhoeae</i>	53.8
<i>Methylobacillus flagellatum</i>	55.4
<i>Bordetella pertussis</i>	54.2
<i>Pseudomonas cepacia</i>	55.4
<i>Escherichia coli</i>	52.6

The amino and carboxy terminal are poorly conserved, although they may have functional significance. Interestingly, the carboxy end is enriched for acidic residues in almost all species analyzed. Although the sequence for *Arabidopsis thaliana* according to the present invention is more divergent than any of the eubacterial RecA proteins found to date, predicted functional domains of the *E. coli* protein [see *J. Bacteriol.* 168:901 (1986)] are largely conserved. Amino acids known to cause recombination deficiency when altered in *E. coli* RecA [see *Biochimie* 73:289 (1991); *CRC Crit. Rev. Biochem. Mol. Biol.* 25:415–456 (1990); and *J. Bacteriol.* 171:2415 (1989)] are invariant in the *Arabidopsis* sequence. However, residues affecting preferentially co-protease activity and/or causing hyper-recombinogenic phenotypes are not so well conserved in the *Arabidopsis* gene. Since this gene is now located in the nucleus of an eukaryote, it is tempting to speculate that it has acquired a different regulatory system and it is able to evolve independently of LexA.

The plastid genome encodes only a small proportion of the proteins needed for functional chloroplasts [see *EMBO J.* 5:204.3 (1986)], and it is thought that most genes have been transferred to the nucleus during evolution [see *Nucleic Acids Res.* 18:65 (1990)]. The base composition and codon usage of these transferred genes have adjusted to reflect their nuclear localization. It has been hypothesized that codon usage is genome specific and provides a basis for species classification comparable to classic systematics [see *Nucleic Acids Res.* 8:1893 (1980)]. Several methods [see *Nucleic Acids Res* 18:65 (1990); *Nucleic Acids Res* 8:1893 (1980); and *FEBS Lett* 95:1 (1978)] were used to compare non-homologous sequences to determine the degree of similarity between the sequenced cDNA according to the present invention and several other *Arabidopsis*, nuclear genes encoding chloroplast proteins. The dinucleotide frequency and base composition (TA/AT ratio, and %G+%C) were not significantly different between the genes examined. However in codon usage distance and the arginine coding ratio, the cloned sequence was indistinguishable from the *Arabidopsis* genes and clearly different from several eubacterial recA genes as indicated in the following table:

TABLE 1

Codon usage in <i>Arabidopsis thaliana</i> nuclear genes encoding chloroplast proteins and several eubacterial recA genes		
Genes*	CGN/AGR Ratio†	Codon usage distance**
EPSP Synthase***	0.62	5.07
Tryptophan Synthetase	0.47	6.28
Acetolactate Synthase	1.36	6.48

TABLE 1-continued

Codon usage in <i>Arabidopsis thaliana</i> nuclear genes encoding chloroplast proteins and several eubacterial <i>recA</i> genes		
Genes*	CGN/AGR Ratio†	Codon usage distance**
Cs Gene	0.33	6.42
Rubisco Activase	0.91	6.88
Average‡	0.74 ± 0.41	6.22 ± 0.68
<i>Arabidopsis recA</i>	1.56	6.87
<i>Anabaena recA</i>	5.00	10.78
<i>Synechococcus recA</i>	8.50	11.39
<i>Escherichia recA</i>	∞ [§]	15.82

*In plant genes (first 6 listed), sequences corresponding to the mature proteins were used for the analysis (introns and chloroplast transit peptides were excluded). References for the *Arabidopsis* genes are listed in Plant Mol. Biol. Reporter 9:104 (1991). The Cs gene codes for a chloroplast protein of unknown function. The eubacterial *recA* genes were obtained from GenBank (release 69).

†Arginine coding ratio, where N = A, C, G, or T and R = A, or G.

**Codon usage distance was determined by a modification of a published procedure [see Nucleic Acids Res 18:65 (1990)]. Briefly, synonymous codons differing only in their third nucleotides were grouped. Termination codons and single codon groups (methionine and tryptophan) were excluded, leaving 21 codon groups with a total of 59 codons. The relative frequency of different codons in each group was calculated. The overall difference in codon usage between any gene and the *Arabidopsis* average was computed by a distance algorithm:

$$D(A, X) = \sum_{i=1}^{i=59} |x(i, A) - x(i, X)|$$

wherein $x(i, A)$ and $x(i, X)$ are the frequencies of the *i*th codon in gene A and in the average *Arabidopsis* nuclear gene encoding a chloroplast protein (determined by pooling the coding sequences of the 5 genes shown).

***5-enolpyruvylshikimate-3-phosphate synthase.

‡The *Arabidopsis* average was calculated from the 5 individual genes shown, and expressed as the mean ± standard deviation. To avoid giving excessive weight to fluctuations in codon usage for rare amino acids, a problem with short proteins, only genes of similar length *recA* were analyzed.

§*Escherichia coli Rec A* lacks arginine residues encoded by AGR.

By Spearman's rank correlation coefficient, the CGN/AGR ratio and codon usage distance are correlated with each other ($r = 0.88$; $p < 0.005$).

These data suggest that the *Arabidopsis recA* gene has adjusted to reflect its localization in the nuclear genome, clearly diverging from even the more closely related cyanobacterial homologs.

The following example IV depicts the treatment of protoplasts in accordance with the present invention.

EXAMPLE IV

Ten ml of protoplasts (1×10^6 protoplasts/ml) in liquid LP* medium [see *In Vitro Cell Dev. Biol.* 25:571 (1989)] were placed in 9-cm Petri dishes. Mitomycin C was added to the desired concentration, and protoplasts were incubated for 12 hours in the dark. Following incubation of the protoplasts with the DNA damaging agent, they were sedimented at 100 xg for 5 minutes. The pellet of intact protoplasts was resuspended in buffer B and reisolated by flotation as described in Example I.

Proteins were then extracted by breaking the protoplast by passage through a 10 μ m nylon mesh, collecting the cell fractions (chloroplasts, mitochondria, and non-sedimenting soluble proteins) following centrifugation on a Percoll gradient as described in Example I, and then dissolving these in buffer containing SDS in order to do gel electrophoresis. Alternatively, with the intact chloroplast fraction isolated from the protoplasts, breaking them by resuspension in 10 mM Na Pyrophosphate, centrifuging in the Eppendorf centrifuge to sediment thylakoid and other membranes, collecting the supernatant solution with its proteins, and resuspending the membranes, both of these to be dissolved in SDS buffer and electrophoresed for Western blot analysis.

A reason for Example IV was to determine if DNA damaging agents affect expression of the proteins immuno-

logically related to *RecA*, and as described, pea protoplasts were incubated with mitomycin C. Mitomycin C is a bifunctional alkylating agent that is activated by reduction and can form interstrand crosslinks [see *Science* 235:1204 (1987)], presumably requiring a recombinational pathway for repair. The treatment increased the steady state level of the chloroplast cross reacting protein similar in Mr to *RecA*, suggesting its involvement in DNA repair/recombination (FIG. 1b). The same blot was probed with an antibody against the γ sub-unit of the chloroplast ATP synthetase as a control for the proper loading of the lanes (FIG. 1c).

In summary, the present invention describes a nucleic acid sequence for a gene that encodes for a *RecA* type of protein in the chloroplasts of higher plants. This is the first time it has ever been found in any higher organisms other than bacteria.

In view of the known roles for *RecA* in *E. coli*, and induction of the pea enzyme by DNA damage, it is likely that the chloroplast enzyme is also concerned with DNA repair. Although it is not scientifically certain at the present that the *Arabidopsis* gene can complement a *recA*-deficient strain of *E. coli*, by using a complementation assay, it has been possible for an isolated a gene from the same *Arabidopsis* cDNA library, to increase the survival of a mutant (*phr*-, *uvrB*-, *recA*-) *E. coli* strain exposed to UV. However, its DNA sequence is quite different from the one isolated by hybridization with *recA* probe according to the present invention. In view of the complex pathways for DNA repair in bacteria [see *Ann. Rev. Genet.* 21:179 (1987)] it is likely that a number of proteins will be needed to interact with *RecA* in chloroplasts as well.

The *recA* gene according to the present invention has a number of uses. For example, by removing the 5' end of the gene, that is the portion of the gene which codes for a "transit peptide" portion of the protein that directs the final product into chloroplasts, this transit peptide could be replaced by an amino acid sequence that directs completed proteins to enter the nucleus.

In order to understand the importance of such "re-direction", one must be aware of the function of *RecA* protein in homologous recombination as found in prokaryotes. Genetic engineering has been vastly more efficient in prokaryotes than in eukaryotes (with the exception of yeast), because in bacteria and yeast the exogenous pieces of DNA are integrated into the chromosome by homologous recombination, a procedure not available in higher plants. By introducing the *RecA* protein, now found only in chloroplasts, into the nuclei of higher plants, it should be possible to increase the frequency of homologous recombination in the chromosomal genes of these higher plants. There are several potential advantages of using the *recA* gene according to the present invention for this purpose. For example, while the gene may be related to prokaryotic progenitors, the gene has been present and functioning in higher plants, and so its codon usage (and other housekeeping aspects) are already adapted to the nuclear environment; the same would certainly not be true of a *recA* gene taken from a bacteria.

Thus, while We have illustrated and described the preferred embodiment of our invention, it is to be understood that this invention is capable of variation and modification, and we therefore do not wish to be limited to the precise terms set forth, but desire to avail ourselves of such changes and alterations which may be made for adapting the invention to various usages and conditions. Such changes and alterations to the present invention include, without limitation, single base substitutions, and deletions, insertions

or translations of the DNA sequences presented herein providing that such alterations do not significantly affect the properties of the altered sequence from that of the cDNA sequences given above. For example, in specific instances it may be more advantageous to insert or delete certain nucleic acids within the sequence give in accordance with the present invention, or to utilize a portion or fragment of the nucleic acid sequence according to the present invention without significantly altering the function of the sequence or resulting expressed peptide. In additions in specific instances it may also be advantageous to insert or delete certain amino acids Within the sequence given in accordance with the present invention, or to utilize a portion or fragment

of the amino acid sequence according to the present invention without significantly altering its function. Accordingly, such changes and alterations are properly intended to be within the full range of equivalents, and therefore within the purview of the following claims.

A description of the specific nucleic and amino acid sequences described in the present invention are provided in the following sequence listing:

Having thus described our invention and the manner and a process of making and using it in such full, clear, concise and exact terms so as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same;

 SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i i i) NUMBER OF SEQUENCES: 6

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1404 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATTACACAGC TAGTCTTGTC TCTGAAGCTG AATCCAAGCT TCACTCCTCT TTCTCCTCTC	60
TTCCCTTTCA CTCCATGTTT TTTCTTTTTCG CCGTCGCTCC GGTTTTCTTC TTGCTACTCC	120
CGCCGCCTCT ATTCTCCGGT TACCGTCTAC GCCGCGAAGA AACTCTCCCA CAAAATCAGT	180
TCTGAATTTCG ATGACAGAAT CAACGGCGCT CTCTCTCCCG ACGCTGATC CCGCTTCCTC	240
GACCGCCAAA AGGCTTTAGA GGCAGCTATG AATGACATTA ACAGTTCATT TGGTAAAGGA	300
AGTGTAACAA GATTGGGGAG TGCTGGTGGA GCATTAGTGG AGACCTTTTC GAGTGGTATT	360
TTGACTCTTG ATCTTGCTTT AGGTGGAGGC CTACCAAAGG GTCGGGTAGT CGAAATATAT	420
GGACCAGAAA GTAGTGCAA GACCACGCTA GCACTCCATG CTATTGCTGA AGTGCAGAAG	480
CTTGGAGGCA ATGCAATGCT TGTTGATGCA GAGCATGCCT TTGATCCAGC GTATTCTAAA	540
GCATTAGGTG TTGATGTAGA AAATTTGATA GTGTGCCAGC CAGATAATGG CGAGATGGCT	600
TTAGAAACTG CAGACCGTAT GTGTCGCTCA GGTGCGGTTG ACCTTATATG TGTGATTCT	660
GTTTCAGCAC TTACTCCACG AGCTGAGATT GAAGGTGAGA TTGGAATGCA GCAAATGGGT	720
TTGCAAGCTC GTCTTATGAG TCAAGCTCTT CGTAAAATGT CAGGAAACGC CTCTAAAGCT	780
GGGTGTACTC TTATTTTCTT AAACCAAATA AGATACAAGA TTGGTGTGTA CTATGGGAAT	840
CCAGAGGTGA CTAGCGGAGG AATTGCGTTA AAGTTCTTCG CGTCGGTCCG TCTAGAAATT	900
CGTTCTGCTG GGAAGATCAA ATCTAGCAA GGGGATGAAG ATATTGGTCT TCGGGCTCGT	960
GTAAGAGTGC AGAAGAGCAA GGTTTCAAGA CCGTATAAGC AAGCAGAGTT TGAGATTATG	1020
TTTGGGGAAO GAGTCAGTAA ACTGGGATGC GTTCTTGATT GTGCTGAAAT TATGGAAGTT	1080
GTGGTCAAGA AAGGTTCTTG GTACAGCTAC GAAGACCAA GGCTCGGGCA AGGAAGAGAG	1140
AAAGCACTGC AGCACTAAG GGAAAACCTT GCTCTTCAAG ACGAAATTGA GAAGAAAGTG	1200
AGATTGTTGA TGTTAGATGG AGAAGTTCAT CGATCAACTC CTTTGATGAG CAGCAGCTCT	1260
TCCTCGGCTT CACATCGCGA AGAAGAAGAA GAAGACTCGC TTGACGATT CCAATGACAT	1320

-continued

AACACTTAAG CTTGAGACTT TCGGATCTAT GGATGTACAA CACTTGATT TCTCTCATCA 1380
 TGTTACCTC TTGTTTCAAG TTTC 1404

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: Not Relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp	Ser	Gln	Leu	Val	Leu	Ser	Leu	Lys	Leu	Asn	Pro	Ser	Phe	Thr	Pro		
1				5					10					15			
Leu	Ser	Pro	Leu	Phe	Pro	Phe	Thr	Pro	Cys	Ser	Ser	Phe	Ser	Pro	Ser		
			20					25					30				
Leu	Arg	Phe	Ser	Ser	Cys	Tyr	Ser	Arg	Arg	Leu	Tyr	Ser	Pro	Val	Thr		
		35					40					45					
Val	Tyr	Ala	Ala	Lys	Lys	Leu	Ser	His	Lys	Ile	Ser	Ser	Glu	Phe	Asp		
	50					55					60						
Asp	Arg	Ile	Asn	Gly	Ala	Leu	Ser	Pro	Asp	Ala	Asp	Ser	Arg	Phe	Leu		
65				70					75					80			
Asp	Arg	Gln	Lys	Ala	Leu	Glu	Ala	Ala	Met	Asn	Asp	Ile	Asn	Ser	Ser		
			85						90				95				
Phe	Gly	Lys	Gly	Ser	Val	Thr	Arg	Leu	Gly	Ser	Ala	Gly	Gly	Ala	Leu		
			100					105					110				
Val	Glu	Thr	Phe	Ser	Ser	Gly	Ile	Leu	Thr	Leu	Asp	Leu	Ala	Leu	Gly		
	115					120					125						
Gly	Gly	Leu	Pro	Lys	Gly	Arg	Val	Val	Glu	Ile	Tyr	Gly	Pro	Glu	Ser		
	130					135					140						
Ser	Gly	Lys	Thr	Thr	Leu	Ala	Leu	His	Ala	Ile	Ala	Glu	Val	Gln	Lys		
145					150					155					160		
Leu	Gly	Gly	Asn	Ala	Met	Leu	Val	Asp	Ala	Glu	His	Ala	Phe	Asp	Pro		
			165					170					175				
Ala	Tyr	Ser	Lys	Ala	Leu	Gly	Val	Asp	Val	Glu	Asn	Leu	Ile	Val	Cys		
			180					185					190				
Gln	Pro	Asp	Asn	Gly	Glu	Met	Ala	Leu	Glu	Thr	Ala	Asp	Arg	Met	Cys		
		195					200					205					
Arg	Ser	Gly	Ala	Val	Asp	Leu	Ile	Cys	Val	Asp	Ser	Val	Ser	Ala	Leu		
	210				215						220						
Thr	Pro	Arg	Ala	Glu	Ile	Glu	Gly	Glu	Ile	Gly	Met	Gln	Gln	Met	Gly		
225				230						235				240			
Leu	Gln	Ala	Arg	Leu	Met	Ser	Gln	Ala	Leu	Arg	Lys	Met	Ser	Gly	Asn		
			245						250				255				
Ala	Ser	Lys	Ala	Gly	Cys	Thr	Leu	Ile	Phe	Leu	Asn	Gln	Ile	Arg	Tyr		
		260						265					270				
Lys	Ile	Gly	Val	Tyr	Tyr	Gly	Asn	Pro	Glu	Val	Thr	Ser	Gly	Gly	Ile		
	275					280						285					
Ala	Leu	Lys	Phe	Phe	Ala	Ser	Val	Arg	Leu	Glu	Ile	Arg	Ser	Ala	Gly		
	290				295						300						
Lys	Ile	Lys	Ser	Ser	Lys	Gly	Asp	Glu	Asp	Ile	Gly	Leu	Arg	Ala	Arg		
305					310					315					320		
Val	Arg	Val	Gln	Lys	Ser	Lys	Val	Ser	Arg	Pro	Tyr	Lys	Gln	Ala	Glu		
			325						330					335			

-continued

Phe	Glu	Ile	Met	Phe	Gly	Glu	Gly	Val	Ser	Lys	Leu	Gly	Cys	Val	Leu
			340					345					350		
Asp	Cys	Ala	Glu	Ile	Met	Glu	Val	Val	Val	Lys	Lys	Gly	Ser	Trp	Tyr
		355					360					365			
Ser	Tyr	Glu	Asp	Gln	Arg	Leu	Gly	Gln	Gly	Arg	Glu	Lys	Ala	Leu	Gln
	370					375					380				
His	Leu	Arg	Glu	Asn	Pro	Ala	Leu	Gln	Asp	Glu	Ile	Glu	Lys	Lys	Val
385					390				395						400
Arg	Leu	Leu	Met	Leu	Asp	Gly	Glu	Val	His	Arg	Ser	Thr	Pro	Leu	Met
				405					410					415	
Ser	Ser	Ser	Ser	Ser	Ser	Ala	Ser	His	Arg	Glu	Glu	Glu	Glu	Glu	Asp
			420					425					430		
Ser	Leu	Asp	Asp	Phe	Gln										
		435													

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGCGAAGA	AACCTCTCCA	CAAAATCAGT	TCTGAATTCG	ATGACAGAAT	CAACGGCGCT	60
CTCTCTCCCG	ACGCTGATTC	CCGCTTCCTC	GACCGCCAAA	AGGCTTTAGA	GGCAGCTATG	120
AATGACATTA	ACAGTTCATT	TGGTAAAGGA	AGTGTAACAA	GATTGGGGAG	TGCTGGTGGA	180
GCATTAGTGG	AGACCTTTTC	GAGTGGTATT	TTGACTCTTG	ATCTTGCTTT	AGGTGGAGGC	240
CTACCAAAGG	GTCGGGTAGT	CGAAATATAT	GGACCAGAAA	GTAGTGGCAA	GACCACGCTA	300
GCACTCCATG	CTATTGCTGA	AGTGCAGAAG	CTTGGAGGCA	ATGCAATGCT	TGTTGATGCA	360
GAGCATGCCT	TTGATCCAGC	GTATTCTAAA	GCATTAGGTG	TIGATGTAGA	AAATTTGATA	420
GTGTGCCAGC	CAGATAATGG	CGAGATGGCT	TTAGAAACTG	CAGACCGTAT	GTGTCGCTCA	480
GGTGCGGTTG	ACCTTATATG	TGTTGATTCT	GTTTCAGCAC	TTACTCCACG	AGCTGAGATT	540
GAAAGTGAGA	TTGGAATGCA	GCAAATGGGT	TTGCAAGCTC	GTCTTATGAG	TCAAGCTCTT	600
CGTAAATGT	CAGGAAACGC	CTCTAAAGCT	GGGTGTACTC	TTATTTTCCT	AAACCAAATA	660
AGATACAAGA	TTGGTGTGTA	CTATGGGAAT	CCAGAGGTGA	CTAGCGGAGG	AATTGCGTTA	720
AAGTTCTTCG	CGTCGGTCCG	TCTAGAAATT	CGTTCTGCTG	GGAAGATCAA	ATCTAGCAAA	780
GGGGATGAAG	ATATTGGTCT	TCGGGCTCGT	GTAAGAGTGC	AGAAGAGCAA	GGTTTCAAGA	840
CCGTATAAGC	AAGCAGAGTT	TGAGATTATG	TTTGGGGAAG	GAGTCAGTAA	ACTGGGATGC	900
GTTCCTTGATT	GTGCTGAAAT	TATGGAAGTT	GTGGTCAAGA	AAGGTTCTTG	GTACAGCTAC	960
GAAGACCAAA	GGCTCGGGCA	AGGAAGAGAG	AAAGCACTGC	AGCACTTAAG	GGAAAACCCT	1020
GCTCTTCAAAG	ACGAAATTGA	GAAGAAAGTG	AGATTGTTGA	TGTTAGATGG	AGAAGTTCAT	1080
CGATCAACTC	CTTTGATGAG	CAGCAGCTCT	TCCTCGGCTT	CACATCGCGA	AGAAGAAGAA	1140
GAAGACTCGC	TTGACGATTT	CCAATGA				1167

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 amino acids

-continued

(B) TYPE: amino acid
 (C) STRANDEDNESS: Not Relevant
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: protein

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala	Ala	Lys	Lys	Leu	Ser	His	Lys	Ile	Ser	Ser	Glu	Phe	Asp	Asp	Arg
1				5					10					15	
Ile	Asn	Gly	Ala	Leu	Ser	Pro	Asp	Ala	Asp	Ser	Arg	Phe	Leu	Asp	Arg
			20					25					30		
Gln	Lys	Ala	Leu	Glu	Ala	Ala	Met	Asn	Asp	Ile	Asa	Ser	Ser	Phe	Gly
		35					40					45			
Lys	Gly	Ser	Val	Thr	Arg	Leu	Gly	Ser	Ala	Gly	Gly	Ala	Leu	Val	Glu
	50					55					60				
Thr	Phe	Ser	Ser	Gly	Ile	Leu	Thr	Leu	Asp	Leu	Ala	Leu	Gly	Gly	Gly
65				70						75					80
Leu	Pro	Lys	Gly	Arg	Val	Val	Glu	Ile	Tyr	Gly	Pro	Glu	Ser	Ser	Gly
				85					90					95	
Lys	Thr	Thr	Leu	Ala	Leu	His	Ala	Ile	Ala	Glu	Val	Gln	Lys	Leu	Gly
			100					105					110		
Gly	Asn	Ala	Met	Leu	Val	Asp	Ala	Glu	His	Ala	Phe	Asp	Pro	Ala	Tyr
		115					120					125			
Ser	Lys	Ala	Leu	Gly	Val	Asp	Val	Glu	Asn	Leu	Ile	Val	Cys	Gln	Pro
	130					135					140				
Asp	Asn	Gly	Glu	Met	Ala	Leu	Glu	Thr	Ala	Asp	Arg	Met	Cys	Arg	Ser
145					150					155					160
Gly	Ala	Val	Asp	Leu	Ile	Cys	Val	Asp	Ser	Val	Ser	Ala	Leu	Thr	Pro
				165					170					175	
Arg	Ala	Glu	Ile	Glu	Gly	Glu	Ile	Gly	Met	Gln	Gln	Met	Gly	Leu	Gln
			180					185					190		
Ala	Arg	Leu	Met	Ser	Gln	Ala	Leu	Arg	Lys	Met	Ser	Gly	Asn	Ala	Ser
		195					200					205			
Lys	Ala	Gly	Cys	Thr	Leu	Ile	Phe	Leu	Asn	Gln	Ile	Arg	Tyr	Lys	Ile
	210					215					220				
Gly	Val	Tyr	Tyr	Gly	Asn	Pro	Glu	Val	Thr	Ser	Gly	Gly	Ile	Ala	Leu
225					230					235					240
Lys	Phe	Phe	Ala	Ser	Val	Arg	Leu	Glu	Ile	Arg	Ser	Ala	Gly	Lys	Ile
				245					250					255	
Lys	Ser	Ser	Lys	Gly	Asp	Glu	Asp	Ile	Gly	Leu	Arg	Ala	Arg	Val	Arg
			260					265					270		
Val	Gln	Lys	Ser	Lys	Val	Ser	Arg	Pro	Tyr	Lys	Gln	Ala	Glu	Phe	Glu
		275					280					285			
Ile	Met	Phe	Gly	Glu	Gly	Val	Ser	Lys	Leu	Gly	Cys	Val	Leu	Asp	Cys
	290					295					300				
Ala	Glu	Ile	Met	Glu	Val	Val	Val	Lys	Lys	Gly	Ser	Trp	Tyr	Ser	Tyr
305				310						315					320
Glu	Asp	Gln	Arg	Leu	Gly	Gln	Gly	Arg	Glu	Lys	Ala	Leu	Gln	His	Leu
				325					330					335	
Arg	Glu	Asn	Pro	Ala	Leu	Gln	Asp	Glu	Ile	Glu	Lys	Lys	Val	Arg	Leu
			340					345					350		
Leu	Met	Leu	Asp	Gly	Glu	Val	His	Arg	Ser	Thr	Pro	Leu	Met	Ser	Ser
	355						360					365			
Ser	Ser	Ser	Ser	Ala	Ser	His	Arg	Glu	Glu	Glu	Glu	Glu	Asp	Ser	Leu
	370					375						380			

-continued

Asp Asp Phe Gln
385

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: cDNA

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATTCACAGC TAGTCTTGTC TCTGAAGCTG AATCCAAGCT TCACTCCTCT TTCTCCTCTC 60
 TTCCCTTTCA CTCCATGTTT TCTTTTTTCG CCGTCGCTCC GGTTTTCTTC TTGCTACTCC 120
 CGCCGCCTCT ATTCTCCGGT TACCGTCTAC 150

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: Not Relevant
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: peptide

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Ser Gln Leu Val Leu Ser Leu Lys Leu Asn Pro Ser Phe Thr Pro
 1 5 10 15
 Leu Ser Pro Leu Phe Pro Phe Thr Pro Cys Ser Ser Phe Ser Pro Ser
 20 25 30
 Leu Arg Phe Ser Ser Cys Tyr Ser Arg Arg Leu Tyr Ser Pro Val Thr
 35 40 45
 Val Tyr
 50

What is claimed is:

1. An isolated nucleic acid molecule encoding a RecA-like protein of *Arabidopsis thaliana* comprising the nucleotide sequence set forth as SEQ ID NO:3.

2. An isolated nucleic acid molecule encoding a RecA-

like protein of *Arabidopsis thaliana* wherein said nucleic acid molecule encodes the amino acid sequence set forth as SEQ ID NO:4.

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