Arabian Journal of Chemistry (2014) 7, 327–334

King Saud University

Arabian Journal of Chemistry

www.ksu.edu.sa
www.sciencedirect.com

ORIGINAL ARTICLE

Genetic characterisation of *Escherichia coli* RecN protein as a member of SMC family of proteins

M.M. Youssef [a,b,*], M.A. Al-Omair [a], S.M. Picksley [c]

[a] *Mansoura University, Faculty of Science, Chemistry Department, Biochemistry Division, Mansoura, Egypt*
[b] *Chemistry Department, College of Science, King Faisal University, Saudi Arabia*
[c] *Department of Biomedical Science, University of Bradford, Bradford BD7 1DP, UK*

Received 15 January 2011; accepted 1 February 2011
Available online 6 February 2011

KEYWORDS

RecN;
SMC;
Tn*10* excision;
Recombination;
Reverse genetic

Abstract The proteins of SMC family are characterised by having Walker A and B sites. The *Escherichia coli* RecN protein is a prokaryotic member of SMC family that involved in the induced excision of Tn*10* and the repair of the DNA double strand breaks. In this work, the Walker A nucleotide binding site of the *E. coli* RecN protein was mutated by changing the highly conserved lysine residue 35 to the aspartic acid (D), designated as $recN_{K35D}$. Reverse genetics was utilized to delete the entire *recN* gene (Δ*recN108*) or introduce the $recN_{K35D}$ gene into the *E. coli* chromosomal DNA. The $recN_{K35D}$ cells showed decreasing in the frequency of excision of Tn*10* from *gal76::*Tn*10* after treatment with mitomycin C compared to $recN^+$ cells. The Δ*recN108* cells showed an uninduced increase frequency of Tn*10* excision from *gal76::*Tn*10* in rec^+ background. While, *recBC sbcBC* Δ*recN108* cells are completely deficient in Tn*10* excision. The recombination proficiency is reduced in cells carrying *recBC sbcBC* cells in addition $recN_{K35D}$ mutation. We observed that the Walker A nucleotide binding site is important for the RecN protein. Strains that deleted *recN* gene are recombination deficient and more sensitive to mitomycin C than strains carrying $recN_{K35D}$.

1. Introduction

The *Escherichia coli recN* gene was originally identified in *recBC sbcB* mutant by Lloyd et al. (1983). The *recN* gene of *E. coli* was cloned (Picksley et al., 1985) and sequenced (Rostas et al., 1987) and the gene product has a molecular weight of 63 kDa (Finch et al., 1985; Picksley et al., 1985; Rostas et al., 1987; Elie et al., 1997). The RecN protein has the predicted characterization for the proteins belonging to the SMC family of proteins (Hirano et al., 1995). This family of proteins plays an important role in chromosomal condensation and segregation, dosage compensation (Hirano et al., 1995, 1997) and DNA recombinational repair (Connelly et al.,

* Corresponding author at: Mansoura University, Faculty of Science, Chemistry Department, Biochemistry Division, Mansoura, Egypt. Tel.: +966 0534319273.
E-mail address: mmm_youssef@yahoo.com (M.M. Youssef).
Peer review under responsibility of King Saud University.

Production and hosting by Elsevier

1878-5352 © 2011 Production and hosting by Elsevier B.V. on behalf of King Saud University.
http://dx.doi.org/10.1016/j.arabjc.2013.11.041

1999; Cao et al., 1990). Members of the SMC family are characterized by having Walker A and Walker B nucleotide binding sites (Walker et al., 1982). The RecN protein belong to subclass of the SMC proteins implicated in DNA repair and recombination that show high sequence similarity in and around the Walker A and Walker B nucleotide binding sites (Hirano et al., 1995; Graumann and Knust, 2009). The *recN* gene product plays an important role in the RecF recombination pathway in *recBC sbcBC* (Lloyd et al., 1983; Picksley et al., 1984b). Picksley et al. (1984a) showed that the *recN* gene product has been involved in the repair of double strand breaks of DNA and that *recN* mutants strains are sensitive to ionisation radiation and mitomycin C. The product of *recN* gene is involved in the induced excision of Tn*10* (Chan et al., 1994; Zhuravel and Boreiko, 2002).

Recombination is an important process that generates genetic variation and preserves the integrity of genome. In *E. coli* K12 the homologous recombination relies on the product of several genes such as *recA* (Clark and Margulies, 1965; Cassuto et al., 1980) *recB* (Howard-Flanders and Theriot, 1966) and *recC* (Emmersom and Howard-Flanders, 1967). Mutations in the *recA* gene cause a major deficiency in the recombination which demonstrate that RecA protein is essential for homologous recombination (Emmerson, 1968). The role of the *recBCD* genes in the recombination is illustrated by the fact that mutation in *recBC* genes was shown to reduce the homologous recombination proficiency of cells to 1% compared to the wild type (Willetts and Mount, 1969). The RecBCD enzyme is an important component of the main pathway of homologous recombination. The RecBCD enzyme consists of three subunits RecB, RecC and RecD proteins encoded by *recB*, *recC* and *recD* genes, respectively (Hickson and Emmerson, 1981). The RecBCD enzyme is an ATP dependent dsDNA 3′–5′ and 5′–3′ exonuclease (Exonuclease V). Moreover, it has also been shown to have ATP dependent ssDNA endonuclease and exonuclease activity and DNA helicase properties (Goldmark and Linn, 1972). The recombination deficiency in *recBC* mutants is suppressed by additional mutation in *sbcBC* genes. The *sbcB* gene codes for DNA exonuclease I, an enzyme which degrade ssDNA from the 3′ end (Kushner et al., 1972; Lloyd and Buckman, 1985). In *recBC sbcBC* cells the recombination process is catalysed by the RecF pathway. The RecF pathway requires a group of genes named *recA*, *recF*, *recO*, *recR*, *recQ*, *recJ*, *recN* and *ruvABC* (Clark and Margulies, 1965; Lloyd et al., 1983; Lovett and Clark, 1984; Sawitzke and Stahl, 1992). Bacterial strains carrying *recBC sbcBC* in addition to *recN* are recombination deficient (Wang and Maier, 2008). Moreover, *recN recJ* mutant reduce the recombination in *recBC sbcBC* cells (Picksley et al., 1984a; Clark et al., 1984; Nagashima et al., 2006). *recN* gene is expressed and regulated by LexA repressor as a part of the SOS response for recovering the damaged DNA (Picksley et al., 1984b). In *recBC sbcBC* a single additional mutation in *recF*, *recO*, *recR*, *recQ*, *recJ*, *recN* and *ruvABC* genes decrease the recombination proficiency (Lovett and Clark, 1984; Kosa et al., 2004).

In the present work we generated two bacterial strains by reverse genetics, one is carrying a *recN* gene mutated in the Walker A nucleotide binding site while the other the entire *recN* gene is deleted. We characterized the *recN* gene by utilizing these two generated bacterial strains in the precise excision of Tn*10* and the recombination process.

2. Materials and methods

The *E. coli* K12 strains and plasmids DNA used in this work are listed in Tables 1 and 2.

2.1. Media

The Luria–Bertani (LB) and 56/2 buffer salts minimal media was made as described by Lloyd et al. (1974). For minimal agar plates 56/2, buffer salts were diluted with equal volume of 3% (w/v) agar solution. The minimal 56/2 agar plates were supplemented with 1 mg of thiamine, 3.3 g glucose and 0.1 g of the required L-amino acids. MacConkey glactose medium was made by dissolving 40 g MacConkey base (Difico) in 900 ml ddH_2O, sterilised by autoclaving. The volume was completed to one litre with sterilised 10% (w/v) glactose. Induced excision of Tn*10* work was preformed as described by Chan et al. (1994).

2.2. Plasmids construction

All recombinant DNA procedures were preformed as described by Sambrook et al. (1989). Plasmid pSP100 (Picksley et al., 1985) carries *recN* gene on 5.6 kb DNA *Hin*d III fragment. pSM106 plasmid (Picksley et al., 1985) was constructed by subcloning 4.9 kb *Hin*d III-*Bgl* II DNA fragment from pSP100 to pBR322 *Hin*d III-*Bam*H I. pMMY106 is similar to pSM106 but carries $recN_{K35D}$ mutation. pMMY109 and pMMY110 were constructed from pSM106, pMMY106 respectively by inserting 1.3 kb blunt end *Hae* II DNA fragment containing the chloramphenicol gene from pHSG415 downstream the *recN* gene in *Psp*OMI blunt end site. pMMY107 was constructed by subcloning 5.6 kb *Hin*d III DNA fragment from pSP100 to pBR322 *Hin*d III site. pMMY108 was constructed by deleting 1.728 kb *Bsr*G I-*Psp*OM I DNA fragment containing the entire *recN* gene from pMMY107 and inserting 1.3 kb blunt end *Hae* II DNA fragment containing the Cm^r gene from pHSG415 instead of the *recN* gene.

2.3. Transformation with a linear DNA fragment

Plasmids pMMY108, pMMY109, and pMMY110 contain a unique restriction site for *Ata* II in the vector (pBR322) sequence. So, pMMY108, pMMY109, and pMMY110 were linearized by digestion with *Ata* II. Bacterial strain N2525 (*recD1009*) was made competent by treatment with cold 0.1 M $CaCl_2$ as described by Sambrook et al. (1989) and exposed to the transforming linear DNA in the same manner as if introducing a circular plasmid DNA. The chloramphenicol resistant transformants were selected and screened for Ampicillin resistance. Ampicillin resistance transformants were discarded while ampicillin sensitive transformants were screened for the mitomycin C sensitivity for Δ*recN*108 and $recN_{K35D}$. P1 transudation was preformed as described by Miller (1972).

2.4. Unique site elimination (USE) mutagenesis

The procedure of USE mutagenesis was carried out according to the manufacturer (Amersham Pharmacia Biotech) instructions.

Table 1 The strains described in the present study.

Strains	Genotype (or relevant phenotype)	Reference or source
AB1157	F⁻ *thi-1 thr-1 araC14 leuB6Δ(gpt-proA2)62 lacY1 tsx-33galK2 λ⁻ Rac⁻ his G4 rfbD1 rpsl31 str^R kdgK51 xylA5 mlt-1 argE3*	Bachmann (1972)
AB2463	As AB1157 but *recA13*	Bachmann (1972)
JC7623	As AB1157 but *recB21 recC22 sbcB15 sbcC201*	Kushner et al. (1971)
MMY096	As AB1157 but Cm^R to Mc^R Cm^R	P1.MMY080 X AB1157
MMY097	As JC6723 but Cm^R to Mc^R Cm^R	P1.MMY080 X JC7623
MMY100	As AB1157 but $recN_{K35D}$ to Mc^SCm^R	P1.MMY094 X AB1157
MMY103	As JC7623 but $recN_{K35D}$ to Mc^S Cm^R	P1.MMY094 X JC7623
MMY104	As AB1157 but Δ*recN108* to Mc^S Cm^R	P1.MMY074 X AB1157
MMY108	As JC7623 but Δ*recN108* to Mc^S Cm^R	P1.MMY074 X JC7623
MMY114	As AB1157 but $recN_{K35D}$ *gal-76::*Tn*10* to Tc^R Mc^S Cm^R	P1.MMY094 X NF471
MMY116	As AB1157 but Δ*recN108 gal-76::*Tn*10* to Tc^RMc^S Cm^R	P1.MMY074 X NF471
MMY118	As AB1157 but *gal-76::*Tn*10* to Tc^RMc^R Cm^R	P1.MMY080 X NF471
MMY123	As JC7623 but Δ*recN108, gal76::*Tn*10* to Tc^RMc^S Cm^R	P1.NF471 X MMY108
MMY124	As JC7623 but $recN_{K35D}$, *gal76::*Tn*10* to Tc^R Mc^S Cm^R	P1.NF471 X MMY103
MMY126	As JC7623 but *gal76::*Tn*10* to Tc^R Mc^R Cm^R	P1.NF471 X MMY097
MMY130	As JC7623 but *gal76::*Tn*10* to Tc^RMc^R	P1.NF471 X JC7623
N2525	As AB1157 but *recD1009*	Lloyd and Buckman (1985)
NF471	As AB1157 but *gal-76::*Tn*10*	Chan et al. (1994)
NF618	As AB1157 but *recN618 gal-76::*Tn*10*	Chan et al. (1994)
SP226	As JC7623 but *recN261*	Picksley et al. (1984b)
SP231	As JC7623 but *recN262*	Picksley et al. (1984b)
SP253	As AB1157 but *recN261*	Picksley et al. (1984b)
SP254	As AB1157 but *recN262*	Picksley et al. (1984b)
SP261	As AB1157 but *tyrA16::*Tn*10*	Lloyd et al. (1974)
KL226	Hfr (CavaIIi) *relA1tonA221*	Lloyd and Buckman (1985)
KL584	F128 *proAB⁺ lacI13 lacZ813 Δ(gpt-lac)5 rpsE⁻ xyl⁻ mtl⁻ recA1*	Lloyd and Buckman (1985)

Table 2 Plasmids DNA used in the present study.

Plasmid	Characterisation	Reference or source
pBR322	pBR322 high copy plasmid Ap^R, Tc^R	Bolivar et al. (1977)
pHSG415	pHSG415 low copy plasmid Ap^R, Cm^R & Km^R	Hashimoto-Goth et al. (1981)
pMMY106	As pSM106 but containing $recN_{K35D}$ gene Ap^R, Tc^S	This work
pMMY107	pBR322 *Hin*d III-5.6 kb *Hin*d III DNA fragment of pSP100 containing *recN* gene Ap^R, Tc^S	This work
pMMY108	pBR322 *Hin*d III-5.6 kb *Hin*d III DNA fragment of pSP100 but Δ*recN* gene (1.728 kb *Bsr*G I-*Psp*OM I) and Insertion of 1.33 kb *Hae* II blunt end DNA fragment of *Cm* gene from pHSG415	This work
pMMY109	Ap^r, Cm^R, Tc^R, Km^S pSM106 digested with *Psp*OM I and inserted 1.3 kb blunt end *Cm* *Psp*OM I site down stream of the *recN* gene pMMY110 pMMY106 ($recN_{K35D}$) digested with *Psp*OM I This work and inserted 1.3 kb blunt end *Cm* gene in *Psp*OM I site down stream of the $recN_{K35D}$ gene	This work
pMMY112	As pSP100 but contain $recN_{K35D}$ Ap^R, Cm^R & Km^S	This work
pSM106	pBR322 *Hin*d III/ *Bam*H I – 4.9 kb *Hin*d III- *Bgl* II DNA fragment of pSP100 containing *recN* gene Ap^R, Tc^S	Picksley et al. (1985)
pSP100	pSP100 low copy plasmid $recN^+$ Ap^R, Cm^R & Km^S	Picksley et al. (1985)

The target mutagenic primer 5′GCGCGGGT**GAC**TCT ATT-GCAAT3′ was used to change the **AAA** codon of lysine 35 of *recN* gene in pSM106 DNA to **GAC** codon of aspartic acid. While, selection mutagenic primer 5′AAACATGAGAA-GTCTGAA GAC3′ was used to eliminate the unimportant unique restriction site of *Eco*R I in pSM106, by changing *Eco*R I recognition site from 5′GAATTC3′ to 5′GAAATC3′. After completing the USE mutagenesis procedure, plasmid DNA was treated with *Eco*R I to identify the presumably mutated plasmids. Five plasmids of those which resist digestion

with *Eco*R I were sequenced (MWG Biotech, Germany) using the following primer 5′GTTGCGACAGCCAGATAGCAC TGCCG3′.

2.5. Sensitivity to mitomycin C

Strains were grown in LB broth to mid-log phase ($O.D_{595}$ ~0.4), washed twice with 56/2 minimal salt buffer and resuspended in the same buffer containing 2 μg/ml mitomycin C. The cells were incubated at 37 °C and samples taken at different times and diluted with 56/2 minimal salt buffer to establish the viable cell count using appropriate serial dilution with 56/2 salt buffer.

2.6. Recombination proficiency

Matings for measuring the recombination proficiency were carried out by growing both the donor and the recipient bacterial strains at 37 °C to OD_{595} ~0.4. The bacterial strains were mixed in a ratio of 1:10 donor to recipient and incubated at 37 °C in static water bath for 30 min (for F' donor) or 40 min (for Hfr donor). The mating mixtures were vortexed vigorously and chilled on ice. Samples were diluted in 56/2 minimal salt buffer and plated on 56/2 agar plates lacking proline, supplemented with 100 μg/ml streptomycin. The number of colony forming unites were counted after 2–3 days.

3. Results

3.1. Mutation of the Walker A nucleotide binding site of recN gene

We are interested in knowing the importance of the Walker A nucleotide binding site to the *E. coli* RecN protein. The Walker A nucleotide binding site of the *E. coli recN* gene was mutated (see Section 2). The mutation was transferred to plasmid pSM106 yielding the plasmid DNA containing GAC codon of aspartic acid instead of AAA codon of lysine residue 35 of the *recN* gene and was designated as pMMY106 (Fig. 1). The mutation was confirmed by partial sequencing (the *recN* gene in plasmid pMMY106 data not shown) and the mutated *recN* gene was designated $recN_{K35D}$.

3.2. Introduction of the $recN_{K35D}$ gene into E. coli chromosomal DNA

The plasmid pMMY110 carries $recN_{K35D}$ gene was linearized with *Ata* II restriction enzyme (Fig. 1), which cut the plasmid only in the vector DNA, and transformed to *E. coli* N2525 (*recD1009*) to Cm^R (Table 3). The Ap^R colonies may produced from undigested plasmid or relegated plasmid inside the bacte-

Table 3 Conjugation recombination proficiency of bacterial strains carrying $recN_{K35D}$ mutation and *ΔrecN108*.

Bacterial strain	Hfr	*F′*
AB157 background		
AB1157 (*rec*$^+$)	1	1
AB2463 (*recA13*)	0.0005	0.43
MMY096 (*rec*$^+$, Cm^R)	0.80	1.07
SP253 (*recN261*)	0.30	0.54
SP254 (*recN262*)	0.50	0.75
MMY100 ($recN_{K35D}$)	0.24	0.60
MMY104 (Δ*recN108*)	0.26	0.95
JC7623 background		
JC7623 (*recBC sbcBC*)	0.70	0.80
MMY097 (*recBC sbcBC*, Cm^r)	0.40	0.63
SP226 (*recN261*)	0.054	0.91
SP231 (*recN262*)	0.014	0.40
MMY103 ($recN_{K35D}$)	0.018	0.21
MMY108 (Δ*recN108*)	0.006	0.68

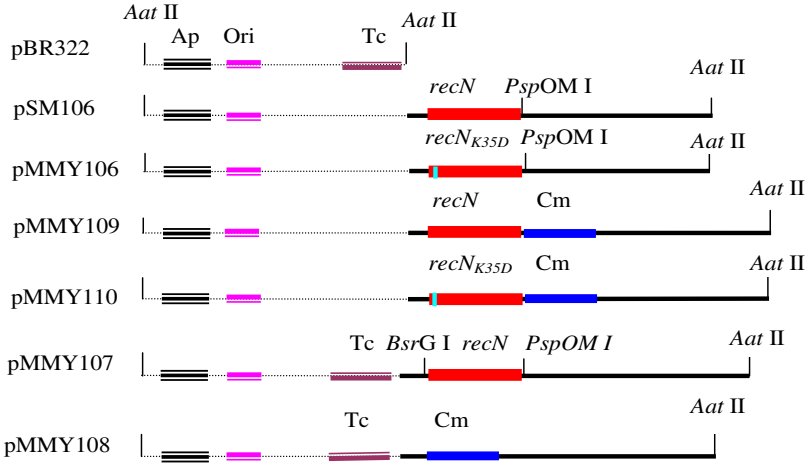

Figure 1 Plasmids construction. All the plasmids constructed in this work are pBR322 derivatives. The *recN* gene in plasmid pSM106 (Picksley et al., 1985) was mutated by site directed mutagenesis to $recN_{K35D}$ (see below) and the new plasmid designated pMMY106. pMMY109 and pMMY110 plasmids were constructed from pSM106, pMMY106, respectively by inserting 1.3 kb blunt end *Hae* II DNA fragment containing the chloramphenicol gene from pHSG415 (Hashimoto-Goth et al., 1981) downstream the *recN* gene in *Psp*OM I blunt end site. pMMY107 plasmid was constructed by subcloning 5.6 kb *Hin*d III DNA fragment containing *recN* gene from pSP100 (Picksley et al., 1985) into pBR322 *Hin*d III site. pMMY108 was constructed by deleting 1.7 kb *Bsr*G I-*Psp*OM I DNA fragment containing the entire *recN* gene from pMMY107 and inserting 1.3 kb blunt end *Hae* II DNA fragment containing the chloramphenicol gene from pHSG415 to 8.2 kb blunt end *Bsr*G I-*Psp*OM I DNA fragment of pMMY107 (instead of the *recN* gene).

rial cell while, Ap^S colonies were screened for Mc^S. The loss of Ap^S and presence of Cm^R, Mc^S mean that the linear DNA has integrated into the chromosomal DNA and the Mc^S presumably indicates the integration of $recN_{K35D}$ into the chromosomal DNA (Fig. 2). The Cm^R, Mc^S, Ap^S strain was designated MMY080. The P1 lysate was made from bacterial strain MMY080 and was used to cross the $recN_{K35D}$ with Cm^r to bacterial strains AB1157 (wt) and JC7623 (*recB21 recC22 sbcB15 sbcC201*). Similarly, pMMY109 was used as a control containing $recN^+$ gene and Cm^R.

3.3. Deletion of the entire recN gene from E. coli chromosomal DNA

The plasmid pMMY108 carries 1.3 kb Cm^R gene instead of *recN* gene and the entire *recN* gene was deleted (designated as *recN108)*. The linear pMMY108 DNA was transformed to *E. coli* N2525 (*recD1009*) similar to pMMY110. The produced Cm^R, Mc^S, Ap^S bacterial strain (*recD1009 recN108*) designated MMY074 (Fig. 3). The P1 lysate was made from bacterial strain MMY074 (*recD1009 recN108*). The P1 lysate of MMY074 was used to cross the *recN108* with Cm^R to bacterial strains AB1157 (wt) and JC7623 (*recB21 recC22 sbcB15 sbcC201*).

3.4. Complementation analysis of recN108, and $recN_{K35D}$ mutant strains

Having generated bacterial strains deleted the entire *recN* gene (*recN108*) and carrying *recN* gene mutated in the Walker A nucleotide binding site ($recN_{K35D}$), we are interested in the examination of mitomycin C sensitivity to these generated bacterial strains. Mitomycin C is a cross linking-agent which causes breaks in both DNA strands and it has been established that *recN* mutant strains are sensitive to mitomycin C (Picksley et al. 1984a). The results of mitomycin sensitivity to strains MMY100 ($recN_{K35D}$), MMY104 (*recN108*) are illustrated in (Fig. 4). The strains having *recN108*, $recN_{K35D}$, *recN261*, *recN262* are more sensitive to mitomycin C than strain AB1157 ($recN^+$) and less sensitive than strain AB2463 (*recA13*). $recN_{K35D}$ cells exhibit sensitivity to mitomycin C as *recN261*, *recN262* cells, however *recN108* cells show *recN*more sensitivity to mitomycin C than $recN_{K35D}$, *recN261* and *recN262* cells.

Bacterial cells *recN108*, $recN_{K35D}$, *recN261*, *recN262* were transfected with plasmid pSP100 ($recN^+$) and the mitomycin C sensitivity was examined (Fig. 5). It is clear that plasmid pSP100 restored the mitomycin resistance to *recN108*, $recN_{K35D}$, *recN261*, *recN262* cells comparable to AB1157 ($recN^+$), but not to the AB2463 (*recA13*).

3.5. Effect of $recN_{K35D}$ mutation and ΔrecN108 on genetic recombination in rec^+ and recBC sbcBC cells

The $recN_{K35D}$ mutation and Δ*recN108* were introduced into AB1157 (rec^+) and JC7623 (*recBC sbcBC*) genetic background and the constructed strains were tested for homologous recombination using Hfr donor cells. The data (Table 3) indicate that $recN_{K35D}$ mutation and Δ*recN108* reduce the homologous recombination in *recBC sbcBC* cells. A strain carrying Δ*recN108* reduces the recombination proficiency more than a strain carrying $recN_{K35D}$ mutation. The effect of $recN_{K35D}$

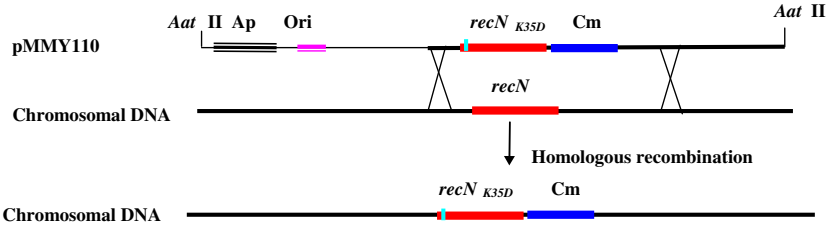

Figure 2 Introduction of the $recN_{K35D}$ gene into *E. coli* chromosomal DNA by reverse genetics. The plasmid pMMY110 (containing $recN_{K35D}$) was linearized by *Aat* II restriction enzyme and transformed into *E. coli* strain N2525 (*recD*1009). Selection was for Cm^R clones and screened for Ap^S and Mc^S. Clones with Cm^R, Ap^S and Mc^S were presumed to have integrated the DNA fragment containing $recN_{K35D}$ gene and Cm resistant gene into the chromosomal DNA by homologous recombination.

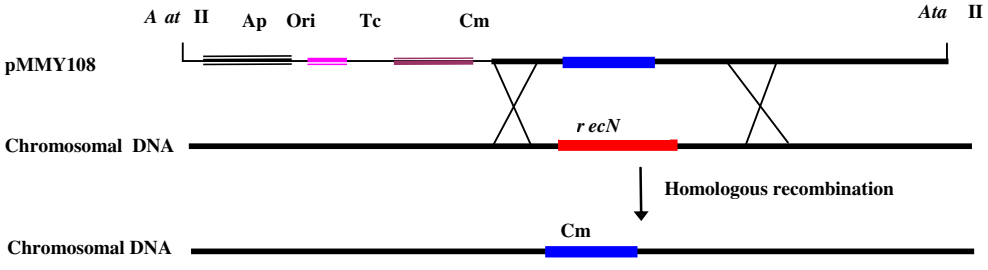

Figure 3 Deletion of the entire *recN* gene from *E. coli* chromosomal DNA. A linear DNA fragment from pMMY108 DNA containing Cm resistant gene and deleted the entire *recN* gene was transformed into *E. coli* strain N2525 (*recD*1009). Selection was for CmR clones and screened for ApS, TcS and McS. Clones with CmR, ApS, TcS, and McS were presumed to have integrated the DNA fragment containing Cm resistant gene and deleted *recN* gene into the chromosomal DNA by homologous recombination.

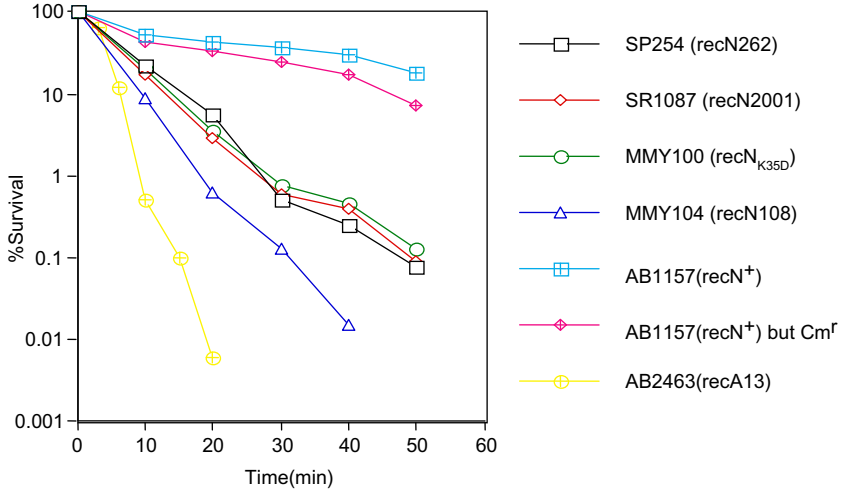

Figure 4 Mitomycin C sensitivity of *E. coli* strains SP254 (*recN262*), SR1087 (*recN2001*), MMY100 recN$_{K35D}$) & MMY104 (*recN108*). Bacterial strains AB1157 (*recN*$^+$), SP254 (*recN262*), SR1087 (*recN2001*), MMY100 recN$_{K35D}$), MMY104 (*recN108*) & AB2463 (*recA13*) were exposed to mitomycin C 2 μg/ml for defined periods of time (min).

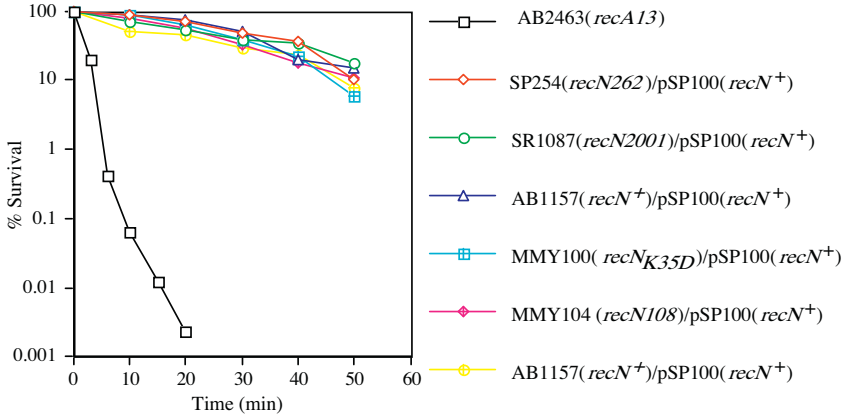

Figure 5 Complementation of the mitomycin C sensitivity of bacterial strains SP254 (*recN262*), SR1087 (*recN2001*), MMY100 recN$_{K35D}$) & MMY104 (*recN108*) by the *recN*$^+$ plasmid pSP100. Bacterial strains AB1157 (*recN*$^+$), SP254 (*recN262*), SR1087 (*recN2001*), MMY100 recN$_{K35D}$), MMY104 (*recN108*) & AB2463 (*recA13*) were transfected by the *recN*$^+$ plasmid pSP100 and exposed to mitomycin C 2 μg/ml for defined periods of time (min).

mutation on the homologous recombination is similar to that of *recN262* and *recN261* mutations. Also, we observed that both *recN$_{K35D}$* mutation and Δ*recN108* are not important as *recN262* and *recN261* mutations for homologous recombination in wild type (*rec*$^+$) strains (Picksley et al. 1984a).

3.6. Effect of recN on the excision of Tn10

Chan et al. (1994) have observed that *recN* gene product is involved in the induced excision of Tn*10*. From this point of view, we are interested in the examination of the effect of the strains carrying *recN$_{K35D}$* mutation and Δ*recN108* on the induced excision of Tn*10* from *gal76::*Tn*10* in AB1157 (*rec*$^+$) and JC7623 (*recBC sbcBC*) backgrounds. Mitomycin C induces the precise excision of Tn*10* from *gal76::*Tn*10* in an *E. coli recN*$^+$ strains. In, both AB1157 (*rec*$^+$) and JC7623 (*recBC sbcBC*) backgrounds the *recN$_{K35D}$* mutation affects in the induced excision of Tn*10* from *gal76::*Tn*10* (Table 4). Our studies show that mitomycin C induces the excision of Tn10 in *recN$_{K35D}$* mutant cells. All the tested revertants were found to be Tc^s and Cm^r. The role of Δ*recN108* in excision of Tn*10* in AB1157 (*rec*$^+$) background is uninducible by mitomycin C. On the other hand, the Δ*recN108* in JC7623 (*recBC sbcBC*) background completely blocks the excision of Tn*10*.

4. Discussion

The members of the SMC family of proteins (Hirano et al., 1995, 1997) and various recombinational repair proteins as RecA (Knight and McEntee; 1985), RecB, RecD (Korangy and Julin; 1992) and SbcC (Connelly et al., 1999) have the Walker A nucleotide binding site (Gly-X-X-X-Lys-Ser/Thr where X is any amino acid) (Walker et al., 1982). In addition, the comparison of the RecN protein sequence of various organisms (Funayama et al., 1999) reveals that the RecN protein contains the Walker A nucleotide binding site. The basic

Table 4 Effect of *recN* mutations on the excision of Tn*10* from *gal76*::Tn*10*.

Bacterial strain	Mitomycin C concentration (ng/ml)			
	0	2.5	5	10
AB1157 background				
MMY118 (*rec*$^+$, Cm^r)	23	236	357	509
MMY114 (*recN*$_{K35D,}$ Cm^r)	21	45	87	111
MMY116 (*recN108,* Cm^r)	413	434	423	441
NF471 (*rec*$^+$)	28	296	468	626
NF618 (recN618)	20	34	21	29
JC7623 background				
MMY130 (*recBC sbcBC*)	12	38	52	68
MMY126 (*recBC sbcBC,* Cm^r)	10	39	61	88
MMY124 (*recBC sbcBC recN*$_{K35D}$Cm^r)	9	25	28	35
MMY123 (*recBC sbcBC recN108,* Cm^r)	0	0	0	0

NB: All bacterial strains used in the excision Tn*10* experiment are *gal76*::Tn*10*.

amino acid lysine residue in the Walker A nucleotide binding site has been shown to be essential for the RecD protein (Korangy and Julin; 1992). To determine the importance of the Walker A nucleotide binding site to the RecN protein, the highly conserved basic amino acid lysine 35 in the Walker A nucleotide binding site of the *E. coli* RecN protein was mutated to an acidic amino acid aspartic acid (Fig. 1).

Many reports have used bacterial strains carrying *recD* mutation and transformed it with linear pieces of DNA containing homology to delete or replace chromosomal genes with genes that had been modified (Chauhudry and Smith, 1984; Russel et al., 1989). In this work, the linear pMMY108 (*recN108*) and pMMY110 ($recN_{K35D}$) plasmids carrying the chloramphenicol and ampicillin resistant genes were introduced into *recD1009* competent cells. The transformants that integrate the linear plasmids DNA into the chromosomal DNA by homologous recombination were identified presumably for loss of the ampicillin resistant gene and accept of the chloramphenicol resistant gene. The deletion of *recN* or reintroduction of $recN_{K35D}$ into the chromosomal DNA identified in clones which shows sensitivity to mitomycin C (Figs. 2 and 3).

The product of *recN* gene is implicated in the repair of DNA double strand breaks (Picksley et al., 1984a; Meddows et al., 2005). Known *recN* mutations are sensitive to the mitomycin C a cross linking-agent (Picksley et al., 1984a,b; Chan et al., 1994; Funayama et al., 1999). The strains carrying $recN_{K35D}$ and *recN108* show sensitivity to mitomycin C (Fig. 4). It is clear that, Δ*recN108* cells are more sensitive to the mitomycin C than $recN_{K35D}$ and the identified *recN* mutations. The pSP100 ($recN^+$) plasmid DNA restores the resistant to the mitomycin C of strains carrying $recN_{K35D}$ and Δ*recN108* to the level of wild type strains ($recN^+$).

The recombination in *rec*$^+$ strains is activated by RecBCD pathway and *recN* gene product not implicated in this pathway. In *recBC* strains the recombination proficiency is restored by additional mutation in *sbcA* or *sbcBC*. In *recBC sbcA* background the recombination is catalysed by the RecE pathway and *recN* gene product is not involved in this pathway (Robbins-Manke et al., 2005). On the other hand, in the *recBC sbcBC* cells the recombination is catalysed by the RecF pathway and *recN* gene product have an important role in the RecF pathway (Picksley et al., 1984a; Wang and Maier, 2008). In this study we observed that *recN108* in *recBC sbcBC* background reduce the homologous recombination more than that any of the *recN* mutation in *recBC sbcBC* background (Table 3).

Many of the SOS genes were found to be implicated in the precise excision of Tn*10* (Chan et al., 1994). *recN* gene is induced as one of the SOS genes under the regulation of LexA repressor to remind the damaged DNA (Picksley et al., 1984b; Kosa et al., 2004). The data (Table 4) indicate that *recN* gene product have a role in the excision of Tn*10* in *rec*$^+$ and *recBC sbcBC* background. The frequency of revertants of *gal*$^+$ is decreased in $recN_{K35D}$ strains than that of the $recN^+$ in AB1157 and JC7623 background.

Acknowledgments

We thank Dr. R.G. Lloyd (UK) and Dr. R. Nagel (Argentina) for bacterial strains they provided to achieve this work.

References

Bachmann, B.J., 1972. Pedigrees of some mutant strains of *Escherichia coli* K 12. Bacteriol. Rev. 36, 525–557.

Bolivar, F., Rodriguez, R.L., Greene, P.J., Betalach, M.C., Heynecker, H.L., Boyer, H.W., Crossa, J.H., Falkow, S., 1977. Construction and characterization of new cloning vehicles. II. A multipurpose cloning system. Gene 2, 95–113.

Cao, L., Alani, E., Kleckner, N., 1990. A pathway for the generation and processing of double-strand breaks during meiotic recombination in *Saccharomyces cerevisiae*. Cell 61, 1089–1101.

Cassuto, E., West, S.C., Mursalim, J., Conlon, S., Howard-Flanders, P., 1980. Initiation of genetic recombination: homologous pairing between duplex DNA molecules promoted by RecA protein. Proc. Natl. Acad. Sci. USA 77, 3962–3966.

Chan, A., Levy, M., Nagel, R., 1994. *recN* SOS gene and induced precise excision of Tn10 in *Escherichia coli*. Mutat. Res. 235, 75–79.

Chauhudry, A.M., Smith, G.R., 1984. A new class of *Escherichia coli* *rec*BC mutants: implications for the role of RecBC enzyme in homologous recombination. Proc. Natl Acad. Sci. USA 81, 7850–7854.

Clark, A.J., Margulies, A.D., 1965. Isolation and characterisation of recombination deficient mutants of *Escherichia coli* K12. Proc. Natl. Acad. Sci. USA 13, 451–459.

Clark, A.J., Sandler, S.J., Willis, K.D., Chu, C.C., Blanar, A.A., Lovett, S.T., 1984. Genes of the RecE and RecF pathways of

conjugational recombination in *Escherichia coli*. Cold Spring Harb. Symp. Quant. Biol. 49, 453–462.

Connelly, J.C., Leau, E.S., Leach, D.R.F., 1999. DNA cleavage and degradation by the SbcCD protein complex from *Escherichia coli*. Nucleic Acids Res. 27, 1039–1046.

Elie, C., Baucher, M., Fondart, C., Forterre, P., 1997. A protein related to eucaryal and bacterial DNA-Motor proteins in the hyperthermophilic *Archaeon sulfolobus acidocaldarius*. J. Mol. Evol. 45, 107–114.

Emmersom, P.T., Howard-Flanders, P., 1967. Cotransduction with thy of a gene required for genetic recombination in *Escherichia coli*. Bacteriology 93, 1729–1731.

Emmerson, P.T., 1968. Recombination-deficient mutants of *Escherichia coli* K12 that map between *thyA* and *argA*. Genetics 60, 19–30.

Finch, P.W., Chambers, P., Emmerson, P.T., 1985. Identification of the *Escherichia coli recN* gene product as a major SOS protein. Bacteriology 164, 653–6658.

Funayama, T., Narumi, I., Kikuchi, M., Kitayama, S., Watanabe, H., Yamamoto, K., 1999. Identification and disruption analysis of the recN gene in the extremely radioresistant bacterium *Deinococcus radiodurans*. Mutat. Res. 435, 151–161.

Goldmark, P.G., Linn, S., 1972. Purification and properties of the *recBC* DNase of *Escherichia coli* K12. J. Biol. Chem. 247, 1849–1860.

Graumann, P.L., Knust, T., 2009. Dynamics of the bacterial SMC complex and SMC-like proteins involved in DNA repair. Chromosome Res. 17, 265–275.

Hashimoto-Goth, T., Franklin, F.C., Nordheim, A., Timmis, K.N., 1981. Specific purpose plasmid cloning vectors I. Low copy number, temperature sensitive, mobilization defective pSC101 derived containment vectors. Gene 16, 227–235.

Hickson, I.D., Emmerson, P.T., 1981. Identification of *Escherichia coli recB* and *recC* gene products. Nature 294, 578–580.

Hirano, T., Mitchison, T.J., Swedlow, R.J., 1995. The SMC family: from chromosome condensation to dosage compensation. Curr. Opin. Cell Biol. 7, 329–336.

Hirano, T., Kobayashi, P., Hirano, M., 1997. Condensins, chromosome condensation protein complexes containing XCAP-C, XCAP-E and a Xenopus homolog of the Drosophila barren protein. Cell 89, 511–521.

Howard-Flanders, P., Theriot, L., 1966. Mutants of *Escherichia coli* K 12 defective in DNA repair in genetic recombination. Genetics 53, 1137–1150.

Knight, K.L., McEntee, K., 1985. Covalent modification of the RecA protein from *E. coli* with the photoaffinity label 8 azidoadenosine 5′ triphosphate. J. Biol. Chem. 260, 867–872.

Korangy, F., Julin, D.A., 1992. Enzymatic effect of a lysine to glutamine mutation in the ATP binding consensus in the RecD subunit of the RecBCD enzyme from *E. coli*. J. Biol. Chem. 267, 1733–1740.

Kosa, J.L., Zdraveski, Z.Z., Currier, S., Marinus, M.G., Essigmann, J.M., 2004. RecN and RecG are required for *Escherichia coli* survival of bleomycin-induced damage. Mutat. Res. 554, 149–157.

Kushner, S.R., Nagaishi, H., Templin, A., Clark, A.J., 1971. Genetic recombination in *Escherichia coli*: the role of exonuclase I. Proc. Natl. Acad. Sci. USA 68, 824–827.

Kushner, S.R., Nagaishi, H., Clark, A.J., 1972. Indirect suppression of recB and recC mutations by exonuclease I deficiency. Proc. Natl. Acad. Sci. USA 69, 1366–1370.

Lloyd, R.G., Buckman, C., 1985. Identification and genetic analysis of *sbcC* mutations in commonly used *recBC sbcB* strains of *Escherichia coli* K12. Bacteriology 164, 836–844.

Lloyd, R.G., Low, B., Birge, G.N., 1974. Isolation and characterisation of an *Escherichia coli* mutant with a temperature sensitivity RecA$^-$ phenotype. Bacteriology 120, 407–415.

Lloyd, R.G., Picksley, S.M., Prescott, C., 1983. Inducible expression of a gene specific to the RecF pathway for recombination in *Escherichia coli* K12. Mol. Gen. Genet. 190, 162–167.

Lovett, S.T., Clark, A.J., 1984. Genetic analysis of the *recJ* gene of *Escherichia coli*. Bacteriology 157, 190–196.

Meddows, T.R., Savory, A.P., Grove, J.I., Moore, T., Lloyd, R.G., 2005. RecN protein and transcription factor DksA combine to promote faithful recombinational repair of DNA double-strand. Mol. Microbiol. 57 (1), 97–110.

Miller, J.H., 1972. Experiments in molecular genetics. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.

Nagashima, K., Kubota, Y., Shibata, T., Sakaguchi, C., Shinagawa, H., Hishida, T., 2006. Degradation of *Escherichia coli* RecN aggregates by ClpXP protease and its implications for DNA damage tolerance. Biol. Chem. 281 (41), 30941–30946.

Picksley, S.M., Attfield, P.V., Lloyd, R.G., 1984a. Repair of DNA double-strand breaks in *Escherichia coli* K12 requires a functional *recN* product. Mol. Gen. Genet. 195, 267–274.

Picksley, S.M., Lloyd, R.G., Buckman, C., 1984b. Genetic analysis and regulation of inducible recombination in *Escherichia coli* K12. Cold Spring Habor Symp. Quant. Biol. 49, 469–474.

Picksley, S.M., Morton, S.J., Lloyd, R.G., 1985. The *recN* locus of *Escherichia coli* K12: molecular analysis and identification of the gene product. Mol. Gen. Genet. 201, 301–307.

Robbins-Manke, J.L., Zdraveski, Z.Z., Marinus, M., Essigmann, J.M., 2005. Analysis of global gene expression and double-strand-break formation in DNA adenine methyltransferase- and mismatch repair-deficient *Escherichia coli*. J. Bacteriol. 187, 7027–7037.

Rostas, K., Morton, S.J., Picksley, S.M., Lloyd, R.G., 1987. Nucleotide sequence and LexA regulation of the *Escherichia coli recN* gene. Nucleic Acids Res. 15, 5041–5049.

Russel, C.B., Thaler, D.S., Dahlquist, F.W., 1989. Chromosomal transformation of *Escherichia coli recD* strains with linearized plasmids. Bacteriology 171, 2609–2613.

Sambrook, J., Fritsch, E.F., Maniatis, T., 1989. Molecular cloning: a laboratory manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.

Sawitzke, J.A., Stahl, F.W., 1992. Phage lambda has an analog of *Escherichia coli recO*, *recR*, and *recF* genes. Genetics 130, 7–16.

Walker, J.E., Saraste, M., Runswick, J., Gay, N.J., 1982. Distantly related sequences in the α- and β-subunits of ATP synthase, myosin, kinases and other ATP- requiring enzymes and a common nucleotide binding fold. EMBO J. 1, 945–951.

Wang, G., Maier, R.J., 2008. Critical role of RecN in recombinational DNA repair and survival of *Helicobacter pylori*. Infect. Immun. 76 (1), 153–160.

Willetts, N.S., Mount, D.W., 1969. Genetic analysis of recombination deficient mutants of *Escherichia coli* K12 carrying *rec* mutations with *thyA*. Bacteriology 100, 923–934.

Zhuravel, D., Boreiko, A., 2002. Regularities of excising transposon Tn10 in rec-mutant *E. coli* cells exposed to gamma radiation. Radiats. Biol. Radioecol. 42 (6), 636–638.