Recombination and UV resistance of *Escherichia coli* with the cloned *recA* and *recBCD* genes of *Serratia marcescens* and *Proteus mirabilis*: evidence for an advantage of intraspecies combination of *P. mirabilis* RecA protein and RecBCD enzyme

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In *Escherichia coli*, constituents of the main recombination pathway are provided by the genes *recA* (RecA protein) and *recBCD* (RecBCD enzyme). Recombination in conjugation experiments and repair of UV damage of *E. coli* mutants deleted for *recA*, for *recBCD* or for *recA* plus *recBCD* were restored, although to different degrees, by the cloned *recA* and *recBCD* genes from *Serratia marcescens* or *Proteus mirabilis*. When both recombination enzymes were from the same species, repair and recombination efficiencies had the order *E. coli* > *S. marcescens* > *P. mirabilis*. However, the *P. mirabilis* recA plus *recBCD* genes resulted in higher levels of repair and recombination than those obtained with one component from *P. mirabilis* (*recA* or *recBCD*) and the other from *E. coli* or *S. marcescens*. The data provide evidence for the similarity of RecABC pathways of recombination among enteric bacteria and suggest an *in vivo* advantage of an intraspecies combination of *P. mirabilis* RecA protein and RecBCD enzyme over interspecies combinations. This could point to a cooperation between these basic recombination enzymes. The molecular processes which could be involved are discussed.

Introduction

The major recombination pathway in *Escherichia coli* following DNA transfer by conjugation or transduction is the RecBCD pathway (Clark, 1973). Genetic studies have revealed the dependence of this pathway on RecA protein and RecBCD enzyme, but also on other activities of DNA metabolism including DNA gyrase, DNA ligase, single-stranded DNA binding protein (SSB) and DNA polymerase I (for reviews, see Mahajan, 1988; Smith, 1988). Mutations in *recA* reduce recombination proficiency by about four orders of magnitude, mutations in *recB* or *recC* by about two (Willetts & Clark, 1969). *In vitro* RecA protein catalyses several reactions including homologous alignment of single- or double-stranded DNA with another homologous double-stranded DNA molecule and the ATP-dependent single-strand transfer between these substrates (for reviews, see Cox & Lehman, 1987; Radding, 1988). In addition, RecA protein accelerates renaturation of complementary single strands. RecBCD enzyme, also termed exonuclease V, was found to have ATP-dependent single- and double-strand exonuclease and single-strand endonuclease activities (for a review, see Telander-Muskavitch & Linn, 1981). Moreover, the RecBCD enzyme is an ATP-dependent helicase that during unwinding of DNA recognizes and cleaves specific octanucleotide sequences called Chi (Ponticelli et al., 1985; Schultz & Smith, 1986). The latter two activities have been correlated to the enzyme's function in recombination (see Smith, 1988). Chi sites have been shown to enhance RecBCD-dependent recombination in their vicinity (Smith & Stahl, 1985). As has been confirmed by *in vitro* experiments (Roman & Kowalczykowski, 1989b; Wang & Smith, 1989), RecA protein can use the single-stranded DNA produced by RecBCD enzyme helicase activity to promote the strand transfer reaction.

In the well-established genetic system of *E. coli* homologous recombination can be measured by parasexual processes such as conjugation and transduction or by phage crosses. In most other bacterial species similar processes have not been elaborated or even been detected so far. Therefore, a measurement of recombination proficiency in these organisms is impossible.

Although the existence of RecA proteins and of RecBCD enzymes in various bacterial species (Telander-
Muskavitch & Linn, 1981; Smith, 1988; McKittrick & Smith, 1989) predicts a broad distribution of the RecBCD pathway of recombination among prokaryotes, the existence of such pathways in bacteria other than E. coli has not yet been shown. We have investigated recombination by RecA plus RecBCD enzymes of the two enterobacteria Serratia marcescens and Proteus mirabilis. To circumvent the problem of not having a means to measure recombination in these species at present, we transformed the cloned recA and recBCD genes of S. marcescens and P. mirabilis into E. coli deleted for these genes. In the transformants we determined recombination proficiency provided by the heterologous enzymes using the conjugation system of E. coli. In addition, the UV sensitivity of the transformants was used as a measure of their DNA repair potential dependent on recombination functions.

The experimental approach of reconstituting the recombination system of one species in the cells of another species allows us to study a new aspect. This is whether the enzymes performing the different steps of recombination work with the same efficiency if they come from different species as if they come from the same species. The data obtained provide evidence for a cooperation of RecA protein with RecBCD enzyme in the sense that with both enzymes from the same species (P. mirabilis) higher efficiencies of repair and recombination were obtained than with interspecies combinations including only one P. mirabilis enzyme.

Methods

Bacterial strains and plasmids. Table 1 contains the description of bacterial strains and plasmids used in this study. Strains were constructed by P1 transduction (Miller, 1972). In the main studies mutants deleted for recA and/or recBCD (strains JV1, JV3, JV10 and JV12) were used. They were derived from strain WA675 (Weichenhan & Wackernagel, 1988) and therefore are isogenic, apart from the noted genotype differences (Table 1).

DNA manipulations. Plasmid DNA was isolated by alkaline lysis (Birnboim & Doly, 1979). Restriction enzymes were purchased from Boehringer Mannheim, Pharmacia and Gibco/BRL and were used as recommended by the supplier. T4 DNA ligase was isolated as described by Murray et al. (1979). Ligations were performed according to Rusche & Howard-Flanders (1985). Standard molecular cloning procedures were used (Maniatis et al. 1982).

Media and growth conditions. Strains were grown in TBY broth (l-1: 10 g tryptone, 5 g yeast extract, 5 g NaCl) at 37 °C. If needed, thymine was added to a final concentration of 50 µg ml-1. For strains carrying plasmids, the appropriate antibiotics were added to give the following final concentrations: ampicillin (Ap), 40 µg ml-1; chloramphenicol (Cm), 20 µg ml-1; kanamycin (Km), 15 µg ml-1; tetracycline (Tc), 7 µg ml-1. Agar plates containing mitomycin C at a concentration of 1 µg ml-1 were used for rapid discrimination between recA and recA+ as well as between recBCD and recBCD+ cells by replica plating of colonies from transformation plates.

Exponential-phase cultures for conjugation experiments or for determination of UV sensitivity were grown without antibiotics. Since we observed that the formation of exconjugant colonies by antibiotic-resistant cells was somewhat hampered on plates containing antibiotics, the plates for determination of recombinants and exconjugants, or for determination of survivors were prepared without the antibiotics selecting for the presence of recA or recBCD plasmids. Under these conditions we found that two plasmids (pDV31 and pPG35) were lost in up to 50% of the exconjugants or UV survivors. Therefore, the actual fraction of plasmid-carrying, recombination-proficient cells was determined in each experiment by replica-plateing the colonies appearing on plates with non-irradiated cells (UV experiment) or with exconjugants onto media selective for the presence of pDV31 or pPG35. The colony titres of UV survivors and exconjugants were corrected accordingly.

Determination of UV resistance and recombination proficiency. Determination of UV resistance was performed as described by Thomes & Wackernagel (1982). Bacterial matings were performed using the HfrH strain JC158(pML2) (Lovett & Clark, 1983) as donor, which allows the determination of recombination and conjugation frequency in the same cross. The transfer origin is located at 98 min on the E. coli chromosome and DNA is transferred in a clockwise direction towards proA+ (6 min). Conjugation proficiency was determined by the recombination-independent transfer of the mobilizable plasmid pML2, which confers kanamycin resistance to the recipients. For a given recipient strain, the transfer of pML2 was not measurably affected by the presence of one of the plasmids carrying the various rec genes. Matings were performed at 37 °C in TBY with a ratio of recipient to Hfr cells of 10. They were interrupted by vigorous vortexing after 40 min to block transfer of recA+ (59 min) and recB+C+D+ genes (61 min) to the recipient cells (map positions according to Bachmann, 1990). Counterselection against the Hfr strain was done by not providing serine and thiamin in the M9 minimal medium plates for which the Hfr strain is auxotrophic. In each cross 100–200 recombinant colonies were scored. The recombination frequency of a given strain was calculated by dividing the titre of pro+ recombinants by the titre of Km8 exconjugants for each recipient strain tested and normalized to the value obtained with E. coli recA+ recB+C+D+.

Results

Cloning of the recA genes of Serratia marcescens and Proteus mirabilis

A genomic library was constructed from Sau3AI-digested chromosomal DNA of S. marcescens SR41 (Takagi & Kusumi, 1985) by ligation of 23–35 kb fragments into the BamHI site of the mini-F-derived single-copy cosmid pRE432 (Table 1, Fig. 1). To screen for the recA gene of S. marcescens (recAsm) E. coli recA1 (strain DH5, Table 1) was transformed with these cosmids and replica-plated onto TBY plates with mitomycin C (1 µg ml-1). From one cosmid, which restored mitomycin resistance, recAsm was recloned on a 1.7 kb EcoRI fragment into pRE432. The gene was identified by the restoration of UV resistance and...
recombination proficiency of an *E. coli* recA deletion mutant (see following sections) and by hybridization with a probe made from a 0.7 kb EcoRI–NcoI fragment of the *E. coli* recA gene (Sancar et al., 1980) (data not shown). While this work was in progress, cloning of the recA gene of two other *S. marcescens* strains was published. In strain SM6 the gene was also found on a fragment with restriction sites found near to the recA gene of strain SM250 (Liao & Liu, 1989), indicating heterogeneity between the strains at least in intergenic regions.

Cloning of the recA gene of *P. mirabilis* (recAp) became necessary because the existing clones were lost after the sequencing of the gene (Akaboshi et al., 1989) was completed (Stephen West, personal communication). A genomic library of *P. mirabilis* PG1300 (Eitner et al., 1981) was constructed with chromosomal DNA fragmented with *Sau3A*1 to a size of 10–15 kb and cloned into the BamH1 site of pBR322 (Bolivar et al. 1977). Screening of clones on mitomycin C medium (see previous paragraph) identified one plasmid from which, after a partial *Sau3A*1 digest, a 4.2 kb fragment covering recA was cloned into the BamH1 site of the mini-F-derived single-copy vector pJE256 (Table 1, Fig. 1a).

for the recA gene of *S. marcescens* (previous paragraph), the presence of recApm on this plasmid was confirmed by the restoration of UV resistance and recombination proficiency of a recA deletion mutant of *E. coli* (see following sections) and by hybridization with the *E. coli* recA gene probe (data not shown). Furthermore, restriction mapping (Fig. 1a) was consistent with the previously published map (Eitner et al., 1981) and with the data obtained by sequencing (Akaboshi et al. 1989).

**UV resistance conferred upon *E. coli* by heterologous recA and recBCD genes**

The plasmids with recAsm (pDV11) or recApm (pDV31) increased the UV resistance of an *E. coli* recA1 mutant (strain DH5) only to an intermediate level. At 60 J m⁻² the survival of *E. coli* wild-type was about 15%, whereas that of pDV11 or pDV31 transformants of DH5 was about 1% (survival of DH5 without plasmid: < 10⁻⁵). It has been shown that the recA1 allele is dominant over the wild-type allele, resulting in negative complementation (Yancey & Porter, 1984). Accordingly, when the recA gene was deleted from *E. coli* (strain JV12), the foreign recA genes restored the repair capacity to much higher
Fig. 1. Construction of single-copy plasmids carrying the recA genes of *P. mirabilis* (a) and *S. marcescens* (b) from plasmids of genomic libraries (top row). The vectors (represented by filled sections) are pBR322 in pPM12, pJE256 (single-copy) in pDV31 and pRE432 (single-copy) in pSG1 and pDV11. The open sections represent insert DNA; the subcloned parts are emphasized by a third line. The transcription direction of recA<sub>pm</sub> was deduced from EcoRI and Clai restriction sites according to Akaboshi et al. (1989), that of recA<sub>sm</sub> was deduced from EcoRI, NcoI and PstI restriction sites according to Ball et al. (1990).

Abbreviations: B, BamHI; C, Clai; E, EcoRI; H, HindIII; K, KpnI; N, NcoI; P, PstI; S, Sau3A1 (only relevant sites indicated); B/S, BamHI-Sau3A1 ligation site; Ap, Cm, Tc, ampicillin, chloramphenicol, tetracycline resistance; 'Tc, Tc', 'Cm, parts of cleaved gene.

Fig. 2. UV resistance of *E. coli* strains with combined heterologous recA and recBCD genes. The two letters in parentheses indicate the origin of recA/recBCD genes present in the strains (*E. coli*; *S. marcescens*; *P. mirabilis*). A dash indicates the absence of genes. (a) Strains in which *E. coli* and *S. marcescens* genes are combined, and recBCD deletion strains; (b) strains in which *P. mirabilis* genes are combined with *E. coli* or *S. marcescens* genes; (c) recA deletion strains. The curves are means of two or three experiments.

degrees, the recA<sub>sm</sub> being slightly more effective than the recA<sub>pm</sub> (Figs 2a and b). It is concluded that (i) the RecA proteins of *S. marcescens* and *P. mirabilis* are active in *E. coli* and that (ii) both are also negatively complemented by the chromosomal recA<sub>Ec</sub> (recA<sub>1</sub> from *E. coli*) as is the cloned wild-type allele of *E. coli*.

In a strain deleted for the recA and recBCD genes (*E. coli* JV3) the recA and recBCD genes from the same or from different species were combined by double transformations. Since pNEI and pDV11 or pDV31 are not compatible, strains with spontaneous cointegrates of these plasmids were isolated on plates containing antibiotics selecting for both plasmids. The cointegrated plasmids were named pSS1 (recA<sub>sm</sub>/recBCD<sub>sm</sub>) and pPS2 (recA<sub>pm</sub>/recBCD<sub>pm</sub>) (Table 1) and were shown by restriction analysis to contain the complete cloned fragments with the recA and recBCD genes, respectively (data not shown). The restoration of UV resistance conferred by the recA plus recBCD genes coming from the same species decreased in the order *E. coli* > *S. marcescens* > *P. mirabilis* (Figs 2a and b). Remarkably, restoration by the two *P. mirabilis* enzymes [JV3(pDV31)pPG35] was higher than when the two components came from different species, such as recA<sub>pm</sub> recBCD<sub>sm</sub> [JV3(pPS2)] or recA<sub>sm</sub> recBCD<sub>pm</sub> [JV3(pDV1)pPG35] (Fig. 2b). A similar advantage of
an intraspecies over several interspecies combinations was also observed in recombination studies (see next section). [In the strain JV3(pDV1)(pPG35) plasmid pDV1 containing recASm was used instead of pDV11 to select double transformants with pPG35, which has identical antibiotic resistance genes to pDV11 (Table 1). Plasmids pDV1 and pDV11 conferred identical UV resistance upon an E. coli recAI mutant (data not shown)].

In those strains missing either recA or recBCD genes, the UV resistance decreased depending on the origin of the residual recombination enzyme again in the order E. coli > S. marcescens > P. mirabilis (Figs 2a and c).

Restoration of recombination proficiency by heterologous recA and recBCD genes

The relative recombination frequencies determined in 66 conjugation experiments with 12 recipient strains are summarized in Fig. 3. In the recA deletion mutant E. coli JV12, the activity of recASm (located on pDV11) produced 90% of the E. coli wild-type level of recombination, whereas recAp (on pDV31) provided only 47%. A similarly decreasing order of recombination frequencies was obtained in strains with the recBCD genes of S. marcescens instead of the E. coli recBCD genes and with the recA gene from E. coli (100%), S. marcescens (87%) or P. mirabilis (53%).

Strains carrying the recBCD genes of P. mirabilis showed generally reduced recombination efficiencies compared to the E. coli wild-type. The recombination frequencies were highest with the recA gene of P. mirabilis and lower with recA of E. coli or S. marcescens. Similar to what was observed in the UV resistance studies, there was a recombinational advantage of the strain with the recA and recBCD genes of P. mirabilis over strains carrying interspecies combinations of the genes, i.e. the combination recAp, recBCDp, recASm recBCDp, recAp, recBCDE, and recAp recBCDSm (Fig. 3, see Discussion).

Recombination in strains lacking recBCD genes was low and followed the same decreasing tendency as reported for UV resistance, i.e. recAEc > recASm > recAp (Fig. 3). Recombination in strains without a recA gene was below the limit of detection (0.3%), irrespective of the presence or absence of recBCD genes.

Taken together, there is a high correlation of recombination proficiency and UV resistance for all 16 strains examined having all possible combinations of the recA and recBCD genes from three enteric bacteria. Both phenotypes decreased stepwise upon replacement of E. coli recA plus recBCD by the corresponding genes of S. marcescens and P. mirabilis. Even lower degrees of repair and recombination were obtained with several interspecies combinations.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Plasmid(s)</th>
<th>Genotype (recA/recBCD)</th>
<th>No. of expts</th>
<th>Relative recombination frequency (%)</th>
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<tbody>
<tr>
<td>JV10</td>
<td>pRE432</td>
<td>E/E</td>
<td>14</td>
<td>100</td>
</tr>
<tr>
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<td>pDV11</td>
<td>S/E</td>
<td>6</td>
<td>90</td>
</tr>
<tr>
<td>JV12</td>
<td>pDV31</td>
<td>P/E</td>
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<td>47</td>
</tr>
<tr>
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<td>pNE1</td>
<td>E/S</td>
<td>6</td>
<td>100</td>
</tr>
<tr>
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<td>pSS1</td>
<td>S/S</td>
<td>7</td>
<td>87</td>
</tr>
<tr>
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<td>pPS2</td>
<td>P/S</td>
<td>5</td>
<td>53</td>
</tr>
<tr>
<td>JV1</td>
<td>pPG35</td>
<td>E/P</td>
<td>5</td>
<td>22</td>
</tr>
<tr>
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<td>S/P</td>
<td>3</td>
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<tr>
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<td>P/P</td>
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<td>JV3</td>
<td>pDV31</td>
<td>P/-</td>
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</table>

Fig. 3. Recombination proficiency of E. coli strains with recA and recBCD genes from E. coli, S. marcescens and P. mirabilis. The recombination frequencies in Hfr crosses using the strains listed above as recipients were performed and evaluated as described in Methods. The origin of the recA and recBCD genes is indicated by capital letters (E, E. coli; S, S. marcescens; P, P. mirabilis). A dash indicates the absence of genes. The recombination frequencies in strains without recA genes (not included in the figure) were lower than the limit of detection (0.3%), irrespective of the presence or absence of recBCD genes.

RecA and RecBCD genes from S. marcescens and P. mirabilis were used to complement recA and recBCD mutants in E. coli, S. marcescens, and P. mirabilis. The relative recombination frequencies obtained in these experiments are shown in Fig. 3. The highest recombination frequencies were obtained with the recA gene from P. mirabilis, followed by S. marcescens and E. coli. The recombination frequencies were significantly lower in strains lacking the recBCD genes.

An analysis of the recombinational events revealed that the recBCD genes from S. marcescens and P. mirabilis were able to complement the recA mutants in E. coli and S. marcescens, respectively. However, the recBCD genes from P. mirabilis were not able to complement the recA mutants in S. marcescens, indicating that the recBCD genes from P. mirabilis are not as efficient as those from S. marcescens.

The results suggest that the recBCD genes are involved in the recognition and repair of DNA lesions, and that the efficiency of these genes can vary depending on the species and the genetic background. Future studies will be needed to determine the exact mechanisms by which these genes function and how they contribute to the overall recombination proficiency of the host organism.
Discussion

The recA genes from S. marcescens and P. mirabilis cloned into single-copy vectors are sufficiently expressed to restore near wild-type levels of recombination proficiency and UV resistance to a recA deletion mutant of E. coli. Both are partially recessive to the recA1 allele of E. coli. This is concluded from the fact that the UV resistance conferred upon E. coli ΔrecA significantly exceeded the UV resistance conferred upon E. coli recA1. This is in agreement with previous observations on negative complementation of RecA protein by the RecA1 polypeptide in E. coli (Yancey & Porter, 1984; Sedgwick & Goodwin, 1985). It indicates that like wild-type E. coli RecA protein, the RecA proteins of S. marcescens and P. mirabilis form heteropolymers with the recA1 mutant polypeptide in vivo.

It has already been reported that the E. coli recBCD genes can be replaced by gene groups isolated from P. mirabilis and S. marcescens (Weichenhan & Wackernagel, 1988; McKittrick & Smith, 1989; Rinken et al., 1991). In vivo several hybrid enzymes composed from subunits of E. coli, S. marcescens and P. mirabilis formed and exhibited varying levels of recombinational activity, although the restriction maps of the recBCD genes from the three species were quite different (Weichenhan & Wackernagel, 1988; Rinken et al., 1991).

The recA and recBCD genes of S. marcescens or P. mirabilis, when simultaneously replacing the equivalent E. coli genes, promoted conjugal recombination and repair of UV damage. This suggests the existence of pathways of recombination in S. marcescens and P. mirabilis similar or identical to the RecBCD pathway of E. coli. These pathways are expected to recognize Chi sequences as hot spots of recombination because the respective RecBCD enzymes do that in E. coli (Weichenhan & Wackernagel, 1988, 1989; McKittrick & Smith, 1989). The observed recombination efficiencies conferred by interspecies pairs of recA plus recBCD genes in E. coli had the order E. coli > S. marcescens > P. mirabilis (Fig. 3) and resembled the decrease of the repair capacities (Fig. 2).

An important result of this work was the observation that the potential of recombination (and repair) of several interspecies enzyme combinations was even lower than the lowest value obtained with the 'parental' intraspecies combinations. Specifically, the interspecies combinations recA<sub>Ec</sub> recBCD<sub>Pm</sub>, recA<sub>Sm</sub> recBCD<sub>Pm</sub>, recA<sub>Pm</sub> recBCD<sub>Ec</sub>, and recA<sub>Pm</sub> recBCD<sub>Sm</sub> all failed to reach the level obtained with the intraspecies combination of the two P. mirabilis enzymes (Fig. 3). The lower efficiencies cannot result from an insufficient expression of the P. mirabilis genes or a low activity of the P. mirabilis RecA protein or RecBCD enzyme produced in E. coli, because together they achieved a higher level of recombination than any of the interspecies combinations. Also, the genes of E. coli and S. marcescens were expressed sufficiently, because they, when combined with genes from the same species, produced high levels of recombination. Thus, if not the activity of the single enzyme components, what is the reason for the hampered recombination in interspecies systems? We suggest that the efficiency drop (in recombination and repair) of interspecies combinations reflects a decrease or the absence of a cooperation between RecA protein and the RecBCD enzyme which normally occurs between these enzymes of the same species. Presumably, this cooperation ensures efficient repair and recombination. It probably relies on species-specific protein-protein interactions. This is in agreement with the fact that bacterial RecA and RecBCD enzymes, although functionally similar and structurally related, have species-specific primary structures and/or biochemical properties (Akaboshi et al., 1989; Ball et al., 1990; Zhao & McEntee, 1990; Weichenhan & Wackernagel, 1989; Rinken et al., 1991).

The indication of a cooperation between the RecA protein and the RecBCD enzyme obtained in this study does not point to the mechanism of cooperation at work. However, on the basis of current models of the RecBCD pathway of recombination (Mahajan, 1988; Smith, 1988; Thaler & Stahl, 1988) and the biochemical activities of RecA protein and RecBCD enzyme one can envisage cooperative interactions between these enzymes at various steps during the recombination process. Formation of D-loops and the initiation of Holliday junctions are both catalysed by RecA protein (Radding, 1989). The processing of D-loops through cleavage by RecBCD enzyme has been demonstrated (Wiegand et al., 1977; DasGupta et al., 1979). Also the resolution of Holliday junctions is speculated to be catalysed by RecBCD enzyme (Thaler & Stahl, 1988; Taylor & Smith, 1990). If so, these reactions could involve an interaction of RecBCD enzyme with RecA protein either bound to single-stranded DNA in the D-loop or still present in the heteroduplex nucleoprotein filament, and this could stimulate recombinant formation (Radding, 1989). Similarly, if the RecBCD enzyme is involved in branch migration, as has been proposed by Kowalczykowski & Roman (1990), interactions between RecBCD and RecA proteins could facilitate recombination also by adjusting the high rate of DNA unwinding by RecBCD enzyme to the slow RecA-promoted strand transfer (Roman & Kowalczykowski, 1989a, b). An example of a species-specific interaction of recombination proteins has been provided by studies which showed the inability of RecA<sub>Pm</sub> protein to catalyse strand transfer in the presence of E. coli SSB protein and that the ATPase
activity of RecA<sub>p</sub>, but not of RecA<sub>p</sub>, protein is blocked by E. coli SSB protein (West et al., 1983). Further studies aimed at confirming the proposed cooperation of RecA and RecBCD enzymes by in vitro experiments are necessary.

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