

Trans-complementation by the RecB nuclease domain of RecBCD enzyme reveals new insight into RecA loading upon χ recognition

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Summary

The loading of RecA onto ssDNA by RecBCD is an essential step of RecBCD-mediated homologous recombination. RecBCD facilitates RecA-loading onto ssDNA in a χ -dependent manner via its RecB nuclease domain (RecBⁿ). Before recognition of χ , RecBⁿ is sequestered through interactions with RecBCD. It was proposed that upon χ -recognition, RecBⁿ undocks, allowing RecBⁿ to swing out via a contiguous 70 amino acid linker to reveal the RecA-loading surface, and then recruit and load RecA onto ssDNA. We tested this hypothesis by examining the interactions between RecBⁿ (RecB⁹²⁸⁻¹¹⁸⁰) and truncated RecBCD (RecB¹⁻⁹²⁷CD) lacking the nuclease domain. The reconstituted complex of RecB¹⁻⁹²⁷CD and RecBⁿ is functional *in vitro* and *in vivo*. Our results indicate that despite being covalently severed from RecB¹⁻⁹²⁷CD, RecBⁿ can still load RecA onto ssDNA, establishing that RecBⁿ does not function at the end of its flexible linker. Instead, RecBCD undergoes a χ -induced intramolecular rearrangement to reveal a RecA-loading surface.

Introduction

The repair of double-stranded DNA (dsDNA) breaks in wild-type *Escherichia coli* requires the functions of RecA and RecBCD proteins ^{1,2}. RecBCD is a heterotrimeric enzyme consisting of RecB, RecC, and RecD subunits ^{3,4}. In its constitutive state, it binds and unwinds from the broken dsDNA ends and simultaneously degrades the 3'-terminated strand at the entry site more extensively than the 5'-terminated strand ^{5,6}. However, the polarity and intensity of nuclease activity is reversed when RecBCD encounters a Chi (χ) sequence (5'-GCTCGTGG-3') ⁷⁻¹⁰. The stable binding of χ to the RecC subunit of RecBCD is suggested to prevent the χ -containing ssDNA from passing through the nuclease domain and possibly redirecting it through an alternative exit, resulting in preservation of 3'-ended χ -containing ssDNA ¹¹. RecBCD then facilitates RecA nucleofilament formation by loading RecA onto the χ -containing ssDNA ¹². The RecA nucleofilament subsequently searches for homologous DNA to promote DNA pairing ¹³. Subsequent maturation of recombination intermediates ensues to complete the repair process ².

The RecB subunit has two domains with distinct functions: a 100 kDa N-terminal helicase domain (RecB¹⁻⁹²⁷; hereafter referred to as RecB^h) and a 30 kDa C-terminal nuclease domain (RecB⁹²⁸⁻¹¹⁸⁰; hereafter referred to as RecBⁿ), connected by a 70 amino acid (aa) linker region (residues 858 to 927 of RecB) serving as a covalent tether between the two structural domains ^{3,14}. The 70 aa linker region is important for RecBCD activities ^{14,15}. Deletion of RecBⁿ from RecBCD results in a mutant enzyme that fails to load RecA after χ -recognition, suggesting that RecBⁿ plays an important role in RecA-loading ¹⁶; moreover, RecBⁿ physically interacts with RecA and the areas of RecBⁿ that can interact with the RecA core region were tentatively identified by computational modeling ¹⁷.

Prior to recognition of χ , RecBCD does not interact with RecA and the surface of RecBⁿ proposed to interact with RecA is buried by interaction with the RecC subunit ³. However, several studies indicate that the buried RecA-interacting region of RecBⁿ is revealed upon recognition of χ to facilitate RecA-loading ¹⁶⁻¹⁸. The discovery that RecB^hCD has helicase activity but no nuclease actively led to the proposal – the ‘nuclease domain swing model’ (Figure 1a) – that upon χ -recognition, RecBⁿ can swing away via its tether to elicit many of the changes occurring upon χ -recognition ¹⁴. Another

potential consequence of this tethered undocking would be exposure of the RecA-interacting region for subsequent RecA-loading^{4,15-17}.

Despite the prominence and value of the nuclease domain swing model, there are no studies showing that RecBⁿ is released upon χ -recognition and that the tether plays the important function of maintaining the RecA-loading domain within proximity of the χ -containing ssDNA. If the model is correct, then a RecBCD enzyme with a severed tether should lose RecBⁿ at χ , and loading of RecA would not ensue (Figure 1b). Here, we show that a functional RecBCD with a severed tether can be reconstituted from a truncated mutant of RecBCD (RecB¹⁻⁹²⁷CD) lacking the nuclease domain and a separated RecB nuclease domain (RecB⁹²⁸⁻¹¹⁸⁰): the severed reconstituted RecBCD complex contains all the residue of the wild-type enzyme but lacks a single peptide bond between amino acid residues 927 and 928. The resulting RecB^hCD-RecBⁿ complex responds to χ sequences, generates χ -containing ssDNA, and loads RecA onto the χ -containing ssDNA. *In vivo*, RecB¹⁻⁹²⁷CD and RecB⁹²⁸⁻¹¹⁸⁰ complement one another to reconstitute nuclease activity, repair UV-damaged DNA and promote χ -dependent recombination. Based on our results obtained from both genetic and biochemical analyses of RecB^hCD-RecBⁿ complex, we conclude that covalent tethering is not required for RecBCD functions, implying that RecBⁿ does not function at the free end of a flexible linker. Rather, we conclude that the RecA-interaction site of RecBⁿ is revealed through χ -induced conformational changes within the holoenzyme. We believe that the linker region plays an important role in RecBCD heterotrimer stability and it may serve to ensure the association of RecBⁿ with the helicase machinery of RecBCD.

Keywords

RecBCD, RecB nuclease domain, swing model, RecA loading, χ recognition, double-strand DNA break repair, homologous recombination.

Results

RecB^hCD forms a complex with RecBⁿ

We generated and purified a mutant of RecBCD that lacks the nuclease domain of RecB, and we designate it as RecB^hCD. To test whether the nuclease domain of RecB (RecBⁿ) can interact with this truncation of RecBCD, we performed a pull-down assay with 6x His-tagged RecBⁿ (^{His}RecBⁿ) ¹⁷ and un-tagged RecB^hCD. Ni-NTA beads retain protein with the 6x His-tag and, therefore, any un-tagged protein co-eluting with His-tagged protein demonstrates an interaction between the two. As shown in Figure 2a, RecB^hCD co-elutes with ^{His}RecBⁿ from the Ni-NTA beads only in the presence of ^{His}RecBⁿ. These results show that a complex is formed between RecB^hCD and ^{His}RecBⁿ.

We next performed a pull-down assay with varying the concentrations of RecB^hCD to measure the affinity between RecB^hCD and ^{His}RecBⁿ. The ratio of eluted [RecB^hCD]/[RecBⁿ] is plotted as a function of the total [RecB^hCD] in Figure 2b, and the data were analyzed with a nonlinear least square (NLLS) algorithm. The analysis yields an apparent dissociation constant (K_d) of $1.1 \pm 0.5 \mu\text{M}$, and the stoichiometry reaches a plateau value at 0.95 moles RecB^hCD per mole RecBⁿ. The affinity is comparable to the previous observation that RecBⁿ and RecA form a stable complex with an apparent K_d of $\sim 1 \mu\text{M}$ under the same conditions ¹⁷.

The RecB^hCD-RecBⁿ complex produces χ -specific ssDNA fragments

We next examined if this reconstituted complex of RecB^hCD and RecBⁿ is functional with regards to χ -recognition by studying whether it can generate χ -specific ssDNA fragments ⁷. The formation of χ -specific ssDNA fragments was assayed using a 4.4 kb linear dsDNA containing a triple- χ sequence in each strand and labeled with ³²P at both 5'-ends (Figure 3a, top panel) ¹⁹. At a sub-stoichiometric amount of enzyme relative to DNA ends (0.1 nM of enzyme and 2.3 nM DNA ends), different χ -specific ssDNA fragments are produced by wild-type RecBCD depending on which DNA end is the entry site (Figure 3a, top panel). RecB^hCD alone can only unwind dsDNA to produce full-length ssDNA, and it does not degrade the ssDNA product despite an increased enzyme concentration (Figure 3b). Like RecBCD, the complex formed between RecB^hCD and RecBⁿ produced χ -specific ssDNA when presented with χ^+ dsDNA (Figure 3a). Since RecBⁿ has a very low affinity for ssDNA ²⁰, it is very unlikely that RecBⁿ is simply binding and digesting the unwound ssDNA products independently of RecB^hCD. If so, the location of such binding would be random, and therefore, a broad range of

degraded ssDNA products should be produced instead of ssDNA products of a specific uniform length. Besides, RecBⁿ alone showed no degradation of linear dsDNA and ssDNA substrates (see last two lanes of Figure 6a).

The affinity of RecB^hCD for RecBⁿ increases in the presence of dsDNA and ATP

We next measured whether the binding affinity of RecB^hCD for RecBⁿ is affected by the presence of dsDNA and ATP. We measured χ -specific ssDNA production at varying concentrations of RecBⁿ while holding the concentration of RecB^hCD constant at 0.1 nM. Under the conditions where dsDNA ends are in large excess of RecB^hCD, all RecB^hCD as well as RecB^hCD-RecBⁿ complexes, are bound to the dsDNA ends. Therefore, the fraction of χ -containing fragments generated relative to the total amount of DNA equals to the ratio of RecB^hCD-RecBⁿ complex to RecB^hCD bound at the ends of dsDNA. Thus, we can monitor the formation of the RecB^hCD-RecBⁿ complex as a function of [RecBⁿ] and determine the binding affinity. Figure 4a shows a representative experiment. When the fraction of χ -specific ssDNA produced is plotted against total [RecBⁿ], a K_d of $0.4 \pm 0.1 \mu\text{M}$ is obtained from NLLS analyses of the data (Figure 4b). The affinity for RecB^hCD binding to RecBⁿ is increased by ~three-fold in the presence of dsDNA and ATP. Importantly, there is good agreement between the pull-down experiment and enzymatic assay.

RecB^hCD recognizes χ despite failure to produce χ -specific fragments

We have shown RecB^hCD alone cannot produce χ -specific ssDNA but can produce χ -specific ssDNA when it associates with RecBⁿ (Figure 3a and 3b). This suggests that RecBⁿ could play two possible roles within the reconstituted RecB^hCD-RecBⁿ complex. First, RecB^hCD alone may not recognize the χ sequence but association with RecBⁿ restores its ability to cleave the DNA up to the 3'-side of χ and then to recognize and attenuate at the χ site. Conversely, it is possible that RecB^hCD intrinsically recognizes χ , but it cannot produce χ -specific ssDNA due to lack of nuclease activity. To distinguish between these two possibilities, we next examined whether RecB^hCD can recognize χ or not.

Previous studies have established that the recognition of χ , under conditions of limiting free $[\text{Mg}^{2+}]$, inhibits DNA unwinding by RecBCD²¹. The time-course of unwinding reaches an apparent plateau at less than the total amount of dsDNA present. This apparent inhibition is reversed by the addition of excess Mg^{2+} , resulting in a burst of

unwinding activity, and nearly complete dsDNA unwinding. This results in a distinctive biphasic time-course of unwinding, which is a characteristic behavior of χ -recognition. When χ is absent (χ^0), neither inhibition at low $[\text{Mg}^{2+}]$ nor significant biphasic kinetics occur. We performed the same assay to determine whether RecB^hCD exhibits the same χ -dependent reversible inhibition of dsDNA unwinding. The fraction of DNA unwound was obtained from quantification of gels, and the time courses are plotted in Figure 5. The amount of χ -containing DNA unwound by both RecBCD and RecB^hCD in 1 mM $\text{Mg}(\text{OAc})_2$ reaches the same apparent plateau at 40 min. However, upon addition of excess Mg^{2+} to a final concentration of 10 mM, the unwinding rate increased in both cases, indicating that both RecBCD and RecB^hCD recognize the χ sequence. Thus, RecB^hCD has the intrinsic capacity to recognize χ , and RecBⁿ has no obligatory role in χ -recognition by the RecB^hCD-RecBⁿ complex; RecBⁿ however is essential for nuclease activity and the related χ -specific ssDNA formation. This finding is in full agreement with earlier studies for RecBC, lacking RecD, enzyme²¹.

The RecB^hCD-RecBⁿ complex facilitates χ -dependent RecA-loading

RecBⁿ is essential for the RecA-loading process¹⁶. So, although the reconstituted RecB^hCD-RecBⁿ complex produced χ -specific ssDNA fragments, whether it could load RecA onto that ssDNA needed to be determined. Consequently, we measured RecABCD-dependent joint molecule formation by RecBCD, RecB^hCD, and RecB^hCD-RecBⁿ enzymes as described previously^{7,12}. The results show that formation of RecA-dependent, χ -dependent joint molecules (the faster migrating “ χ -dep” joint molecules in Figure 6a) by the RecB^hCD-RecBⁿ complex is similar to that of the wild-type RecBCD enzyme. In contrast, RecB^hCD alone failed to produce χ -dependent joint molecules and produced only χ -independent joint molecules (from the full-length ssDNA products of unwinding) at a slower rate as previously observed^{7,12}. The yields of χ -dependent joint molecule formed after 10 minutes were $14.4 \pm 1.4\%$ and $13.4 \pm 1.1\%$ of the input linear dsDNA substrate for wild-type RecBCD and RecB^hCD-RecBⁿ enzymes, respectively (Figure 6b). RecB^hCD alone produced χ -independent joint molecules ($4.0 \pm 0.4\%$ at 10 minutes); this slower rate is comparable to that of mutant RecBCD enzymes that lack RecA-loading function^{16,19}. Incubation of RecBⁿ domain alone with linear dsDNA or with ssDNA for 10 min showed no effect (Figure 6a, last two lanes). These findings affirm that the RecB^hCD-RecBⁿ complex is capable of loading RecA onto the χ -containing ssDNA,

and importantly, that the covalent attachment – tethering –between the RecB helicase and RecBⁿ domains is not necessary for the RecA-loading process

The RecB^hCD-RecBⁿ complex is DNA repair and nuclease proficient *in vivo*

To corroborate our *in vitro* findings, we determined the *in vivo* proficiency of RecB^hCD-RecBⁿ with regards to its DNA repair function by measuring sensitivity to ultraviolet (UV) irradiation, and to its nuclease activity by measuring infectivity of T4 2⁻ phage. Cells expressing RecB^hCD-RecBⁿ, RecB^hCD, and wild-type RecBCD proteins on plasmids in a *recBCD* null strain were compared. As shown in Figure 7, cells expressing RecB^hCD protein alone are highly UV sensitive, comparable to the strain that lacks *recBCD* genes (Figure 7). Interestingly, co-expression of RecBⁿ and RecB^hCD proteins alleviated the UV sensitivity: the ability to repair the UV-induced DNA damage is comparable to the cells that are expressing wild-type RecBCD protein. This result suggests that the RecB nuclease domain is indeed capable of interacting *in trans* with RecB^hCD enzyme *in vivo* and protecting cells from UV-induced DNA damage.

If the RecB nuclease domain interacts with RecB^hCD *in vivo*, then it is expected to have nucleolytic activity. To determine whether the RecB^hCD-RecBⁿ complex has nucleolytic activity, we assayed T4 2⁻ phage sensitivity. Wild-type T4 phage with a functional gene 2 product is resistant to RecBCD-dependent DNA degradation due to the protection afforded by the binding of gene 2 protein to dsDNA ends of T4 phage DNA. However, T4 2⁻ phages lacking gene 2 product make plaques only on the strain lacking RecBCD nuclease activity. Table 1 shows plaque formation by T4 2⁻ in different backgrounds. In the strain expressing RecB^hCD and RecBⁿ proteins, viability T4 2⁻ phage is decreased by almost a thousand-fold compared to the strain expressing RecB^hCD alone and is reduced only ~10-fold compared to wild-type RecBCD. These results further confirm the ability of RecBⁿ to associate *in trans* with RecB^hCD *in vivo* to confer exonucleolytic activity to the cells.

The RecB^hCD-RecBⁿ complex promotes γ -stimulated homologous recombination *in vivo*.

We further investigated the functionality of the RecB^hCD-RecBⁿ complex *in vivo* by measuring γ -stimulated recombination between λ *red gam* phages which lack both the RecBCD-inhibiting Gam protein, and the λ recombination system, Red²². Cells expressing RecB^hCD-RecBⁿ complex showed a ~10-fold increase in λ recombinants and

a ~4-fold higher γ -stimulated crossover activity compared to the cells expressing RecB^hCD alone (Table 2); these values approach those of wild-type RecBCD. These results further confirm that the RecBⁿ indeed interacts with RecB^hCD *in vivo* to reconstitute a holoenzyme that is functional for γ -stimulated recombination in cells.

Discussion

RecBCD enzyme plays an essential role in the recombinational DNA repair of dsDNA breaks in *E. coli*. It is a multifunctional enzyme that initiates the DSB repair by nucleolytically processing the DSB. Its DNA resection activity serves as a prototype for dsDNA processing and mediator function in all organisms. Homologs or analogs specifically involved in resection exist in all organisms: in Eukaryotes, the Sgs1-Dna2-RPA-Top3-Rmi1 complex in *Saccharomyces cerevisiae* and the BLM-DNA2-RPA-TOP3 α -RMI-RMI2 complex in humans comprise functional analogs of the χ -activated RecBCD complex^{2,23-25}.

RecBCD also possesses another essential activity: it mediates the delivery of RecA onto ssDNA that is complexed with SSB. This loading of RecA by RecBCD in response to χ -activation is a crucial step of recombinational dsDNA break repair; however, the detailed mechanism by which this occurs is not fully understood. RecBCD enzyme, specifically the nuclease/RecA-loading domain, is known to interact with RecA and to load RecA onto ssDNA, but only after recognition of χ . The isolated nuclease domain of RecB interacts directly with RecA and regions potentially responsible for such interactions were identified¹⁷. Before recognition of χ , the RecA-interacting surface on RecBⁿ is occupied through the interactions with the RecC subunit³. In response to χ , by an unspecified structural mechanism, the concealed RecA-interacting interface of RecBⁿ is revealed to facilitate RecA-loading onto ssDNA^{12,16,17,26}.

One model, the ‘nuclease domain swing model’, described in the Introduction, proposed that upon χ -recognition, conformational changes in RecBCD liberate RecBⁿ from its binding site on RecC resulting in the exposure of the RecA-interacting surface of RecBⁿ. The 70 aa linker was envisioned to tether the loading-domain in proximity to the newly generated ssDNA (Figure 1a-(iii)). RecA then interacts with RecBⁿ and is nucleated on the χ -containing ssDNA (Figure 1a-(iv))^{4,14-17}. A prediction of the simplest form of this model is that without a tether, if RecBⁿ were to be released, none of the RecBⁿ-dependent events downstream of χ -recognition would occur.

We examined this model by severing the link between RecB^hCD and RecBⁿ. We discovered that we could reconstitute the activities of wild-type RecBCD, despite the absence of a contiguous covalent linker. Pull-down experiments showed that the RecB^hCD forms 1:1 complex with RecBⁿ in the absence of DNA with an affinity, similar to that observed between RecA and RecBⁿ ($K_d \sim 1 \mu\text{M}$)¹⁷. In the presence of dsDNA and

ATP, the affinity between RecB^hCD and RecBⁿ increases slightly ($K_d = 0.4 \pm 0.1 \mu\text{M}$). As is evident from the enzymatic assays and consistent with the equilibrium binding constant, RecB^hCD is predominantly free and not bound to RecBⁿ until concentrations greater than $\sim 0.4 \mu\text{M}$ (e.g., see Figure 4), suggesting that a function of the linker is to ensure interaction of nuclease and RecA-loading domain with the RecBCD holoenzyme by creating a unimolecular species of RecB^h and RecBⁿ.

Unexpectedly, we discovered that the reconstituted complex formed between RecB^hCD and RecBⁿ can process χ -containing dsDNA to produce χ -specific ssDNA as does wild-type RecBCD enzyme. Also, the reconstituted RecB^hCD-RecBⁿ complex is RecA-loading proficient like the wild-type RecBCD enzyme. Hence, the interactions between RecBⁿ and RecB^hCD are functional and sufficient for producing χ -specific ssDNA and RecA-loading. This conclusion is supported by *in vivo* observations of decreased plaque formation of T4 2 γ phage in RecB^hCD-RecBⁿ expressing strain, showing that RecBⁿ and RecB^hCD form an active nuclease complex in cells. Furthermore, the RecB^hCD-RecBⁿ complex showed χ -dependent crossover hotspot activity in classical lambda phage crosses, confirming reconstitution of a functional RecBCD complex. These physiological measurements are slightly reduced compared to wild-type RecBCD, implying incomplete saturation of RecB^hCD with RecBⁿ, again consistent with a function of the tether being to produce a single polypeptide comprising RecB^hCD and RecBⁿ rather than relying on bimolecular complex formation.

However, our findings that RecB^hCD and RecBⁿ can reconstitute typical RecBCD functions is in contradiction with the swing-model for RecA loading. Specifically, the results show that an intact covalent tether is unnecessary; thus, RecBCD has reorganized itself after χ -recognition and the RecA interaction site of RecBⁿ was revealed without covalent tethering. Thus, in contrast to the prevailing model, non-covalent interactions between RecBⁿ and RecB^hCD play an important role in the association of RecBⁿ with the rest of the enzyme even after recognition of χ . Based on our results, we propose that χ recognition causes conformational changes in both the RecBⁿ and RecB^hCD proteins. As a result, rather than swinging freely as a ball on a tether, RecBⁿ functions while remaining attached to the rest of the enzyme but in a different conformation. These unexpected findings raise the question of what is the function of the 70-aa linker? Our attempts to purify truncated RecB proteins with shorter linkers (RecB¹⁻⁸⁶⁶ and RecB¹⁻⁸⁹⁸) revealed that the RecBCD heterotrimer was unstable, suggesting that

the linker is likely a “strap” that is important to the stability of the RecBC complex within the heterotrimer.

Consequently, we propose a new model of RecA-loading by RecBCD in response to χ . RecBCD unwinds and degrades the duplex DNA from the DNA end (Figure 8(i)). Before the recognition of χ , the RecBⁿ remains associated with the RecC subunit, and the RecA-loading surface is concealed (Figure 8(ii)). RecBCD recognizes χ and the recognition of χ induces conformational changes in RecBCD causing rearrangement of interactions with the RecA-loading domain, RecBⁿ (Figure 8(iii)). These structural rearrangements both reveal the RecA-interaction interface and modify the degradative focus of RecBⁿ to produce 3'-ended, χ -containing ssDNA and facilitate RecA-loading on to it (Figure 8-(iv)).

Acknowledgements

We would like to thank Drs. Gerald Smith and Susan Amundsen of Fred Hutchinson Cancer Research Center, Seattle, USA for generously providing the strains and phages for the *in vivo* nuclease and recombination assays. These studies were supported by NIH grant R35 GM131900 to S.C.K.

Authors contributions

S.C.K., and M.S. conceived the study. S.C.K., M.S., J.W., and T.L.P. designed experiments. Experiments were performed by J.W., and T.L.P. and Y.K.W. assisted T.L.P. in genetic experiments. T.L.P., J.W., and S.C.K. analyzed the data and wrote the manuscript. S.C.K. acquired funding and supervised the project.

Declaration of interests

The authors declare no competing interests.

Inclusion and diversity statement

We support inclusive, diverse, and equitable conduct of research.

Figure legends

Figure 1. Illustration of the ‘nuclease domain swing model’ for RecBCD. (a) Upon recognition of the χ sequence, the nuclease domain is released to enable the subsequent loading of RecA onto a newly generated χ -containing ssDNA. (i) RecBCD binds to a duplex DNA end. (ii) The duplex DNA is unwound by the slow and fast motors (RecB and RecD respectively) of RecBCD. The nuclease domain preferentially degrades 3'-ended ssDNA-strand over the 5'-ended ssDNA-strand. The RecA-interacting region of the RecB nuclease domain is concealed through the interactions with the RecC subunit. (iii) χ recognition by RecBCD releases the RecB nuclease domain, revealing the RecA-interacting interface of RecBⁿ. RecA now interacts with RecBⁿ. (iv) RecBCD nucleates RecA onto the χ -containing ssDNA and the RecA-ssDNA filament grows. (b) Illustration of expected outcome of the nuclease swing model for an altered RecBCD with a severed tether. (i) RecB^hCD and RecBⁿ form a stable complex and the complex binds to a duplex DNA end. (ii) The RecB^hCD-RecBⁿ complex unwinds and degrades duplex DNA similar to wild-type RecBCD; the RecA-interacting interface of RecBⁿ is concealed. (iii) Upon recognition of χ , the interaction between RecB^hCD and RecBⁿ is reduced, causing RecBⁿ to detach and swing out from the rest of the enzyme. (iv) As a result, no loading of RecA onto χ -specific ssDNA is observed.

Figure 2. RecB^hCD forms a stable complex with RecBⁿ. The pull-down assay was performed using ^{His}RecBⁿ and RecB^hCD, as described in STAR methods. (a) A representative pull-down experiment; incubation, wash and elution aliquots were analyzed using 12% SDS-PAGE. ^{His}RecBⁿ and RecB^hCD (1 μ M each) were incubated with Ni-NTA beads, and an aliquot was removed at the end of incubation and loaded onto Lane 1. Lane 2 is the 3rd wash of the Ni-NTA beads with interaction buffer, and Lane 3 is the elution of Ni-NTA beads with 300 mM imidazole. A control was performed in the absence of ^{His}RecBⁿ by incubating Ni-NTA beads with RecB^hCD (2 μ M), and the incubation, wash and elution aliquots were loaded onto Lanes 4, 5, and 6, respectively. The RecB^hCD and ^{His}RecBⁿ markers represent the equivalent of 2 μ M and 1 μ M, respectively. (b) Determining the binding affinity of RecB^hCD for RecBⁿ. Pull-down assays were performed with 0.5 μ M ^{His}RecBⁿ and increasing amounts of RecB^hCD. The

ratio of RecB^hCD to ${}^{\text{His}}\text{RecB}^n$ eluted from the bead was plotted as a function of total $[\text{RecB}^h\text{CD}]$. The solid line is a simulation using equation (2) and K_d of $1.1 \pm 0.5 \mu\text{M}$.

Figure 3. The reconstituted complex of RecB^hCD and RecB^n recognizes χ and produces χ -specific ssDNA fragments. (a) dsDNA ($10 \mu\text{M}$ nt) with χ (χ^+) or without χ (χ^0) was reacted with either 0.1 nM RecBCD or $0.1 \text{ nM RecB}^h\text{CD}$ plus $1 \mu\text{M RecB}^{\text{nuc}}$. (b) dsDNA ($10 \mu\text{M}$ nt), χ^+ or χ^0 , was reacted with various concentrations of RecB^hCD . The location of the triple- χ sequence on the dsDNA is indicated in the inset and the asterisk (*) indicates the position of the $\gamma^{32}\text{P}$ label.

Figure 4. The affinity of RecB^n for RecB^hCD is increased in the presence of dsDNA and ATP. χ -specific ssDNA production was performed with $0.1 \text{ nM RecB}^h\text{CD}$, $20 \mu\text{M}$ (nt) χ^+ DNA and varying amounts of RecB^n . A representative experiment is shown in (a). The fraction of χ -specific ssDNA produced was quantified and plotted as a function of the total $[\text{RecB}^n]$ in (b). Data were analyzed (as described in STAR Methods) and yield an apparent K_d of $0.4 \pm 0.1 \mu\text{M}$. The solid line is a simulation using equation (4) and $K_d = 0.4 \mu\text{M}$.

Figure 5. RecB^hCD recognizes χ as shown by reversible inactivation of dsDNA unwinding upon χ recognition. Either χ^0 or χ^+ DNA ($10 \mu\text{M}$ nt) was reacted with 0.1 nM RecBCD or $0.2 \text{ nM RecB}^h\text{CD}$. Aliquots were removed at the times indicated, and excess Mg^{2+} was added after 40 min (indicated by arrows) to a final concentration of 10 mM . Comparison of the time courses of the fraction of DNA unwound by RecBCD with that of RecB^hCD is shown. Data are the mean \pm SEM from two independent experiments.

Figure 6. $\text{RecB}^h\text{CD-RecB}^n$ loads RecA onto χ -containing ssDNA to form χ -specific joint molecule. (a) The χ -dependent (χ -dep) and χ -independent (χ -indep) joint molecules (JM) formed, and the χ -specific ssDNA fragments produced as a function of time. C_1 and C_2 are control lanes with 5'-labeled linear dsDNA and ssDNA (heat-denatured dsDNA), respectively. The last two lanes are the reaction mixtures containing linear dsDNA and ssDNA with RecB^n alone. (b) Percentage of joint molecules formed relative to the input of linear dsDNA are plotted. Data points are the percentage of joint molecules formed by

RecBCD (circles), RecB^hCD-RecBⁿ (triangles), and RecB^hCD (rectangles) proteins. Data are the mean \pm SEM from three independent experiments.

Figure 7. Co-expression of RecB^hCD and RecBⁿ proteins confers DNA repair proficiency to *E. coli* cells. A *recBCD* null strain expressing wild-type RecBCD, RecB^hCD, RecB^hCD-RecBⁿ proteins was subjected to UV irradiation. Percentage of cells surviving at various doses of UV irradiation are compared. Error bars of some data-points are minimal, hence not visible on the graph. Data are the mean \pm SEM from the three independent experiments.

Figure 8. Model illustrating the prospective mechanism of χ -dependent RecA-loading by the RecBCD enzyme and double-strand break repair. (i) RecBCD binds to a duplex DNA end. (ii) The slow motor (RecB) and the fast motor (RecD) unwind duplex DNA. The differential translocation speed between two motor creates a loop ahead of slow RecB motor. The unwound duplex DNA is degraded by RecB nuclease domain, and the 3'-end ssDNA is preferentially degraded over the 5'-ended ssDNA. (iii) RecBCD recognizes the χ sequence, and χ remains transiently bound to the RecC subunit. The χ -induced conformational changes in RecBCD leads to domain rearrangements of RecB nuclease while remaining attached to the rest of the RecBCD enzyme. (iv) The structural rearrangements affecting RecBⁿ cause attenuation of nuclease activity leaving χ -containing ssDNA with the χ sequence at the 3'-end and reveal the RecA-interacting interface to load RecA onto the χ -containing ssDNA. (v) After RecA nucleation, growth of the RecA filament needed for the homology search ensues.

Table 1: Exonuclease activity of RecBCD mutants *in vivo*.

<i>E. coli</i> strain	T4 phage titer ^a	T4 2 ⁻ phage titer ^a
AB1157 (WT)	0.8 ± 0.1	1.8 ± 0.1 × 10 ⁻⁴
ΔrecCBD::FRT	1	1
ΔrecCBD::FRT (pRecBCD)	1.0 ± 0.1	2.5 ± 0.3 × 10 ⁻⁴
ΔrecCBD::FRT (pRecB ¹⁻⁹²⁷ CD)	2.0 ± 0.1	1.1 ± 0.1
ΔrecCBD::FRT (pRecB ¹⁻⁹²⁷ CD & pRecB ⁿ)	0.8 ± 0.2	2.9 ± 1.7 × 10 ⁻³

^aRelative values: T4 wild-type or T4 2⁻ phage titers from the indicated strains are divided by the titer on ΔrecCBD::FRT strain. Data are the mean ± SEM from three independent experiments.

Table 2: Recombination proficiency and χ activity of the RecBCD mutants *in vivo*.

Strains	λ Recombinant frequency (J ⁺ R ⁺ recombinants, %)		χ activity
	Cross 1	Cross 2	
	(1081 x 1082)	(1083 x 1084)	
AB1157 (WT)	8.7 ± 0.6	7.7 ± 0.6	5.1 ± 0.1
ΔrecCBD::FRT	0.1 ± 0.01	0.2 ± 0.05	1.1 ± 0.1
ΔrecCBD::FRT (pRecBCD)	8.7 ± 0.01	7.9 ± 0.3	5.7 ± 0.9
ΔrecCBD::FRT (pRecB ¹⁻⁹²⁷ CD)	0.9 ± 0.2	0.7 ± 0.4	1.5 ± 0.2
ΔrecCBD::FRT (pRecB ¹⁻⁹²⁷ CD & pRecB ⁿ)	7.2 ± 0.7	6.9 ± 0.04	4.1 ± 0.3

Data are the mean ± SEM from two independent experiments.

STAR Methods

Key resources table

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Bacterial and phage strains		
AB1157 (Wild-type)	<i>E. coli</i> Genetic Resources at Yale CGSC, The Coli Genetic Stock Center	CGSC#: 1157
BW25113	<i>E. coli</i> Genetic Resources at Yale CGSC, The Coli Genetic Stock Center	CGSC#: 7636
AB1157, but Δ recCBD:: FRT	This study	N/A
V330	Smith, G. R. ²⁷	N/A
594	Smith, G. R. ²⁸	N/A
C600	Smith, G. R. ²⁸	N/A
λ 1081	Smith, G. R. ²⁸	N/A
λ 1082	Smith, G. R. ²⁸	N/A
λ 1083	Smith, G. R. ²⁸	N/A
λ 1084	Smith, G. R. ²⁸	N/A
T4 phage	Smith, G. R. ²⁸	N/A
T4 2 ⁺	Smith, G. R. ²⁸	N/A
Chemicals and recombinant proteins		
ATP disodium, crystalline	Cytiva (formerly known as GE Healthcare life sciences)	CAT#27100603
Adenosine 5'-O-(3-Thiophosphate), Tetralithium Salt (ATP γ S)	Millipore Sigma	CAT#119120-25MG
ATP, [γ - ³² P] 6000Ci/mmol 10mCi/ml EasyTide, 250 μ Ci	PerkinElmer	CAT# BLU502Z250UC
Phosphoenol-pyruvate	Roche	CAT#10108294001
EcoRI-HF	NEB	CAT#R3101S
Ncol	NEB	CAT#R0193S
Ndel	NEB	CAT#R0111S
SexAI	NEB	CAT#R0605S
XbaI	NEB	CAT#R0145S
Klenow Fragment (3' – 5', exo $^{-}$)	NEB	CAT#M0212S
T4 Polynucleotide Kinase (T4 PNK)	NEB	CAT# M0201S
L-Lactic dehydrogenase from rabbit muscle	Sigma-Aldrich	CAT#L2500-5KU
Pyruvate Kinase from rabbit muscle	Sigma-Aldrich	CAT#P1506-50KU
Proteinase K, recombinant, PCR grade	Roche	CAT#03115828001
USB [®] Shrimp alkaline phosphatase	Affymetrix	CAT#70092Z
Ampicillin sodium salt	Sigma-Aldrich	CAT#A9518-25G
Chloramphenicol	Sigma-Aldrich	CAT#C0378-25G
Kanamycin sulfate from <i>Streptomyces kanamyceticus</i>	Sigma-Aldrich	CAT#K1377-5G

Streptomycin dihydrochloride pentahydrate	Sigma-Aldrich	CAT#S9007-5G
Oligonucleotides (primers are described in the plasmid construction section)		
Recombinant DNA		
pBR322	NEB	CAT#N3033S
pBR322-3F3H	Kowalczykowski, S. C. ¹⁸	N/A
pPB520	Emmerson, P. T. ²⁹	N/A
pMS421	Weinstock, G. M. ³⁰	N/A
pPB800	Emmerson, P. T. ²⁹	N/A
pPB800-TAAs	This study	N/A
pKD46	<i>E. coli</i> Genetic Resources at Yale CGSC, The Coli Genetic Stock Center	N/A
pKD3	Addgene	CAT#45604
pET15b-30	Julin, D. A. ³¹	N/A
pGL10	Ray, M. K. ³²	N/A
pGB ^{nuc}	This study	N/A
Software and algorithms		
Gel pro analyzer	Media Cybernetics	https://mediacy.com
ImageQuant software	Cytiva	https://www.cytivalifesciences.com/
Scientist 3.0	Micromath Scientist	N/A
Prism 5.0	GraphPad	https://www.graphpad.com/
Image J	NIH.GOV	https://imagej.nih.gov/ij
Other		
Bio-Spin® Columns, Bio-Gel® P-30	BIO-RAD	CAT#7326231
Ni-NTA Magnetic Agarose Beads	QIAGEN	CAT#36113

Lead contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead contact, Stephen C. Kowalczykowski (sckowalczykowski@ucdavis.edu).

Materials availability

No restrictions for use of materials from this study.

Experimental model and subject details

Bacterial strains and phages

The following *Escherichia coli* strains were used in the experiments as described in the method details. AB1157 cells as wildtype, the *recCBD* operon deleted AB1157

(Δ recCBD::FRT), V330 (Δ (recC-argA) 234 $\lambda^- F^-$)²⁷, 594 (*lac*-3350 *galK2 galT22 rpsL179* $\lambda^- F^-$), and C600 (*thr-1 leuB6 thi-1 lacY1 tonA21 supE44 rfbD1* $\lambda^- F^-$)²⁸. The following phage strains were also used in the study. λ 1081 (*susJ6 b1453 cl857* $\chi^+ D123$), λ 1082 (*b1453* $\chi^+ D123 susR5$), λ 1083 (*susJ6 b1453* $\chi^+ 76 cl857$), λ 1084 (*b1453* $\chi^+ 76 susR5$), T4 phage (gene 2⁺), and T4 2⁺ (gene 2 *amN51*). All the phages were generous gifts from Gerald R. Smith²⁸.

Buffers and Reagents

Buffers were made from reagent grade chemicals with Milli-Q water. ATP (Cytiva, USA) and ATP γ S (Millipore Sigma, USA) stocks were adjusted to pH 7.5, and concentration was determined spectrophotometrically using $\epsilon_{260} = 1.54 \times 10^4 \text{ M}^{-1} \text{ cm}^{-1}$.

Method details

Purification of proteins

6x His-tagged RecBⁿ (^{His}RecBⁿ) was purified as described¹⁷. The plasmid for overexpression of RecB¹⁻⁹²⁷ and RecD was made by replacing bases 960 to 965 of pPB800²⁹ with two TAA stop codons, and this plasmid is then transformed into a Δ recCBD *E. coli* strain V330²⁷ carrying pPB520 (*recC*⁺)²⁹ and pMS421 (*lacI*^q)³⁰. This strain was grown, lysed, and RecB^hCD was purified chromatographically in the same way as wild-type RecBCD as described previously³³. We also generated two longer truncations of the RecB nuclease domain to generate RecB¹⁻⁸⁶⁶ and RecB¹⁻⁸⁹⁸. We expressed them together with RecC and RecD subunits as was done for the RecB¹⁻⁹²⁷ truncation. However, we failed to purify stable heterotrimeric RecBCD complexes with these longer deletions, despite clear expression of all the subunits.

Both RecB^hCD and ^{His}RecBⁿ are stored in buffer B (20 mM Tris-HCl, pH 7.5, 0.1 mM EDTA, 0.1 mM DTT, 100 mM NaCl, 50% (v/v) glycerol) at -80°C. RecB^hCD and ^{His}RecBⁿ have extinction coefficients of $\epsilon_{280} = 4.2 \times 10^5 \text{ M}^{-1} \text{ cm}^{-1}$ and $4.6 \times 10^4 \text{ M}^{-1} \text{ cm}^{-1}$ in buffer B, respectively. These values are determined by comparing the absorbance spectra of aliquots of protein in buffer B to spectra taken in 6 M guanidinium-HCl. The extinction coefficients of either RecB^hCD or ^{His}RecBⁿ in 6 M guanidinium-HCl at 280 nm was calculated from the amino acid sequence as described³⁴. RecA and SSB were purified as described³⁵.

Preparation of DNA substrates

DNA substrate χ^0 was prepared from circular plasmid pBR322, while χ^+ DNA was prepared from pBR322 3F3H, (a pBR322 derivative with two sets of three tandem χ -sequences) ¹⁹. These circular plasmid DNA were purified by cesium chloride density gradient centrifugation ³⁶. The molar concentration of DNA was determined using an extinction coefficient of $6290 \text{ M}^{-1} \text{ cm}^{-1} \text{ nt}^{-1}$ at 260 nm. Plasmid DNA was linearized using NdeI (NEB, Ipswich, MA) and radioactively labeled at the 5'-end by sequential reaction with shrimp alkaline phosphatase (USB Corp, Cleveland, OH) and T4 polynucleotide kinase (NEB, Ipswich, MA) and [γ -³²P] ATP (Perkin Elmer, Wellesley, MA) followed by purification with P30 BioSpin columns (Bio-Rad, Hercules, CA). 3'-labeling was performed by adding Klenow fragment (exo⁻) of Polymerase I (NEB, Ipswich, MA) and [α -³²P] ATP (Perkin Elmer, Hopkinton, MA) to the linearized DNA and purified as described above.

Generation of Δ recCBD strain of *E. coli* and plasmid constructions:

Generation of Δ recCBD::FRT (flipase recognition target (FRT)) AB1157

strain: For the generation of Δ recCBD::FRT AB1157 strain ³⁷, the homologous regions of *recC* and *recD* genes (underlined), along with the chloramphenicol acetyltransferase gene (*cat*) of pKD3 plasmid was PCR amplified using the forward primer, 5'-
GCTGGTGGAATATAACCCATCAACTCGGGCAACCGCGCTGGCACCGCGCCAATCTC
GTGTAGGCTGGAGCTGCTTC-3' and reverse primer 5'-
GAGCTTCCTCAAGCATCGCAATATAATCTCGCCGCTCTGAAAAGCCGTTTCGC
ATATGAATATCCTCCTTAG -3'. The purified PCR product was then transformed into a BW25113 strain carrying pKD46 plasmid ³⁷. The P1 lysate of BW25113 transformants were later transduced into AB1157 cells. The *cat* gene was removed by FLP recombinase to obtain AB1157 Δ recCBD::FRT strain as described by Daysenko and Wanner method of one-step inactivation of genes in *E. coli* ³⁷.

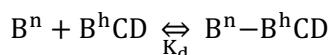
Construction of pPB800-TAAs: A 1.2 kb region of *recB* gene was PCR amplified using a forward primer 5'-
CGCTGGCAACGCCCTATTAAATCGACATCCAGCCG-3' and a reverse primer 5'-
CGGCTGGATGTCGATTAAAGGCGTTGCCAGCG-3' containing two stop codons at the 928th and 929th positions of *recB* gene. The PCR amplified region was digested with Ncol and SexAI enzymes and cloned into the Ncol and SexAI digested pPB800 vector (pKK223-3 based *recB* and *recD* overexpression plasmid ²⁹) to obtain pPB800-TAAs plasmid. The pPB800-TAAs contains two TAA stop codons in the places of 928th and

929th amino acids of RecB. It expresses the RecB¹⁻⁹²⁷ and RecD polypeptides without RecBⁿ domain. We also constructed vectors for expressing RecB¹⁻⁸⁶⁶ and RecB¹⁻⁸⁹⁸ truncated RecB proteins using following primers. RecB-866 forward primer – 5'-GTTGCCAGGCAATTATTAATCGCATAACGCTTC-3' and RecB-866 reverse primer – 5'-GAAGCGTTATGCGATTAATAAATTGCCTGGCAAAC-3'; RecB-898 forward primer- 5'-CAACGATTGCCCGGCTATGATGGCGCGTCACCAGC-3' and RecB-898 reverse primer 5'-GCTGGTGACGCCATCATTAGCCGGCAATCGTTG-3'. The DNA sequencing was performed to confirm the integrity of the DNA sequence and presence of stop codons.

Construction of pGB^{nuc}: The XbaI-EcoRI restriction digested 1.2 kb DNA fragment containing RecBⁿ gene from the pET-15b-30 vector³¹ was cloned into a low copy number plasmid pGL10 vector³² at the XbaI-EcoRI sites. DNA sequencing was performed to confirm the integrity and presence of RecBⁿ gene, and expression of RecBⁿ was also confirmed.

Protein-protein interaction assays using Ni-NTA magnetic beads

Ni-NTA magnetic beads (QIAGEN, Valencia, CA) were used to study the interactions between ^{His}RecBⁿ and RecB^hCD as described¹⁷. RecBⁿ (0.5 μM) was incubated with various amounts of RecB^hCD at the indicated conditions in 50 mM Tris-acetate pH 7.5, 50 mM NaCl, 50 mM imidazole, 0.2% Triton X-100 for 15 min. Ni-NTA beads were added to a final concentration of 1%, and the beads were immobilized, washed, and eluted as described¹⁷. Eluted fractions were analyzed on 12% SDS-PAGE, followed by staining with Coomassie brilliant blue and quantified on a Gel Pro Analyzer (Media Cybernetics, Bethesda, MD). The amount of protein eluted was calculated by comparison to known quantities of each protein. The binding isotherm was analyzed by assuming one RecBⁿ binds to one RecB^hCD as described in Scheme 1:



Scheme 1

where Bⁿ represents RecBⁿ, and B^hCD stands for RecB^hCD. The dissociation constant K_d is defined in the equation (1):

$$K_d = \frac{[B^n][B^hCD]}{[B^n - B^hCD]} \quad (1)$$

Since RecB^hCD can only bind to the Ni-NTA beads when it forms a complex with the His⁺RecBⁿ, the amount of RecB^hCD eluted from the Ni-NTA beads equals the amount of RecB^hCD-RecBⁿ complex formed. The ratio of [RecB^hCD-RecBⁿ] to total [RecBⁿ] is given in equation (2):

$$\frac{[B^n - B^hCD]}{B_T^n} = \frac{K_d (1 + B_T^n + B^hCD_T) - \sqrt{(K_d + B_T^n - B^hCD_T) + 4K_d B^hCD_T}}{2B_T^n} \quad (2)$$

where Bⁿ_T and B^hCD_T stand for the total concentrations of RecBⁿ and RecB^hCD, respectively. Data were analyzed by nonlinear least square (NLLS) analysis using Scientist (Micromath, St. Louis, MO) and equations (1) and (2) to determine K_d.

χ-specific ssDNA formation assay

χ-specific ssDNA formation assay were performed by mixing 10 μM (nts) radioactively labeled dsDNA, 0.1 nM RecBCD (or 0.1 nM RecB^hCD plus 1 μM RecBⁿ) and 1 μM SSB in 25 mM Tris-acetate, pH 7.5, 10 mM Mg(OAc)₂ unless noted otherwise. This mixture was incubated at 37°C for 3 min, and the reaction is initiated by addition of ATP to 5 mM. 10 μL aliquots were removed at each specified time points and quenched with 65 mM EDTA followed by deproteinization with 2% (w/v) SDS and 1 mg/ml proteinase K (Roche, Indianapolis, IN). These were loaded onto a 1% agarose gel and run at 40 V for 16 hr. The gel was dried and exposed to a phosphor screen and quantified on a Storm phosphorImager (GE Healthcare, Piscataway, NJ).

The fraction of χ ssDNA produced $f_{Chi}(t)$ at time t was calculated using equation (3):

$$f_{chi}(t) = \frac{\frac{c_{Chi}(t)}{c_{ds}(t) + c_{ss}(t) + c_{chi}(t)} - \frac{c_{Chi}(0)}{c_{ds}(0) + c_{ss}(0) + c_{chi}(0)}}{1 - \frac{c_{Chi}(0)}{c_{ds}(0) + c_{ss}(0) + c_{chi}(0)}} \quad (3)$$

where $c_{Chi}(t)$, $c_{ds}(t)$ and $c_{ss}(t)$ are the counts of the bands corresponding to the χ ssDNA, dsDNA and ssDNA at time t , respectively. Since DNA is in excess, all the RecB^hCD-RecBⁿ complexes should be bound to dsDNA. Thus, the fraction χ ssDNA produced

should reflect the ratio of RecB^hCD - RecB^n complexes formed to total $[\text{RecB}^h\text{CD}]$. This relation can be expressed in terms of K_d , total $[\text{RecB}^n]$ and $[\text{RecB}^h\text{CD}]$ as given in equation (4):

$$f_{Chi}(t) = \frac{[\text{RecB}^n - \text{RecB}^h\text{CD}]}{[\text{RecB}^h\text{CD}]_{total}} = \frac{K_d(1 + B_T^n + B^h\text{CD}_T) - \sqrt{(K_d + B_T^n - B^h\text{CD}_T) + 4K_d \cdot B^h\text{CD}_T}}{2 \cdot B^h\text{CD}_T} \quad (4)$$

Data were analyzed using NLLS with Scientist (Micromath, MO) to determine K_d .

χ -dependent reversible inactivation assay

χ -dependent reversible inactivation of DNA unwinding was performed as described²¹. The reaction mixture was the same as the regular χ ssDNA assay (25 mM Tris-acetate, 5 mM ATP, 1 μ M SSB monomers) except that the concentrations of RecBCD and RecB^hCD were 0.1 nM and 0.2 nM, respectively, and the concentration of Mg(OAc)_2 was 1 mM. Assay temperature was at 37 °C, and 40 min after the reaction was initiated by addition of 5 mM ATP, excess Mg(OAc)_2 was added to a final concentration of 10 mM. Aliquots were removed at specified time points and processed as described above.

Joint molecule formation assay

Coupled joint molecule formation reactions for RecA-RecBCD, RecB^hCD , and RecB^hCD - RecB^n were conducted as described earlier^{7,12}. Briefly, reactions were carried out in 25 mM Tris-acetate (pH 7.5), 8 mM Mg(OAc)_2 , 5 mM ATP, 1 mM dithiothreitol, 1 mM phosphoenolpyruvate, 2 units/ml pyruvate kinase, 10 μ M (nucleotides) 5'-end-labeled NdeI-linearized χ^+ -pBR322 3F3H dsDNA, 20 μ M (nucleotides) supercoiled circular χ^+ -pBR322 3F3H DNA, 5 μ M RecA protein, 2 μ M SSB protein and either 0.3 nM RecBCD, 0.9 nM RecB^hCD , or 0.3 nM RecB^hCD with 1 μ M RecB^{nuc} . When the RecB^n concentration was varied as indicated, reactions contained 0.3 nM RecB^hCD . Reactions were terminated at indicated times by adding stop buffer. The reaction products were separated on a 1% (w/v) TAE (40 mM Tris-acetate (pH 8.2) and 1 mM EDTA) agarose gel at 600V·h, visualized, and quantified using Amersham Biosciences Storm 840 PhosphorImager and ImageQuant software.

UV sensitivity test

E. coli strain AB1157 Δ recCBD::FRT containing pMS421 (for *lacI*^q expression) pPB520 (RecC expression), pPB800 (RecB and RecD expression), pPB800-TAAs (for RecB⁹²⁷ expression without RecBⁿ and RecD expression), and pGBⁿ (RecBⁿ expression on a low copy number plasmid pGL10) were grown overnight in LB broth containing spectinomycin (20 μ g/ml), chloramphenicol (25 μ g/ml), ampicillin (100 μ g/ml) and kanamycin (30 μ g/ml) antibiotics. An aliquot (50 μ l) of an overnight culture was inoculated into 5 ml of LB medium and was allowed to grow till early log phase ($OD_{600} = 0.5$) at 37 °C. Serial dilutions of cells were made, and 5 μ l of diluted cells were spotted on LB agar plates. The plates were irradiated with UV light (254 nm) using a Spectroline short wave UV lamp (model-XX-15F, Spectronics corporation, NY, USA) for 0, 4, 8 and 12 seconds at a UV dose of 0.3 J/m²/s. The colonies that survived UV irradiation after incubation at 37 °C for 20 hours in the dark were scored.

T4 2⁻ plaque assay

E. coli strain AB1157 Δ recCBD::FRT expressing RecBCD mutant enzymes from plasmids pPB520, pPB800, pPB800-TAAs, and pGBⁿ were grown overnight in LB broth containing chloramphenicol (25 μ g/ml), ampicillin (100 μ g/ml) and kanamycin (30 μ g/ml) as needed. The pPB800, pPB800-TAAs, pPB520, and pGBⁿ are the low-copy expression vectors having 10-20 copies per cell and these proteins were expressed under *lacI*^q repression (from the pMS421 plasmid) without IPTG induction. An aliquot (50 μ l) of an overnight culture was inoculated into 5 ml of LB medium containing suitable antibiotics, was allowed to grow till early log phase ($OD_{600} = 0.5$) at 37 °C. Early log cell culture (0.1 ml) was mixed with 3 ml of LB top agar and spread on LB bottom agar plates. Plates were allowed to dry for 15 min. Serial dilutions of the phage stock (10⁹ plaque forming units/ml) were made in suspension medium (50 mM Tris-HCl, pH 7.5, 100 mM NaCl, 1 mM MgSO₄, 0.01% gelatin), and 5 μ l of each dilution was spotted on LB agar plate containing bacterial cells. These plates were incubated at 37 °C overnight, and the number of countable plaques formed under lower dilution was counted. T4 or T4 2⁻ phage titers from strains expressing RecBCD and derivatives were divided by the titer from strain AB1157 Δ recCBD::FRT with an efficiency of plating (EOP) about 3 \times 10¹⁰/ml.

Lambda recombination and χ activity assay

The bacteriophage λ crosses were performed between λ phage 1081, λ phage 1082, λ phage 1083, and λ phage 1084 (described in experimental model and subject

details section). Cross 1 was performed between phage 1081 × 1082, and cross 2 between phage 1083 × 1084. The frequencies of J⁺R⁺ recombinants of the mixed λ phage crosses (cross 1 and cross 2) from the *recBCD* null strains expressing RecBCD mutant enzymes from pPB520, pPB800, pPB800-TAAs, and pGBⁿ vectors determined by plating them on *E. coli* strain 594 (*sup*⁰) for recombinants, also on strain C600 (*sup**E*) for the total phage titer. The χ activity in these crosses was determined by the method of Stahl and Stahl ²² using the equation, χ activity = $\sqrt{(t \div c) \text{ cross 1} \div (t \div c) \text{ cross 2}}$, where (t ÷ c) is the ratio of turbid (t) to clear (c) plaques from cross 1 or cross 2, among J⁺R⁺ recombinants as described ²⁸.

Quantification and Statistical analysis

Data are presented as mean, \pm Standard Error of the Mean (SEM) or Standard Deviation (SD), unless otherwise stated. At least three independent experiments have been performed for each experiment. Data from the protein-protein interactions using Ni-NTA magnetic beads and the χ -specific ssDNA formation assays were analyzed by nonlinear least square (NLLS) analysis using Scientist software (Micromath, MO). The gels were quantified using Gel Pro Analyzer (Media Cybernetics, Bethesda, MD). Data from the χ -dependent reversible inactivation, and the joint molecule formation assays were quantified using Amersham Biosciences Storm 840 PhosphorImager and analyzed using the ImageQuant software (GE Healthcare, Piscataway, NJ). Graphs and image processing were done using the Prism 5.0 (Graphpad, USA) and ImageJ (nih.gov) software programs.

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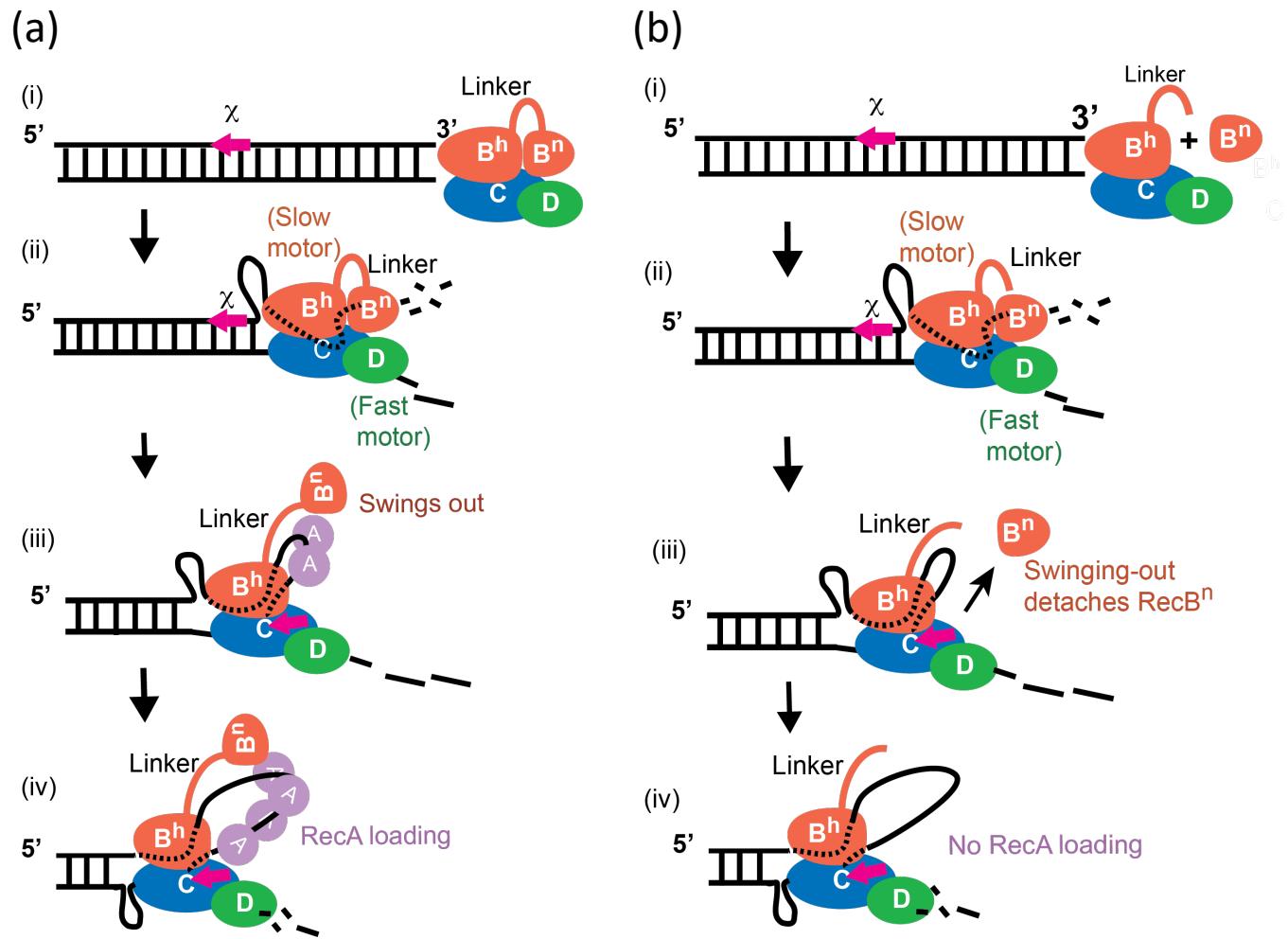
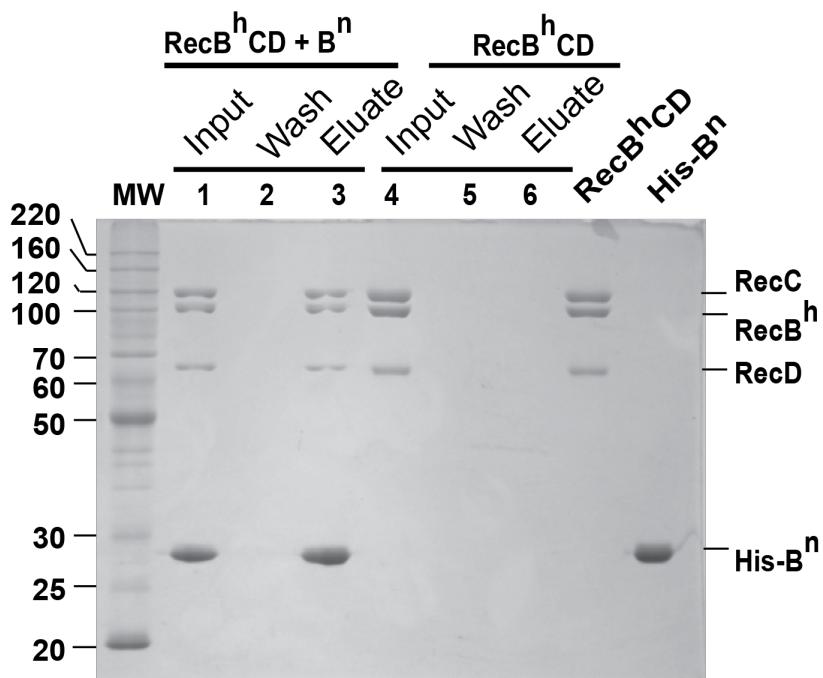


Figure 1

(a)



(b)

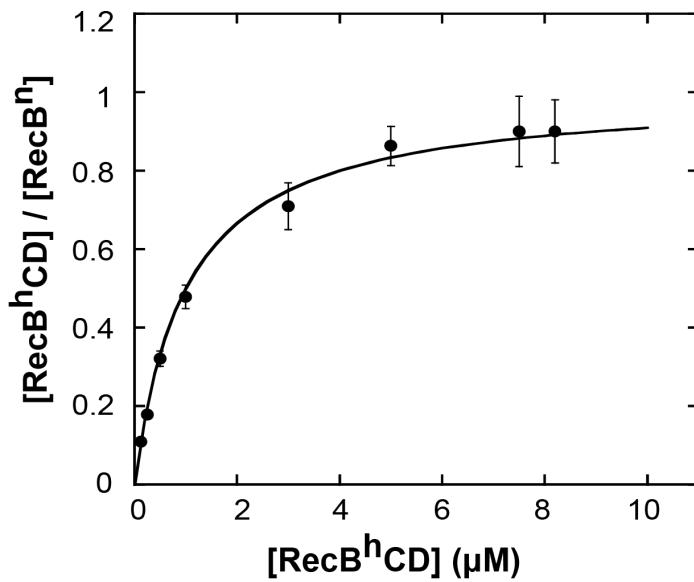
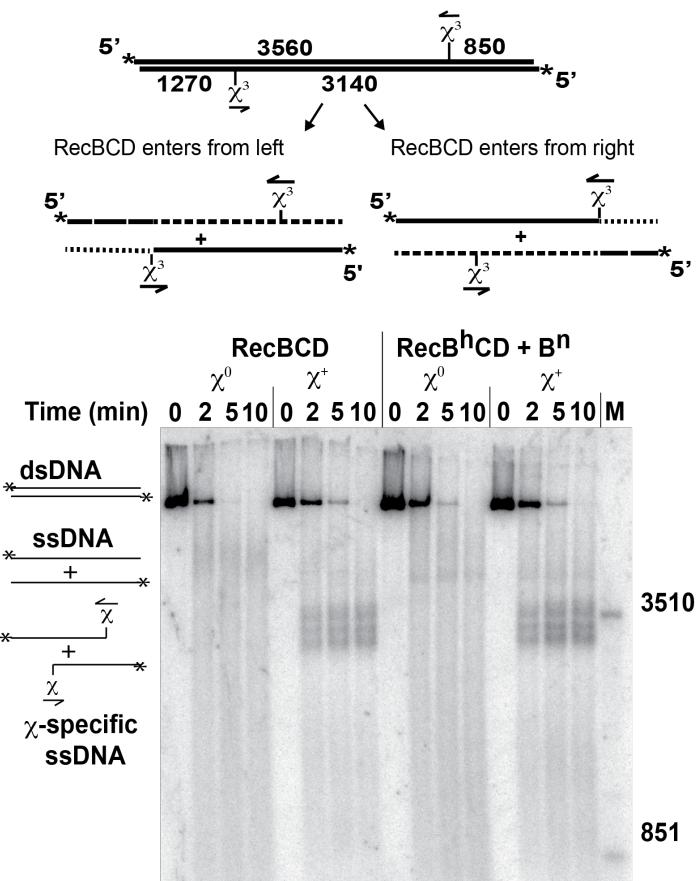


Figure 2

(a)



(b)

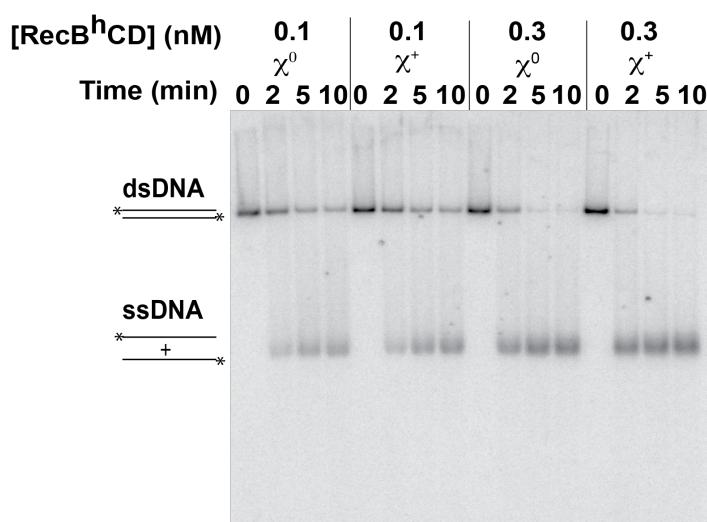


Figure 3

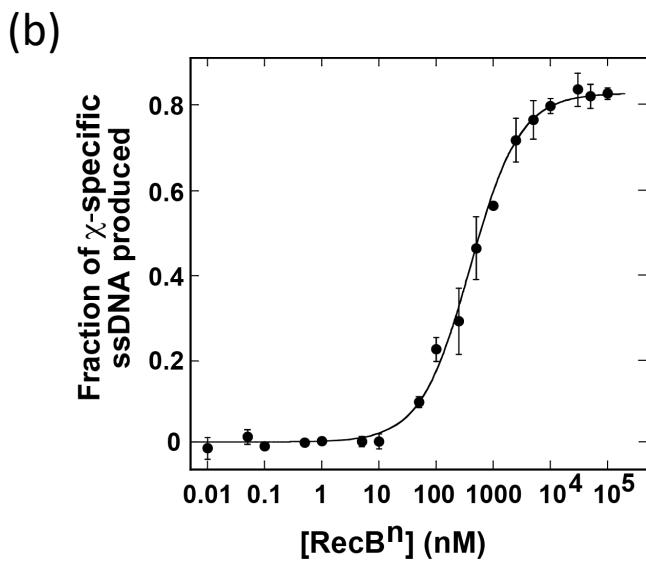
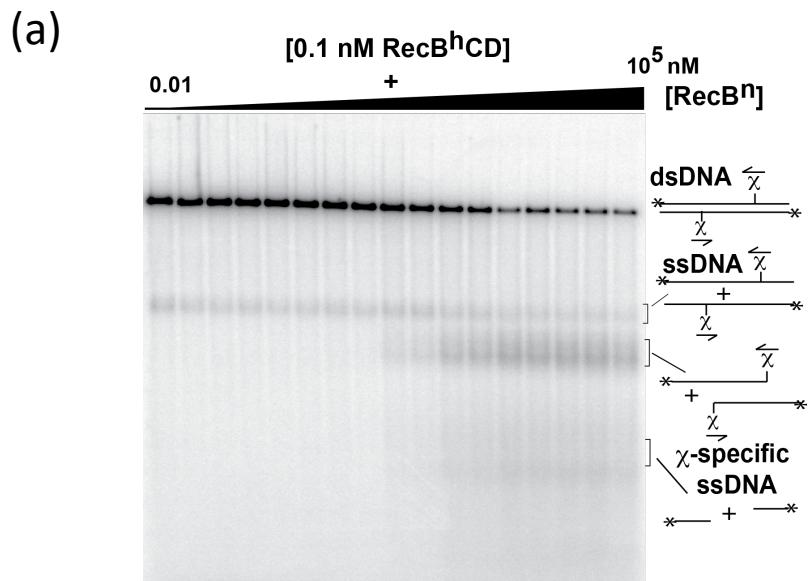


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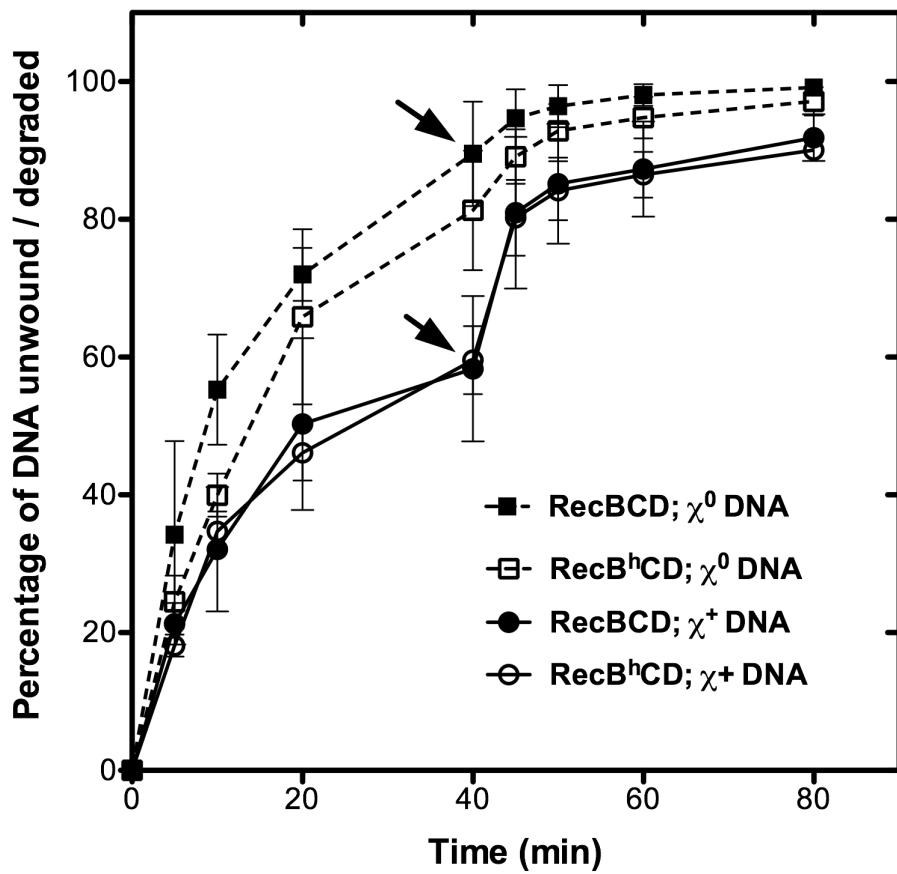
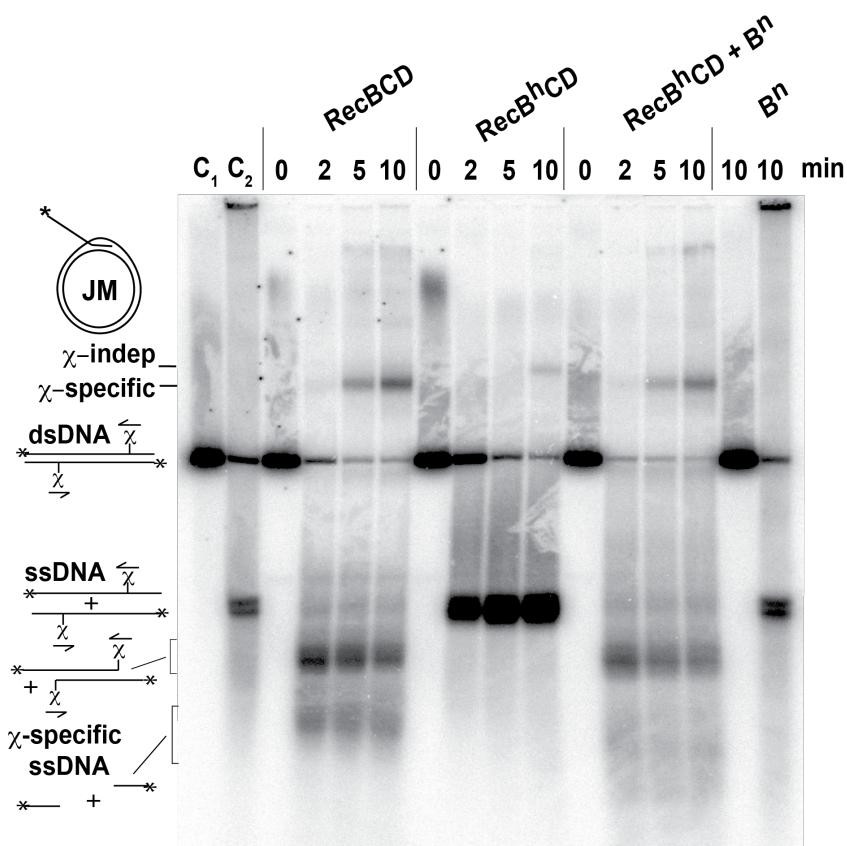


Figure 5

(a)



(b)

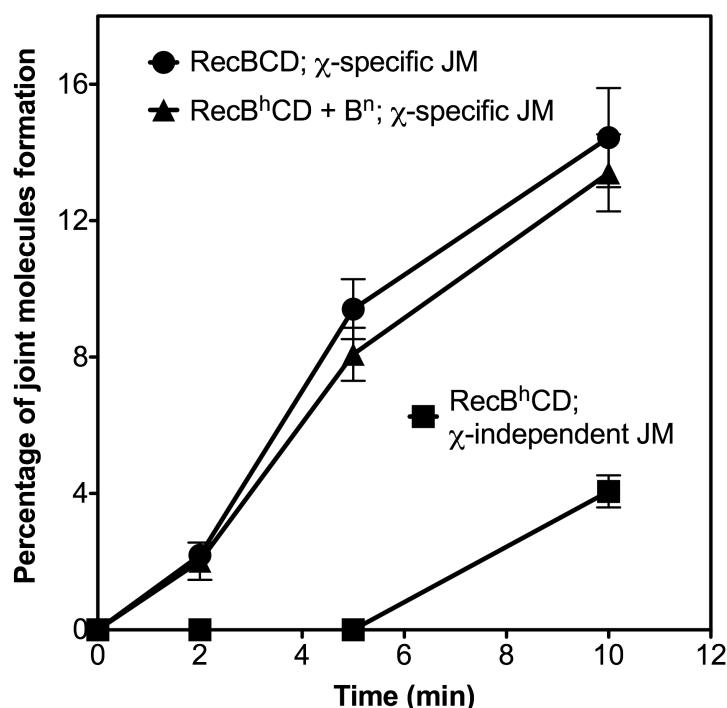


Figure 6a and b

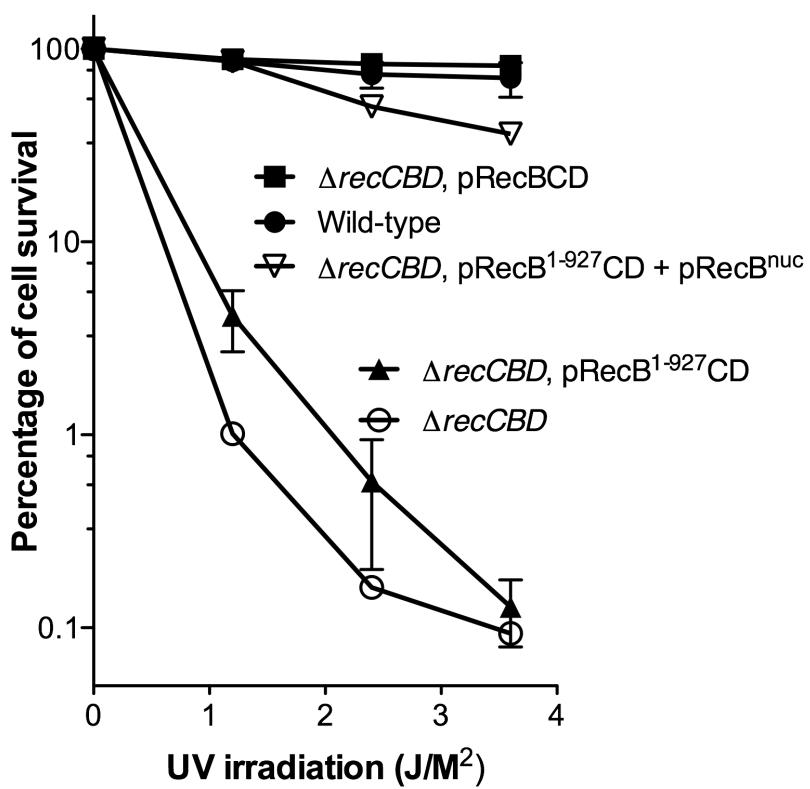


Figure 7

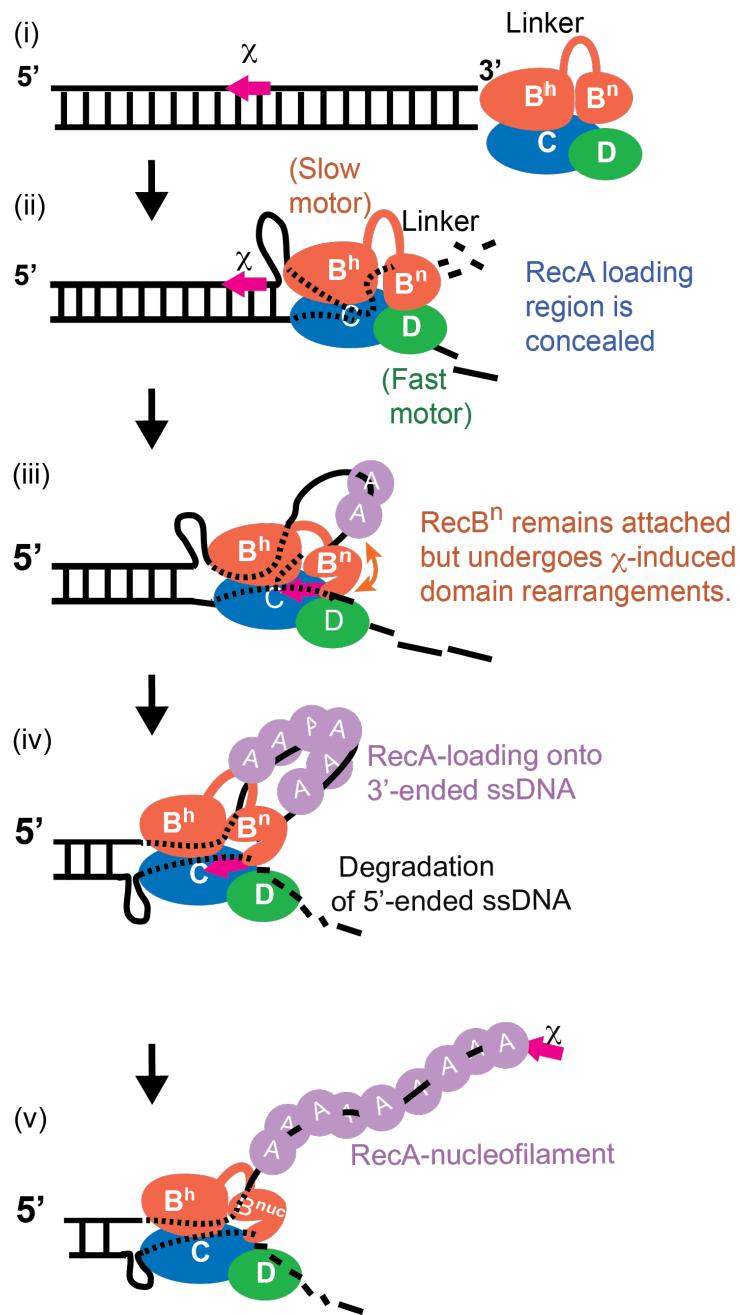


Figure 8