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Genetic Control of Multiple Pathways of Post-Replicational Repair in *uvrB* Strains of *Escherichia coli* K-12

DAVID A. YOUNGS* AND KENDRIC C. SMITH
Department of Radiology, Stanford University School of Medicine, Stanford, California 94305

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The effect of the *recA*, *uvrD*, *exrA*, and *recB* mutations and of post-irradiation treatment with chloramphenicol on the survival and post-replicational repair after ultraviolet irradiation of *uvrB* strains of *Escherichia coli* K-12 was examined. Each of these mutations or treatments was found to decrease survival and the extent of repair. The interactions of the inhibitory effects of the *uvrD*, *exrA*, and *recB* mutations and chloramphenicol treatment were determined by examining the survival and repair characteristics of the several multiple mutants. The survival results suggest that the post-replication repair process in *uvrB* strains may be subdivided into at least five different branches. These include three branches that are blocked by the *exrA*, *recB*, or *uvrD* mutation, a fourth branch that is blocked by any one of these mutations and is also sensitive to chloramphenicol treatment, and at least one additional branch that is not sensitive to either of these mutations or to chloramphenicol treatment. The extent of post-replicational repair observed with each of the strains is in general agreement with the pathways postulated on the basis of the survival data, although there are several apparent exceptions to this correlation.

Two systems for the "dark repair" of ultraviolet (UV) radiation-damaged deoxyribonucleic acid (DNA) were described previously, excision repair and post-replicational repair (9). The *uvrA* and *uvrB* strains of *Escherichia coli* K-12 do not excise pyrimidine dimers from their DNA after UV irradiation (1, 10, 20), and they lack a UV-specific endonuclease activity that appears to be required for the first incision event of the excision repair process (2). Thus, the only known dark-repair system remaining in the *uvrA* and *uvrB* strains is the post-replicational repair process.

Post-replicational repair is thought to involve the closure of gaps that arise in newly synthesized DNA as the replication complex proceeds past UV-induced lesions (16, 17). This process appears to involve a recombinational event such that the missing DNA in the newly synthesized strand is replaced by parental DNA. The resultant gap in the donating strand and any other small, single-stranded regions are presumably repaired by the action of one or more of the DNA polymerases and polynucleotide ligase.

Although very little is known of the actual enzymology of post-replicational repair, any mutation or treatment that sensitizes a *uvrA* or *uvrB* strain to UV irradiation could be presumed to act by inhibiting the post-replicational repair process. The *recA*, *recB*, *recC* (6), *recF* (8), *exrA* (12), and *uvrD* (14) mutations are among those known to sensitize *uvrA* and *uvrB* strains to killing by UV radiation. In addition, post-irradiation incubation in a growth medium containing chloramphenicol (7) or sodium arsenite (T. G. Rossman, M. S. Meyn, and W. Troll, Mutat. Res., in press) results in sensitization of the *uvrA* and *uvrB* strains. An inhibitory affect of the *recA* (19, 22), *recB* (present data and reference 15), *recF* (15), *exrA* (19, 24), and *uvrD* (present data) mutations and of chloramphenicol treatment (present data and reference 18) on the gap-filling process has been directly demonstrated.

The present report concerns the interaction of the inhibitory effects of the *recB*, *exrA*, and *uvrD* mutations and chloramphenicol treatment on the post-replicational repair process. The results suggest that each of these three mutations inhibits a separate branch of the post-replicational repair process and a common, chloramphenicol-sensitive branch as well.

(A preliminary report of these data was presented at the second annual meeting of the American Society for Photobiology, Vancouver, British Columbia, Canada, July 1974.)

MATERIALS AND METHODS

Bacterial strains. The properties and sources of the *E. coli* K-12 strains used in the present experiments are given in Table 1. The transduction and mating techniques were described previously (24). For the genetic crosses described in Table 1, the selection was first for the nutritional marker as indicated. The presence or absence of the desired radiation-sensitizing marker was then ascertained by determining the relative UV, X-ray, or methyl methane sulfonate sensitivity of the recombinants as required.

Experimental conditions. The media, growth conditions, irradiation and pulse-labeling conditions, and alkaline sucrose gradient procedures were described previously (24). The UV fluences indicated in this paper are average incident fluences. The incident fluence was determined as described previously (24) and was corrected for sample absorption using a fluence attenuation factor determined empirically by comparing the survival of the *uvrB recA* strain when irradiated at varying cell densities. The correction factors determined in this manner were markedly different from those obtained by the Morowitz procedure (13), presumably because of problems in measuring sample absorption at 254 nm due to light-scattering effects (11).

Chloramphenicol (Sigma Chemical Co.) was used at a final concentration of 100 μg/ml and was freshly prepared for each experiment.

Molecular weight calculations. To avoid a speed-dependent effect on the sedimentation rate of large DNA molecules (e.g., reference 4), the centrifugation speeds used in the present experiments were varied from 20,000 rpm (using a SW50.1 rotor) for samples from unirradiated cells, to 40,000 rpm for samples of small DNA pieces from irradiated cells. This is a variation from the general technique described previously (24).

M_n values for all samples were calculated directly from the gradient profiles. The limits for such calculations were chosen so as to exclude, as completely as possible, the very-low-molecular-weight material at the top of the gradients.

The M_n values were calculated relative to a ^{14}C-labeled bacteriophage T2 DNA marker by the relationship

$$M_n = \frac{[\Sigma f_i/d_i^{2.63} \text{ for phage T2 DNA}]}{[\Sigma f_i/d_i^{2.63} \text{ for } E.\ coli \text{ DNA}]} \times 55 \times 10^6$$

where f_i is the fraction of recovered counts, and d_i is the average distance sedimented, of each *i*th fraction. A value of 55 $\times$ 10^6 was used as the single-stranded molecular weight for bacteriophage T2 DNA (5).

RESULTS

Figure 1 shows the UV survival curves obtained with each of the various strains, and the D_{37} values are given in Table 2. For convenience in presenting the data, the multiple mutants have been grouped into three classes. The survival results show that the class 1 strains all have quite similar sensitivities to UV irradiation. The class 2 strains, which contain two sensitizing mutations in addition to *uvrB5*,

TABLE 1. *List of strains*

Strain designation	Genotype[a]	Derivation, reference, or source
DY200	F$^-$ *uvrB5 exrA recB21 uvrD3 leuB rha lac str thyR*	P1·SR255 × DY181 (select Thy$^+$)
DY199	F$^-$ *uvrB5 exrA uvrD3 leuB rha lac str thyR*	P1·SR255 × DY181 (select Thy$^+$)
DY197	F$^-$ *uvrB5 recB21 uvrD3 rha lac str leuB thyR*	P1·SR255 × DY179 (select Thy$^+$)
DY161	F$^-$ *uvrB5 exrA recB21 rha lac str metE leuB thyR*	P1·AB2470 × DY146 (select Thy$^+$)
DY157	F$^-$ *uvrB5 recB21 rha lac str metE leuB thyR*	P1·AB2470 × DY145 (select Thy$^+$)
DY155	F$^-$ *uvrB5 recA56 rha lac str metE leuB thyR*	JC5088 × DY145 (select Thy$^+$)
DY180	F$^-$ *uvrB5 exrA rha lac str leuB thyA thyR*	P1·N14-4 × DY146 (select Met$^+$)
DY181	F$^-$ *uvrB5 exrA uvrD3 rha lac str leuB thyA thyR*	P1·N14-4 × DY146 (select Met$^+$)
DY178	F$^-$ *uvrB5 rha lac str leuB thyA thyR*	P1·N14-4 × DY145 (select Met$^+$)
DY179	F$^-$ *uvrB5 uvrD3 rha lac str leuB thyA thyR*	P1·N14-4 × DY145 (select Met$^+$)
DY145	F$^-$ *uvrB5 rha lac str metE leuB thyR thyA*	P1·DY99 × DY143 (select Mal$^+$)
DY146	F$^-$ *uvrB5 exrA rha lac str metE leuB thyR thyA*	P1·DY99 × DY143 (select Mal$^+$)
DY143	F$^-$ *uvrB5 rha lac str metE malB leuB thyR thyA*	P1·AB2499 × KH21 (select Bio$^+$)
KH21	F$^-$ *rha lac str metE malB leuB bio thyR thyA*	R. B. Helling
DY99	F$^-$ *exrA lac str metE thyR thyA*	24
N14-4	F$^-$ *uvrD3 trp gal str*	14
SR255	F$^-$ *recB21 leu thr thi pro arg his lac ara gal mtl xyl str tsx thyR*	P1·AB2470 × AB2497 (select Thy$^+$)
AB2470	F$^-$ *recB21 leu thr thi pro arg his lac ara gal mtl xyl str tsx*	A. J. Clark
AB2497	F$^-$ *leu thr thi pro arg his lac ara gal mtl xyl str tsx thyA thyR*	R. P. Boyce
JC5088	Hfr KL16 *recA56 thr ilv spc*	J. D. Gross

[a] The exrA mutation was originally obtained from *E. coli* B_{s-1}.

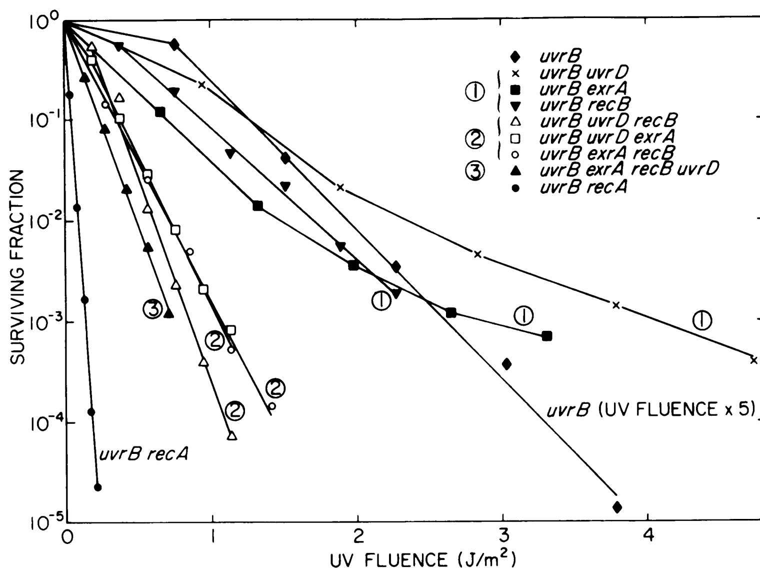

FIG. 1. *Survival of uvrB strains after UV irradiation. Exponential-phase cells grown in minimal medium were irradiated (254 nm) with stirring in DTM buffer (minimal medium without organic components) at room temperature, diluted in 0.67 M phosphate buffer, and plated on minimal medium solidified with Difco Noble agar as described previously (24). Each survival curve represents the average of two or more independent experiments. The strain numbers and D_{37} values are given in Table 2.*

show similar D_{37} values and are more sensitive than the class 1 strains. The class 3 strain, containing all three additional mutations, was somewhat more sensitive than the class 2 strains but not as sensitive as the *uvrB recA* strain, which lacks both known dark-repair systems.

The effect of post-irradiation treatment with chloramphenicol on survival is shown in Fig. 2. The results indicate that the *uvrB* strain is sensitized by the chloramphenicol treatment, with the major affect being a reduction in the shoulder of the survival curve (Fig. 2A). Each of the class 1 strains (Fig. 2B, C, and D) and the *uvrB recA* (Fig. 2B) strain showed little or no sensitization to UV radiation by the chloramphenicol treatment. The *uvrB urvD* strain did show some sensitization after the survival had decreased to 10^{-2} or less (Fig. 2D). The *uvrB exrA* strain was protected to a small extent by the chloramphenicol treatment, especially at survival levels greater than 10^{-3} (Fig. 2C).

The initial yield of single-strand breaks or gaps in newly synthesized DNA in *uvrB recA* cells was 68 per *E. coli* genome per J/m² (Fig. 3). This corresponds closely to the number of pyrimidine dimers produced, approximately 65 per genome per J/m² (16). The extent of strand breakage immediately after the pulse-labeling period was also checked for each of the other strains listed in Table 2 (data not shown). These values were somewhat lower than observed with the *uvrB recA* strain, presumably because of repair which occurred during the pulse-labeling period, as suggested by Sedgwick (19). Thus, the initial level of strand breakage is most likely the same for each of the strains, approximately one break or gap per pyrimidine dimer (16, 19).

The extent of repair of gaps produced in newly synthesized DNA after UV irradiation was examined. The results of the pulse-label gradient studies are shown in Fig. 4 and are summarized in Table 2. They indicate that each of the mutations, *exrA*, *recB*, and *uvrD*, as well as chloramphenicol treatment, partially inhibits post-replicational repair in a *uvrB* strain. This is shown by the decreased levels of DNA strand rejoining observed in the class 1 strains, or in the *uvrB* strain after chloramphenicol treatment, compared with that found with the *uvrB* strain in the absence of chloramphenicol. Each of the class 2 and 3 multiple mutants also showed decreased repair compared with the *uvrB* strain. However, the extent of repair observed with certain of the class 2 and 3 strains overlapped with that found for the class 1 strains. The unusual strains are *uvrB exrA* (Fig. 4D), which has an inordinately large slope (i.e., reduced repair capacity) compared with the other class 1 strains, and *uvrB recB uvrD* (Fig.

4G), which has a smaller slope value than the other class 2 and 3 strains. The class 3 strain (Fig. 4H) also shows a smaller slope value than predicted on the basis of the relative sensitivities of the strains.

The *uvrB recA* strain showed essentially no post-replicational repair. The results obtained after 80 min of incubation in minimal medium were not significantly different from those obtained when the cells were lysed immediately after pulse-labeling (compare the two lines in Fig. 3).

Table 2 also gives the number of unrepaired DNA daughter strand gaps per genome per D_{37} fluence. These values indicate that the more sensitive strains show a smaller number of unrepaired gaps per D_{37} fluence than do the more resistant strains.

The extent of degradation of newly synthesized DNA to acid-soluble material is indicated by the data in Table 3. The amount of degradation generally increased with increasing sensitivity of the cells to killing by UV radiation. The data in Table 3 also indicate an inverse correlation between the amount of acid-insoluble radioactivity present at the end of the 10-min pulse-labeling period and the sensitivity of the strain.

TABLE 2. *Extent of unrepaired, DNA daughter strand gaps (DSG) after post-replicational repair*

Strain	Slope[a]	DSG per genome per J/m²	D_{37} values[b] (J/m²)	DSB per genome per D_{37} fluence
uvrB (DY178)	0.097	2.7	5.9	16
uvrB + CAP[c]	0.40	11	2.9	32
Class 1				
uvrB recB (DY157)	0.56	16	0.70	11
uvrB uvrD (DY179)	0.40	11	0.86	9.5
uvrB exrA (DY180)	0.67	19	0.41	7.8
Class 2				
uvrB exrA uvrD (DY-181, DY199)	0.62	17	0.27	4.6
uvrB recB uvrD (DY-197)	0.35	9.8	0.31	3.0
uvrB exrA recB (DY-161)	0.67	19	0.21	4.0
Class 3				
uvrB exrA recB uvrD (DY200)	0.53	15	0.15	2.2
uvrB recA (DY155)	2.5	70	0.027	1.9

[a] From the data shown in Fig. 4. Units are: 10^8 per dalton per J/m².

[b] The D_{37} values listed were taken from the data shown in Fig. 1 and represent the UV fluence required to reduce the surviving fraction from 1.0 to 0.37.

[c] CAP, Chloramphenicol treatment.

DISCUSSION

The *uvrA* and *uvrB* strains of *E. coli* K-12 lack the UV-specific endonuclease required for the initial event of the excision repair process (2). Thus, each of the mutations or treatments that sensitizes the *uvrA* or *uvrB* strains to UV irradiation may be presumed to inhibit post-replicational repair, the only dark-repair process known to act on pyrimidine dimers in these cells. The present UV survival studies indicate that the *recA*, *exrA*, *recB*, and *uvrD* mutations, and also post-irradiation chloramphenicol treatment, sensitize *uvrB* strains to killing by UV radiation, in confirmation of earlier results (see Introduction).

The survival curves of the multiple mutants were analyzed by the method of Brendel and Haynes (3), involving a calculation of the survival level expected for an additive interaction of two mutations based on the known survival values for each of the parent strains. The results of this analysis indicate that the *exrA*, *recB*, and *uvrD* mutations interact synergistically. That is, each of the class 2 strains is more sensitive than predicted for a strictly additive interaction of the sensitizing mutations. Thus, these three mutations appear to act on independent repair pathways that compete, to some extent, for the same substrate.

The class 3 strain was also more sensitive than predicted for an additive interaction, with one exception. If the survival level expected for an additive interaction was calculated using the observed survival values for the *uvrB recB uvrD* and *uvrB exrA* strains, then the class 3 strain was more sensitive than predicted for UV fluences less than ~0.4 J/m² but was less sensitive than predicted after higher fluences. This may indicate that after UV fluences greater than 0.4 J/m² the presence of both the *uvrD* and *recB* mutations partially blocks a repair pathway that is blocked completely by an *exrA* mutation.

Thus, the *exrA*, *uvrB*, and *recB* mutations appear to act mainly on independent, competing pathways of post-replicational repair. However, the results of the chloramphenicol experiments modify this conclusion somewhat. The class 1 mutants were sensitized only slightly, or

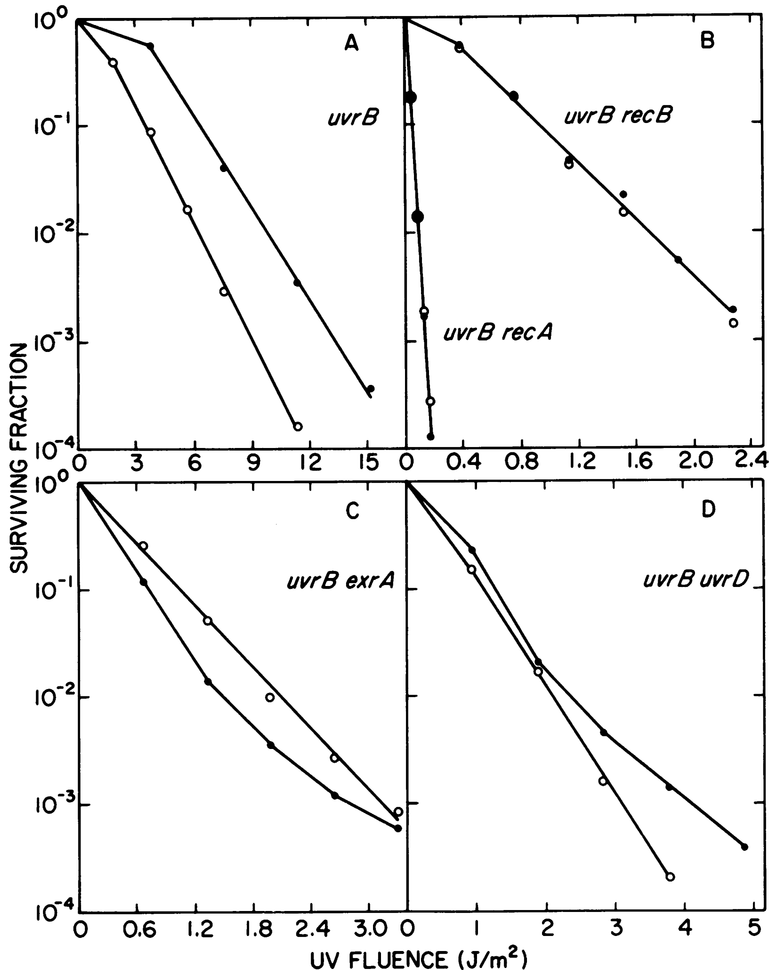

FIG. 2. *Effect of post-irradiation chloramphenicol treatment on survival of uvrB strains. Cells were grown and irradiated as indicated in the legend for Fig. 1. After irradiation, samples of the cells to be treated with chloramphenicol (O) were added to an equal volume of minimal medium containing twice the normal concentration of organic components and 200 µg of chloramphenicol per ml, incubated for 80 min at 37 C, and then diluted and plated as indicated in the legend for Fig. 1. Samples that were not treated with chloramphenicol (●) were diluted and plated immediately after irradiation. (No change in survival was observed in irradiated cells incubated in the medium without chloramphenicol [23].) Each survival curve represents the average of at least two experiments.*

not at all, by post-irradiation chloramphenicol treatment (Fig. 2), suggesting that the *exrA*, *uvrD*, and *recB* mutations all block a fourth, chloramphenicol-sensitive repair pathway in addition to their action on independent pathways.

At least one additional branch of the post-replicational repair process must be postulated to account for the fact that the *uvrB recA* strain is much more sensitive than the class 3 strain. The *recF* mutation may be able to inhibit this branch of repair since the data of Rothman et al. (15) indicate that a *uvrB recB recF* strain is much more sensitive than our class 3 strain. Thus, the available survival data indicate the existence of at least five different branches of the post-replicational repair process in *uvrB* cells. This is shown schematically in Fig. 5.

The results of the post-replicational repair studies indicate that no significant amount of repair occurred in *uvrB recA* cells (Fig. 3). This is consistent with the results of Smith and Meun (22) who found no repair in *recA* or *uvrB recA* cells after a UV fluence of 6.3 J/m². However, Smith (21) did observe repair in *recA* cells after a UV fluence of 1.5 J/m², and

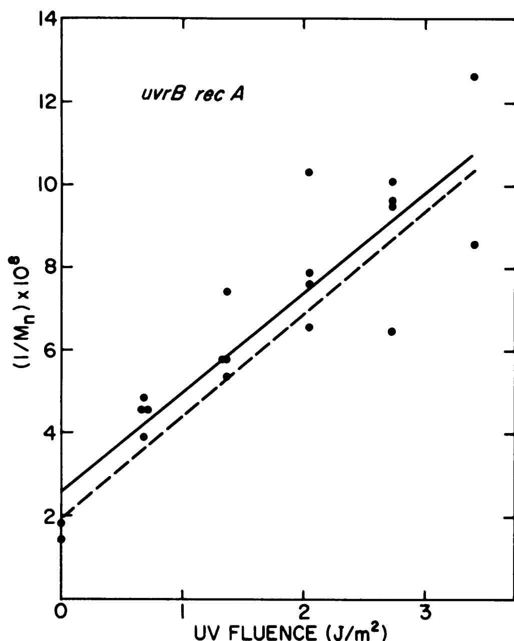

FIG. 3. *Effect of UV irradiation on the size of newly synthesized DNA in the uvrB recA strain. The cells were grown and irradiated as indicated in the legend for Fig. 1, pulse-labeled for 10 min as described previously (24), and then immediately lysed on alkaline sucrose gradients. The inverse of the number average molecular weight is shown as a function of the UV fluence. The dashed line is identical to that fitted to the data points shown in Fig. 4D for the uvrB recA strain and indicates the extent of strand breakage after 80 min of incubation in minimal medium to allow post-replicational repair to occur.*

Sedgwick (19) found limited repair in a *uvrB recA* strain derived from *E. coli* B/r. The reasons for these differences are not clear.

Our results also show that the *exrA*, *uvrD*, and *recB* mutations, as well as chloramphenicol treatment, each result in a partial inhibition in the amount of repair that occurs in the *uvrB* strain (Fig. 4 and Table 2). Ganesan and Smith (7) found that chloramphenicol did not inhibit post-replicational repair in a *uvrB* strain after a UV fluence of 6 J/m². In addition, Smith and Meun (22) reported that a *recB* or *recC* mutation had no inhibitory effect on post-replicational repair after UV fluences up to 18 J/m². However, the present results indicate that both chloramphenicol treatment and the presence of a *recB* mutation partially inhibit post-replicational repair. These differences in experimental results are probably due to the following factors. (i) A speed-dependent effect on the sedimentation velocity of large DNA molecules (e.g., reference 4) would have obscured small levels of unrepaired, DNA daughter strand gaps in the previous experiments. (ii) The earlier experiments used low UV fluences, which would have resulted in only in a small level of unrepaired, DNA daughter strand gaps. (iii) The *recB* and *recC* strains used in the earlier experiments were *uvr*⁺, which could have resulted in a lower level of breaks in newly synthesized DNA because of removal of dimers by excision repair. (iv) A more resistant, and therefore presumably more repair-proficient, series of strains (derived from AB1157 rather than W3110) was used in the earlier experiments. However, the conclusion made by Ganesan and Smith (7), on the basis of survival data, that chloramphenicol blocks a repair pathway which can also be inhibited by a *recA* or *recB* mutation, still holds and is supported by the present results.

Our results showed an inverse correlation between the number of unrepaired gaps per D_{37} fluence and the relative sensitivities of the different classes of strains (Table 2). This suggests that unrepaired gaps may be less efficient in producing lethality in the more resistant strains. The high value observed for *uvrB* cells treated with chloramphenicol suggests that some of the inhibitory effect of this compound on repair may be reversible. This possibility has not been examined experimentally.

There was also a good correlation between the sensitivities of the different classes of strains and the extent of DNA degradation observed. This is illustrated by the data in Table 3, section B, which gives the relative amounts of radioactivity remaining acid insoluble after the 80-min incubation period. These results take into account the possible differences in DNA synthesis as well as degradation.

Within a given class of mutants there was a good correlation between the relative sensitivity to killing and the ability to repair daughter strand gaps (i.e., D_{37} and slope values in Table 2). However, between the different classes of strains there are several inconsistencies in the correlation between sensitivity and repair capability. There are several possible explanations for the lack of strict correlation between survival and the extent of repair among all nine different strains used in the present study. (i) The increased DNA degradation or decreased DNA synthesis characteristic of the more sensitive strains may have resulted in an effect on cell survival that was not reflected in the repair studies. (ii) The experimental procedure used for the repair experiments may not have allowed sufficient time for repair to occur in all strains,

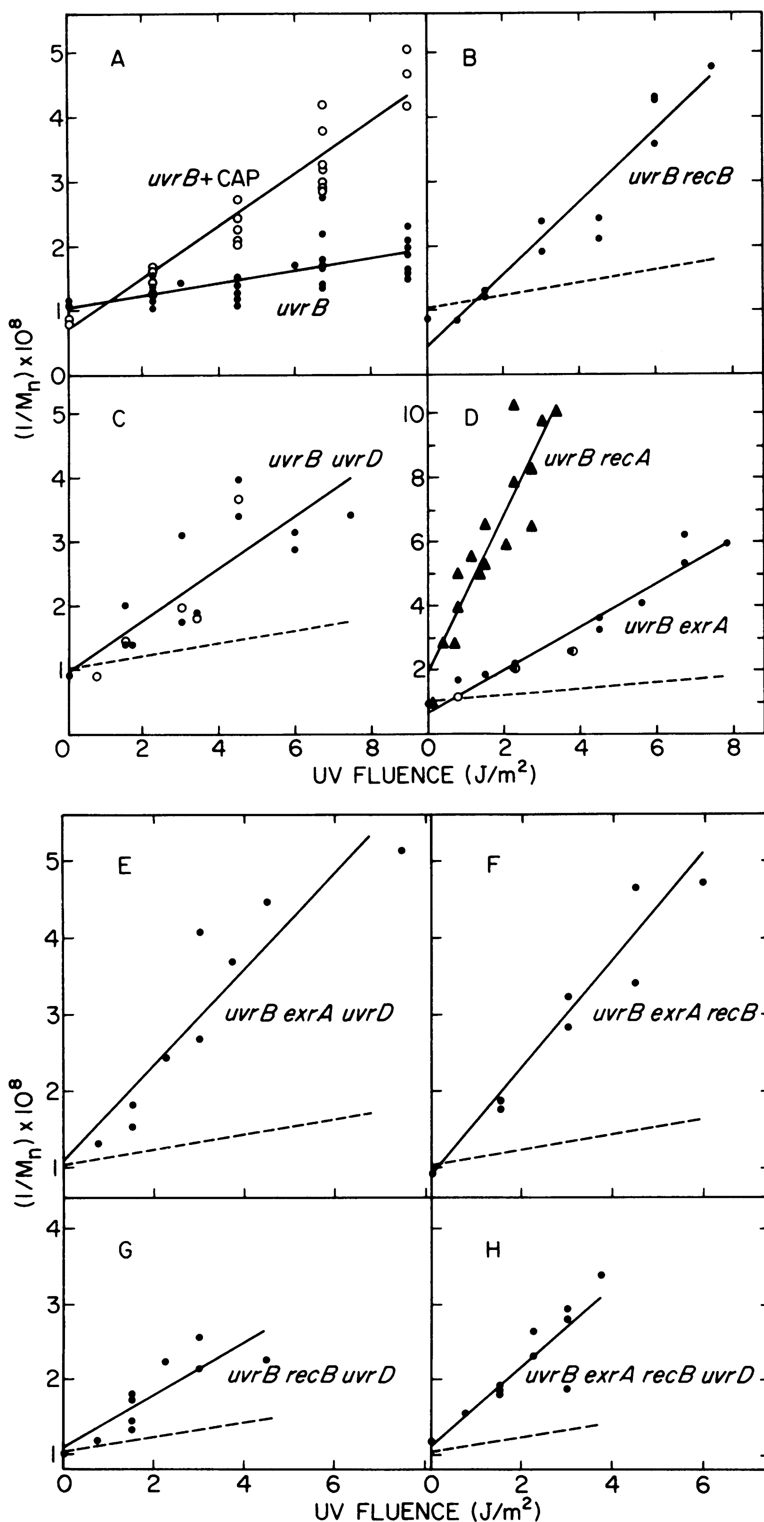

FIG. 4. *Post-replicational repair in uvrB strains of E. coli K-12. The cells were pulse-labeled as indicated in the legend for Fig. 3 and then incubated for 80 min at 37 C in minimal medium before lysis on alkaline sucrose gradients. The open symbols indicate that chloramphenicol (CAP) was present at 100 µg/ml during the 80-min incubation period. The dashed lines in each section have the same slope and intercept values as that fitted to the uvrB data without CAP treatment (A). The strain numbers and slope values are given in Table 2. Note the change of scale for (D).*

TABLE 3. *Degradation of newly synthesized DNA after UV irradiation*[a]

Strain	Amt of acid-insoluble radioactivity[b]								
	Sampled immediately after pulse-labeling (A)			Sampled 80 min after pulse-labeling (B)			Degradation during 80-min incubation (B/A)		
	0 J/m²	4.7 J/m²	9.3 J/m²	0 J/m²	4.7 J/m²	9.3 J/m²	0 J/m²	4.7 J/m²	9.3 J/m²
uvrB	1.0	0.78	0.48	1.2	0.87	0.45	1.2	1.1	0.95
uvrB + CAP[c]	1.0	0.80	0.48	1.0	0.66	0.30	1.1	0.82	0.63
Class 1									
uvrB recB	1.0	0.49	0.26	1.4	0.55	0.20	1.4	1.1	0.76
uvrB uvrD	1.0	0.49	0.35	1.2	0.34	0.16	1.3	0.70	0.46
uvrB exrA	1.0	0.61	0.47	1.2	0.52	0.28	1.2	0.85	0.60
Class 2									
uvrB exrA uvrD	1.0	0.59	0.34	1.2	0.31	0.15	1.2	0.54	0.43
uvrB recB uvrD	1.0	0.35	0.20	1.2	0.17	0.082	1.2	0.49	0.41
uvrB exrA recB	1.0	0.40	0.21	1.3	0.33	0.093	1.3	0.82	0.46
Class 3									
uvrB exrA recB uvrD	1.0	0.27	0.15	1.2	0.13	0.059	1.2	0.49	0.38
uvrB recA	1.0	0.24	0.12	1.2	0.12	0.056	1.2	0.52	0.46

[a] The cells were irradiated and then pulse-labeled for 10 min as for the gradient experiments. Samples were taken immediately after resuspension of the pulse-labeled cells and after 80 min of incubation in minimal medium at 37 C. Triplicate samples were prepared as described previously (24). The numbers listed are the average of two experiments and represent the amount of trichloroacetic acid-insoluble radioactivity in the samples incubated for 80 min in minimal medium relative to the unirradiated sample taken immediately after the pulse-labeling period. The fact that the values for unirradiated cells are greater than 1 indicates that some residual incorporation of label occurred during the 80-min incubation period.

[b] Relative to unirradiated time-zero samples.

[c] CAP, Chloramphenicol treatment.

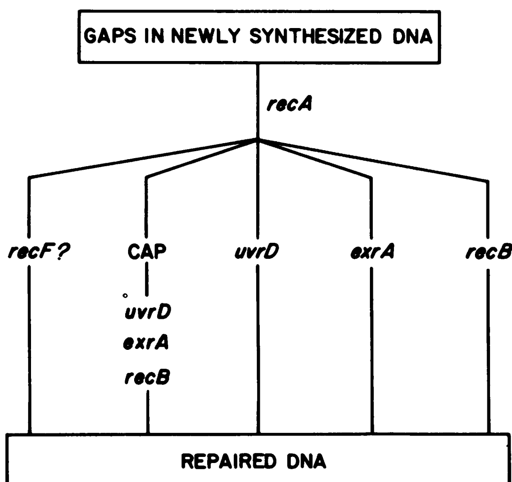

FIG. 5. *Proposed pathways of post-replicational repair in uvrB strains of E. coli K-12. The involvement of recF is suggested by the data of Rothman et al. (15).*

although most repair in a *uvrB exrA* strain was found to be complete in 60 min (24). (iii) The end points of cell survival and repair of gaps in newly synthesized DNA are quite different. Thus, it is possible that the mutations examined inhibit repair processes that are not reflected in our repair studies but are important in determining cell survival. For example, the repair of any gaps in the parental strands remaining after the recombinational steps of post-replicational repair would not be measured in our repair experiments but could well influence survival. Although there are several inconsistencies in the correlation between the repair data and the proposed multiple pathways, the survival data are highly reproducible and their analysis clearly supports the multiple pathway concept.

In conclusion, our studies suggest the following. (i) The post-replicational repair process in *E. coli uvrB* cells consists of at least five independent branches. (ii) Three of the branches are

blocked by *exrA*, *uvD*, or *recB* mutations. (iii) One branch is blocked by either the presence of any one of these mutations or by post-irradiation incubation in a growth medium containing chloramphenicol. (iv) At least one branch is blocked neither by the three mutations nor by chloramphenicol treatment. This part of the post-replicational repair process may prove to be inhibited by the presence of a *recF* mutation (15). A schematic description of the five proposed branches of the post-replicational repair process is shown in Fig. 5.

ACKNOWLEDGMENTS

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ADDENDUM IN PROOF

Recently, S. G. Sedgwick (Proc. Natl. Acad. Sci. U.S.A. **72**:2753–2757, 1975) found that chloramphenicol prevented a small amount of post-replication repair and completely eliminated mutation fixation in *E. coli* $WP2_s$ *uvrA* cells, and suggested that an inducible product is involved in these two processes. The postreplication repair pathway that we have shown to be inhibited by chloramphenicol and by the *recB*, *exrA*, and *uvrD* mutations may possibly be the same as the inducible, mutagenic repair pathway described by Sedgwick.

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