

## Multiple, Independent Components of Ultraviolet Radiation Mutagenesis in *Escherichia coli* K-12 *uvrB5*

NEIL J. SARGENTINI\* AND KENDRIC C. SMITH

Department of Radiology, Stanford University School of Medicine, Stanford, California 94305

Received for publication 21 August 1979

Reversion systems involving the *lacZ53*(amber) and *leuB19*(missense) mutations were developed to study the mutant frequency response of *Escherichia coli* K-12 *uvrB5* (SR250) to ultraviolet radiation (254 nm). A one-hit mutant frequency response was discernible at ultraviolet radiation fluences below  $\sim 0.5 \text{ J m}^{-2}$ . At higher fluences the overall mutant frequency response could be resolved into one-hit and two-hit components. A new interpretation of the published data on *E. coli* K-12 indicates that SR250 is not unique in this respect. In addition, the Lac reversion system showed enhanced mutagenesis after ultraviolet radiation fluences of  $\sim 1$  to  $3 \text{ J m}^{-2}$ , whereas the Leu reversion system did not. We conclude that the complex ultraviolet radiation mutant frequency response curves for *E. coli* K-12 *uvrB5* were the result of three independent mutagenic processes for Lac reversion and two for Leu reversion.

The nonlinear nature of the mutant frequency response (MFR) to UV radiation was noted in the early radiation mutagenesis studies on bacteria (15). Witkin (39) proposed that this nonlinearity resulted from a two-hit process. When the logarithm of the mutant frequency (MF) was plotted against the logarithm of the UV radiation fluence, a straight line with a slope of 2 was obtained (1) [the slope is equal to the exponent of the fluence parameter in an equation for MF, i.e.,  $\text{MF} = (\text{fluence})^n$ ]. This treatment of the data seemed to substantiate the two-hit nature of UV radiation mutagenesis. Much discussion has occurred concerning the nature of these two hits (reviewed in reference 43).

Although log-log plots are valuable in illustrating some concepts (41), other approaches to the treatment of mutagenesis data are also useful (17, 19, 21, 37). Doudney (17, 21) noted that, when the MFR to UV radiation in *Escherichia coli* B/r was plotted with linear coordinates, a distinct linear (one-hit) region was evident, although the adjacent MFR at higher or lower fluences was nonlinear. Using this plotting technique, he (19, 20) has identified three operationally different regions of a UV radiation-induced MFR curve for *E. coli* B/r *uvrA*. At the lowest fluences ( $< 2 \text{ J m}^{-2}$ ; fluences were corrected by the method of Doudney [20]), the MFR curve ( $F^2$  region) was nonlinear and was probably proportional to the square of the fluence. This suggested a two-hit mechanism, one being a lesion blocking the synthesis of DNA (17, 18, 21) and inducing SOS (error-prone) repair (14, 33), and the other hit was assumed to be the premuta-

tional lesion. At intermediate fluences (2 to  $3 \text{ J m}^{-2}$ ), a linear (one-dimer [1DM]) MFR in relation to fluence was observed (19). This suggested that all of the cells in the population had received sufficient radiation for the full induction of error-prone repair, and thus premutational lesions produced mutations with one-hit kinetics. Other experiments supported this conclusion. For example, if the physiology of the cells was altered by giving an inducing UV radiation fluence as a pretreatment (19) or by incubating a *tif-1* strain at  $42^\circ\text{C}$  (41, 42), then the UV radiation-induced MFR was linear even in the usual  $F^2$  region. Beyond the 1DM region was a so-called two-dimer (2DM) region that again conformed to a two-hit process (19). However, in this region the UV radiation-induced MFR was not altered by preinducing the cells (19, 43). This region of two-hit kinetics was thought to reflect the increasing importance of two interacting lesions (19), such as overlapping daughter strand gaps (16, 34-36).

In the work reported here, a new one-hit MFR region was noted at low UV radiation fluences ( $< 0.5 \text{ J m}^{-2}$ ). This one-hit error-prone mechanism provided an explanation for the less than two-hit UV radiation mutant frequency responses commonly found for *E. coli* K-12 strains. Based upon our data, we suggest that UV radiation mutagenesis in *E. coli* K-12 *uvrB5* involves multiple mechanisms.

### MATERIALS AND METHODS

**Bacterial strains.** The *E. coli* K-12  $F^-$  strains used in this study were SR250 (formerly called DY145;

reference 44) *uvrB5 leuB19 metE70 thyA36 deo(C2?) rha-5 lacZ53 rpsL151*  $\lambda^-$  and SR735 (also known as RFS817) *thi-1 relA1 rpsL220*  $\Delta$ (*ara-leu*)498  $\Delta$ *lac-3*  $\lambda^-$ . This latter strain was obtained from B. Bachmann (CGSC no. 5735). The genotype symbols are those used by Bachmann et al. (2). The allele designations were suggested by B. Bachmann (personal communication). The *lacZ53* marker is the amber mutation from *E. coli* K-12 Hfr300 YA14 and has been known as *lacY14* (5). The *leuB19* marker has also been called *leuB1* (26, 27) and originated in *E. coli* B (25).

**Media.** Cells were cultured in 0.4% glucose-salts medium (23) supplemented with thiamine·HCl at 0.5  $\mu$ g/ml, D-biotin at 1  $\mu$ g/ml, thymine at 10  $\mu$ g/ml, 1 mM L-leucine, and 1 mM L-methionine. Survival and reversion to Lac<sup>+</sup> were assayed on modified glucose-salts plates (27 ml) solidified with Noble agar (Difco) (38) at 1.6%, containing lactose at 0.4% and glucose at 300 or 1,200  $\mu$ g/ml. These plates are referred to as  $\Delta$ glu-300 or  $\Delta$ glu-1200 plates, respectively. Plates lacking any glucose ( $\Delta$ glu-0) were used to quantitate spontaneous Lac<sup>+</sup> mutants present when the culture was harvested. The small amount of glucose in the  $\Delta$ glu plates was necessary to allow the expression of induced mutants and also to allow relatively small numbers of auxotrophs to grow into colonies for the estimation of viability. Survival and reversion to Leu<sup>+</sup> were assayed on analogous plating media. Thus,  $\Delta$ leu-1 represents L-leucine at 1.0  $\mu$ g/ml. LB medium (30) was supplemented with thymine at 10  $\mu$ g/ml (LBt).

**Transduction procedure.** Donor strains were lysogenized by bacteriophage P1::Tn9(Cm<sup>r</sup>)ets (kindly provided by M. Casadaban). Lysogenizations and transductions were performed generally as described by Miller (30).

**UV radiation mutagenesis procedure.** Cells in the logarithmic phase of growth ( $\sim 2.5 \times 10^8$  colony-forming units per ml) were centrifuged (6,000  $\times g$  for 6 min), washed (1 $\times$ ), and resuspended in 67 mM phosphate buffer, pH 7.0 (12) at an optical density at 650 nm of 0.2 in a Zeiss PMQII spectrophotometer. These cells were UV irradiated as required and plated to assay for mutants or viability. Mutant colonies were counted when their number no longer increased (after 3 days at 37°C). Data were compiled from at least four experiments per UV radiation fluence with four mutant selection and three viability plates per fluence. These tabulated data may be obtained from us.

**Irradiation.** An 8-W General Electric germicidal lamp, emitting primarily at 254 nm, was situated at a distance of 47 cm from the cell sample. Cell suspensions (10 ml in a 9.0-cm-inside-diameter glass petri dish bottom) were irradiated on a rotating platform. The UV radiation fluence rate was  $\sim 0.2$  or  $\sim 0.04$  J m<sup>-2</sup> s<sup>-1</sup> (after the fluence rate was reduced with metal screens) and was checked before each experiment with a germicidal photometer (International Light, Inc., no. IL-254) whose calibration was verified by uranyl oxalate actinometry (modified from Bowen [4]). All manipulations were carried out under General Electric "gold" fluorescent lights to prevent photoreactivation. The stated UV radiation fluences have been corrected for cell-masking effects (e.g., the measured incident fluence  $\times 0.89$ , for optical density at 650 nm = 0.20, gives the corrected average incident fluence) according

to an empirically derived relationship based on the survival of a *uvrB5 recA56* strain irradiated at various cell concentrations (45).

**Quantitation of mutagenesis.** The UV radiation-induced MF was calculated per average mutant selection plate by a modified version of the formula of Bridges (6):  $MF = \{[M_i - M_{po} + M_o(1 - SF_c)](1 \times 10^8)\} / [(S_c)(\text{volume plated})]$  where  $M_i$  is the number of mutant colonies arising from irradiated cells on  $\Delta$ nutrient plates (i.e.,  $\Delta$ glu or  $\Delta$ leu),  $M_{po}$  is the number of mutant colonies arising from nonirradiated cells on  $\Delta$ nutrient plates,  $M_o$  is the number of mutant colonies arising from nonirradiated cells on plates lacking the growth-limiting nutrient (i.e., glucose or leucine),  $SF_c$  is the surviving fraction of irradiated cells as influenced by the concentration technique used,  $1 \times 10^8$  is the factor included to normalize mutant frequencies to the number of mutants per  $1 \times 10^8$  survivors,  $S_c$  is the colony-forming units per milliliter in the irradiated cell suspension plated in the mutant assays, and volume plated is the volume of cell suspension plated (e.g., 0.2 ml) in the mutant assays.

**Chemical mutagenesis.** Mutagenesis by 2-aminopurine nitrate (Calbiochem) or sodium bisulfite was performed by the method of Miller (30). An overnight LBt culture of strain SR250 was diluted  $10^{-6}$  in phosphate buffer, and 0.6 ml was added to 30 ml of LBt  $\pm$  2-aminopurine nitrate at 600  $\mu$ g/ml. For bisulfite mutagenesis, the overnight culture was pelleted, washed, and resuspended in 0.2 M acetate buffer (pH 5.2)  $\pm$  1 M sodium bisulfite. After shaking for 30 min at 37°C, these latter cells were pelleted, washed, and resuspended in LBt at a 10-fold dilution. For both mutagenesis techniques, the seeded LBt was divided into 12 2.5-ml cultures  $\pm$  mutagen and incubated with aeration for 24 h at 37°C. Culture volumes of 0.2 ml were spread upon two  $\Delta$ leu-0 plates per culture. Cultures were also assayed for colony-forming units per milliliter on  $\Delta$ glu-300 plates.

## RESULTS

**Characterization of the *leuB19* mutation.** The *leuB19* deficiency does not appear to be a nonsense mutation because of the inability of Leu<sup>+</sup> revertants to support the growth of various amber or other bacteriophage T4 mutants (R. Bockrath, personal communication). However, a more conclusive test was performed. A total of 107 independent Leu<sup>+</sup> revertants of strain SR250 were induced by UV radiation fluences of either 0.25, 2.5, or 5.0 J m<sup>-2</sup>. Transducing lysates were prepared from these revertants, and all were able to transduce strain SR735  $\Delta$ (*ara-leu*) to Leu<sup>+</sup>. A transducing lysate prepared from SR250 *leuB19* did not transduce this strain to Leu<sup>+</sup>. Since no known suppressor loci are cotransducible (i.e., less than 2 min away) with the *leuB* locus (2), this is good evidence that all of the Leu<sup>+</sup> revertants of SR250 were due to mutations within the *leuB* locus.

2-Aminopurine nitrate, a mutagen that induces AT  $\rightleftharpoons$  GC transition mutations (22), was

tested for its ability to revert strain SR250 to  $\text{Leu}^+$ . The resultant mutant frequencies from two replicate experiments, using 12 cultures each, were  $42 \pm 12$  and  $59 \pm 9$   $\text{Leu}^+$  per  $10^8$  cells from 2-aminopurine nitrate-treated cultures or  $2.5 \pm 2.2$  and  $1.6 \pm 0.9$   $\text{Leu}^+$  per  $10^8$  cells, respectively, from nontreated cultures. In two experiments with sodium bisulfite, a mutagen that specifically induces GC  $\rightarrow$  AT transition mutations (30), the resultant average mutant frequencies were  $1.3 \pm 1.1$  and  $1.3 \pm 1.0$   $\text{Leu}^+$  per  $10^8$  cells compared with  $1.9 \pm 1.2$  and  $2.4 \pm 1.7$   $\text{Leu}^+$  per  $10^8$  cells for the respective nontreated control sets of cultures. These data are consistent with the *leuB19* mutation being the result of a GC  $\rightarrow$  AT transition and revertible by an AT  $\rightarrow$  GC transition.

**Determination of optimum conditions for the quantitation of UV radiation mutagenesis.** Experiments were performed to determine a nutrient concentration that would allow maximal mutation ( $\text{Lac}^+$  or  $\text{Leu}^+$ ) expression. Cells were UV irradiated and spread on mutant selection plates containing various concentrations of glucose or leucine. On the basis of these data, glucose concentrations of 300 or 1,200  $\mu\text{g}/\text{ml}$  were chosen for experiments in which nonconcentrated cells or cells concentrated 10-fold, respectively, would be plated for  $\text{Lac}^+$  mutants. A leucine concentration of 1  $\mu\text{g}/\text{ml}$  was chosen for experiments in which fivefold-concentrated cells would be plated for  $\text{Leu}^+$  mutants. The amount of limiting nutrient (especially in the case of glucose) used in these experiments represents an amount sufficient for maximal mutation yield without production of an inordinately large number of spontaneous mutant colonies per plate.

Variability in the number of viable cells plated in the UV radiation mutagenesis experiments was not considered to be important because in an experiment in which different numbers of nonirradiated cells were plated, the value for spontaneous mutants arising on the mutant selection plates (corrected for preexisting mutants) was largely unaffected by the number of viable cells plated (data not shown).

**Reversion to  $\text{Lac}^+$  or  $\text{Leu}^+$  after low UV radiation fluences.** The initial data obtained by plating 10-fold-concentrated cells on  $\Delta\text{glu-1200}$  plates suggested a linear increase in the  $\text{Lac}^+$  MFR with fluence up to  $0.4 \text{ J m}^{-2}$ . This plating procedure, while yielding substantial numbers of radiation-induced mutants, is complicated by the large background of spontaneous  $\text{Lac}^+$  mutants and can only be of value for low UV radiation fluences. To look at the MFR over the fluence range  $0.0$  to  $1.2 \text{ J m}^{-2}$ , noncon-

centrated cells were spread on  $\Delta\text{glu-300}$  plates. Both sets of data are presented in Fig. 1 and indicate linearity up to  $\sim 0.5 \text{ J m}^{-2}$ . The pooled data points are defined by the relation:  $\text{Lac}^+$  mutants per  $10^8$  cells =  $414 \times$  fluence, obtained by fitting a straight line through the data points for  $0.0$  to  $0.5 \text{ J m}^{-2}$  for strain SR250.

The UV radiation-induced MFR (*leuB19*  $\rightarrow$   $\text{Leu}^+$ ) also appeared to be linear up to  $\sim 0.5 \text{ J m}^{-2}$  (Fig. 2). A straight line was fitted through the data points for  $0.0$  to  $0.35 \text{ J m}^{-2}$  to yield the relation for strain SR250:  $\text{Leu}^+$  mutants per  $10^8$  cells =  $50.6 \times$  fluence.

**Reversion to  $\text{Lac}^+$  or  $\text{Leu}^+$  after higher UV radiation fluences and plotted with linear coordinates.** To determine whether these linear MFR curves correspond to the 1DM region described by Doudney (19) (suggesting that *E. coli* K-12 is always induced for error-prone repair) or to a heretofore unnoticed type of linear MFR, the MFR (*lacZ53*  $\rightarrow$   $\text{Lac}^+$ ) was measured over the UV radiation fluence range  $0.0$  to  $9.0 \text{ J m}^{-2}$  for strain SR250. Figure 3 shows that at UV radiation fluences of  $>0.5 \text{ J m}^{-2}$  the  $\text{F}^2$ , 1DM, and 2DM regions of the MFR described by Doudney (19) can be seen in our data. Thus, two linear MFR regions are observed for  $\text{Lac}$  reversion, a linear MFR below  $\sim 0.5 \text{ J m}^{-2}$  and a 1DM region for  $\sim 1$  to  $3 \text{ J m}^{-2}$ . When our *leuB19*  $\rightarrow$   $\text{Leu}^+$  data for UV radiation fluences of  $0.0$  to  $6.5 \text{ J m}^{-2}$  were plotted with linear coordinates (Fig. 4), a 1DM region could not be discerned.

**UV radiation-induced reversion to  $\text{Lac}^+$  or  $\text{Leu}^+$  plotted with logarithmic coordi-**

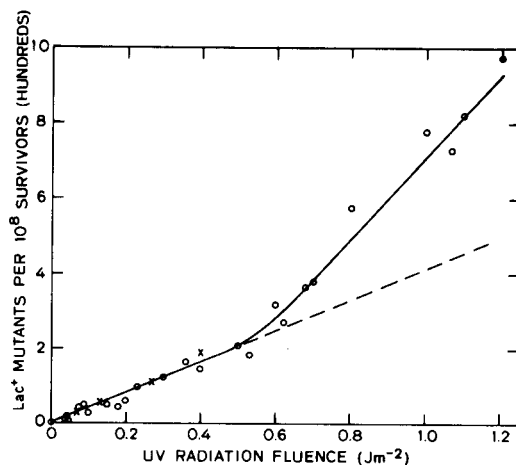


FIG. 1. UV radiation mutagenesis to  $\text{Lac}^+$  of *E. coli* K-12 *uvrB5* (SR250). Symbols:  $\circ$ , 0.2 ml of nonconcentrated cells spread upon  $\Delta\text{glu-300}$  plates;  $\times$ , 0.2 ml of 10-fold-concentrated cells spread upon  $\Delta\text{glu-1200}$  plates. A straight line has been visually fitted to the data for  $0.0$  to  $0.5 \text{ J m}^{-2}$ .

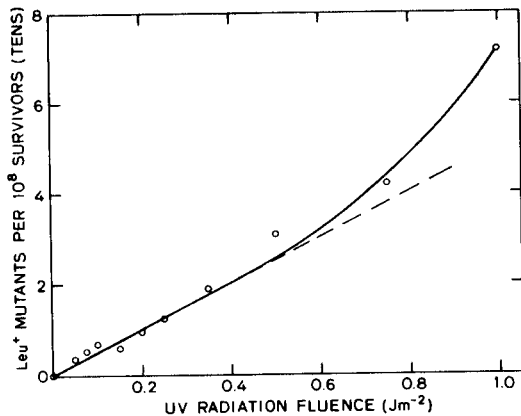


FIG. 2. UV radiation mutagenesis to  $Leu^+$  of *E. coli* K-12 *uvrB5* (SR250). A straight line has been visually fitted to the data for 0.0 to  $0.35 J m^{-2}$ .

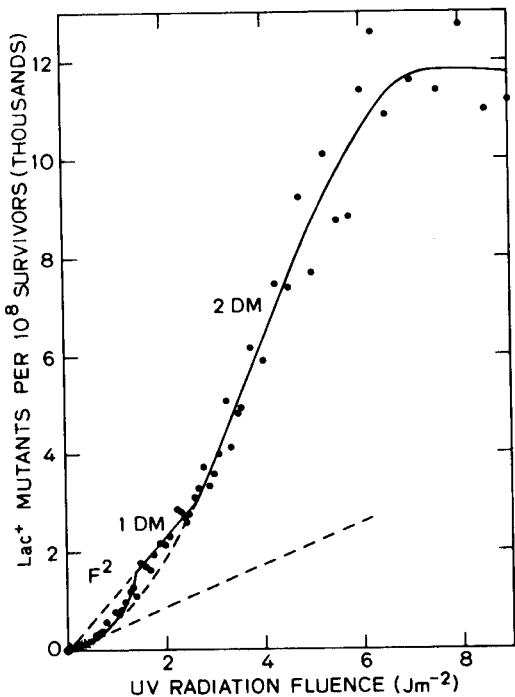


FIG. 3. UV radiation mutagenesis to  $Lac^+$  of *E. coli* K-12 *uvrB5* (SR250). Symbols: ●, 0.2 ml of non-concentrated cells spread upon  $\Delta glu-300$  plates; ×, 0.2 ml of 10-fold-concentrated cells spread upon  $\Delta glu-1200$  plates. The terms  $F^2$ , 1DM, and 2DM are defined in the text. The lower dashed line is an extension of the line through the data for 0.0 to  $0.5 J m^{-2}$  shown in Fig. 1. The upper dashed line fits the 1DM region. These curves have been visually fitted to the data.

notes. When the  $Lac^+$  MFR data (Fig. 3) were plotted with logarithmic coordinates (Fig. 5), the low-fluence linear region, but not the 1DM re-

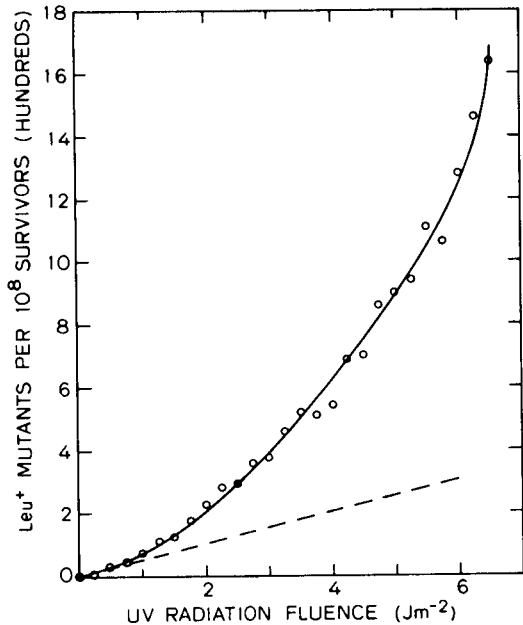


FIG. 4. UV radiation mutagenesis to  $Leu^+$  of *E. coli* K-12 *uvrB5* (SR250). The dashed line is an extension of the line through the data for 0.0 to  $0.35 J m^{-2}$  shown in Fig. 2. These curves have been visually fitted to the data.

gion, became clearly evident. We believe that these data points fit the relation  $MF = aF + bF^2$  and thus should continually curve upward until a slope of 2.0 is reached. At fluences greater than  $6 J m^{-2}$ , the reversion system no longer appears to respond to increasing amounts of radiation. A straight line was fitted through the data points, and its slope was calculated. The line through the  $Lac^+$  UV radiation MFR data points for 0.5 to  $6.0 J m^{-2}$  has a slope of 1.59. The line " $Lac^+$  mutants per  $10^8$  cells =  $414 \times$  fluence" (derived from Fig. 1) drawn through the data points for 0.038 to  $0.5 J m^{-2}$  (Fig. 5) emphasizes the change in rate of UV radiation mutagenesis in the region of  $0.5 J m^{-2}$ .

The slope value of 1.59 is markedly different from the value of 2.0 frequently associated with the UV radiation mutagenesis of *E. coli* B/r (1). If we make the assumption that the low-fluence linear MFR region (0 to  $0.5 J m^{-2}$ ) is the result of a linear process that operates at least up to  $6.0 J m^{-2}$ , an extrapolated line between 0.5 and  $6.0 J m^{-2}$  may be used to determine the contribution of this process to the total observed MFR. After subtracting the contribution of the linear process, the data points corresponding to the corrected MFR (Fig. 5) could be fitted with a line having a slope of 2.0. Also, the 1DM region

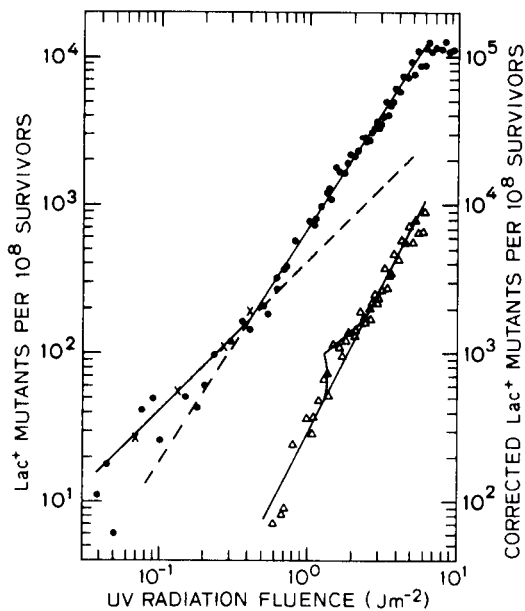


FIG. 5. UV radiation mutagenesis to  $Lac^+$  of *E. coli* K-12 *uvrB5* (SR250). Symbols: ●, 0.2 ml of non-concentrated cells spread upon  $\Delta$ glu-300 plates; ×, 0.2 ml of 10-fold-concentrated cells spread upon  $\Delta$ glu-1200 plates; Δ,  $Lac^+$  mutant data corrected as described in the text. These curves have been visually fitted to the data.

is more evident in the corrected data plot than in the uncorrected data plot, since the linear process had effectively obscured the 1DM region.

Since the corrected  $Lac^+$  data points (Fig. 5) fit the relation " $Lac^+$  mutants per  $10^8$  cells =  $bF^2$ ," the fluence coefficient,  $b$ , can be determined by finding the corrected mutant frequency at  $1.0 J m^{-2}$ ; it is 300 ( $Lac^+$  mutants  $\cdot 10^{-8}$  cells  $\cdot J^{-2} \cdot m^4$ ). Thus, combining the relation for the linear process with that for the calculated two-hit process, we obtained a quadratic formula for UV radiation-induced reversion to  $Lac^+$ :  $Lac^+$  mutants per  $10^8$  cells =  $414 \times \text{fluence} + 300 \times (\text{fluence})^2$ . Similar calculations were performed with the  $Leu^+$  data (Fig. 6), which had a slope of 1.54 for  $0.5$  to  $6 J m^{-2}$ , and yielded the relation:  $Leu^+$  mutants per  $10^8$  cells =  $50.6 \times \text{fluence} + 26 \times (\text{fluence})^2$ . The curves defined by these relations were virtually congruent with the experimental MFR curves (data not shown).

## DISCUSSION

### New linear MFR observed in *E. coli* K-12.

UV radiation mutagenesis data obtained for  $Lac$  (Fig. 1) and  $Leu$  (Fig. 2) reversion in *E. coli* K-12 *uvrB5* (SR250) indicated a previously unde-

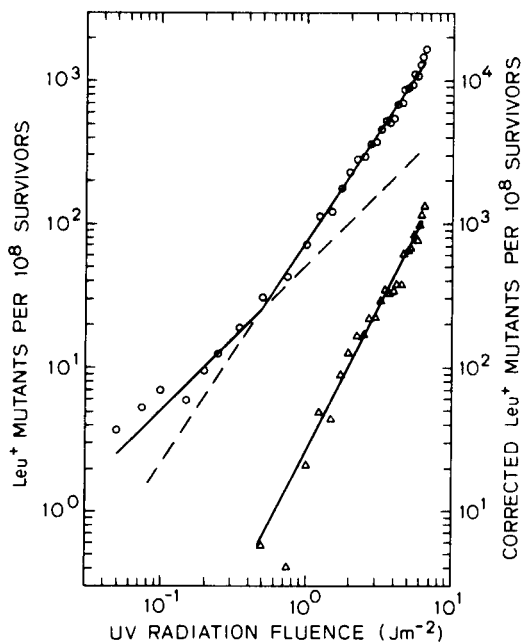


FIG. 6. UV radiation mutagenesis to  $Leu^+$  of *E. coli* K-12 *uvrB5* (SR250). Symbols: ○, experimental data; Δ,  $Leu^+$  mutant data corrected as described in the text. These curves have been visually fitted to the data.

tected linear or one-hit mutant frequency response region. This linear region supplements the  $F^2$ , 1DM, and 2DM regions previously described by Doudney (19) for *E. coli* B/r. The presence of this linear region allowed us to explain why our UV radiation MFR curves had slopes of 1.59 ( $Lac^+$ ) or 1.54 ( $Leu^+$ ) for fluences of  $0.5$  to  $6.0 J m^{-2}$  when plotted with log-log coordinates. Data for *E. coli* B/r on a similar plot fit a line with a slope of  $\sim 2.0$ , i.e., a two-hit process (39). We assumed that the linear process, although evident only at fluences less than  $\sim 0.5 J m^{-2}$  (Fig. 1 and 2), actually operated at the same rate up to  $\sim 6 J m^{-2}$ . When the effect of the linear process was subtracted from the total UV radiation mutagenesis data, the remaining data had a slope of 2.0 ( $\Delta$  in Fig. 5 and 6) on a log-log plot. This suggested that, whereas UV radiation mutagenesis in *E. coli* B/r was generally a two-hit process, in strain SR250 both one-hit and two-hit processes were important to UV radiation mutagenesis.

To determine whether *E. coli* K-12 (SR250) was unique in possessing the linear process, we surveyed the published UV radiation mutagenesis data. Since data obtained at UV radiation fluences less than  $0.5 J m^{-2}$  were not generally available, we chose to determine the slopes of

available data plotted with log-log coordinates. These slopes (Table 1) were expected to indicate the presence of both one-hit and two-hit processes in the same fashion as that for strain SR250 (Fig. 5 and 6). The UV radiation-induced MFR slopes for the most commonly tested *E. coli* B/r strains, WP2 and WP2<sub>s</sub>, were consistently found to be near 2.0. In contrast, the *E. coli* K-12 strains, when plated on defined-selective media as we had done, consistently had slopes that were less than 2.0. This analysis suggests that *E. coli* K-12 strains, regardless of excision-repair

proficiency, generally employ both one-hit and two-hit mutagenic processes. In some systems, broth supplementation was correlated with MFR slopes of approximately three (Table 1).

**New interpretation of the 1DM region of mutagenesis.** Doudney (19), using a Trp nonsense reversion system, suggested that UV radiation mutagenesis in *E. coli* B/r *uvrA* (WP2<sub>s</sub>) consisted of two processes. One process was non-linear (F<sup>2</sup> region) until it was fully induced (1DM region), whereupon it continued to operate as a linear process up to 6 J m<sup>-2</sup>. The second process

TABLE 1. Slopes calculated for straight lines fitted to UV radiation MFR data plotted with log-log coordinates

<i>E. coli</i>	Excision repair genotype	Reversion system <sup>a</sup>	Plating medium <sup>b</sup>	MFR slope <sup>c</sup>	Fluence range (J m <sup>-2</sup> )	References
<b>B/r strains</b>						
WP2	+	<i>trpE65</i>	Δtrp ± CAA	2.1 ± 0.1	1.5-220	1, 7, 9-11, 13, 31
WP2	+	<i>trpE65</i>	ΔNB	1.4 - 1.8	2-50	19, 31
WP2 <sub>s</sub>	<i>uvrA155</i>	<i>trpE65</i>	ΔNB, Δtrp ± CAA	2.0 ± 0.2	0.3-6	1, 7, 10, 13, 16, 19, 20, 31, 40
WU36-10	+	<i>tyr</i>	Δtyr	3.1	10-50	8
WU36-10	+	<i>leu</i>	Δleu	1.7	10-50	8
WU36-10-89	<i>uvrA</i>	<i>leu</i>	ΔNB	2.0 } <sup>d</sup> <1.0 }	0.053-0.37 0.66-4.5	32
<b>K-12 strains</b>						
AB1157	+	<i>his-4</i>	Δhis	1.3	15-120	24
AB1884	<i>uvrC34</i>	<i>his-4</i>	Δhis	1.5	2.5-15	24
AB1886	<i>uvrA6</i>	<i>his-4</i>	Δhis	1.7	1-15	24
PAM579	<i>uvrB</i>	<i>his-4</i>	Δhis	1.6	1-15	24
AB1885	<i>uvrB5</i>	<i>his-4</i>	Δhis	1.2	2.5-15	24
SR315	<i>uvrB5</i>	<i>leuB19</i>	Δleu	1.3 } <sup>d</sup> 2.7 }	1-4 4-8.5	3
SR312	<i>uvrA6</i>	<i>leuB19</i>	Δleu	1.4 } <sup>d</sup> 2.6 }	1-4 4-8.5	3
AB1157, JC3872	+	<i>his-4</i>	ΔNB	1.6 - 1.9	5-120	24, 28
JC3912, AB1886	<i>uvrA6</i>	<i>his-4</i>	ΔNB	1.4 - 1.7	0.25-15	24, 28
JC3890, TK603	<i>uvrB301</i>	<i>his-4</i>	ΔNB	1.7 ± 0.2	0.25-2	28, 29
AB1884	<i>uvrC34</i>	<i>his-4</i>	ΔNB	1.1 } <sup>d</sup> ~2 }	1-5 5-15	24
PAM579	<i>uvrB</i>	<i>his-4</i>	ΔNB	1.8	1-15	24
AB1885	<i>uvrB5</i>	<i>his-4</i>	ΔNB	2.0 } <sup>d</sup> <1 }	1-5 5-15	24
DY174	+	<i>leuB19</i>	ΔNB	2.0	3-80	37
DY178, SR315	<i>uvrB5</i>	<i>leuB19</i>	ΔNB	2.5-2.8	0.5-8	3, 37
SR312	<i>uvrA6</i>	<i>leuB19</i>	ΔNB	3.3	1-6.5	3
SR329	<i>uvrA155</i>	<i>leuB19</i>	ΔNB	2.9	1-8	3
SR314	<i>uvrA6 uvrB5</i>	<i>leuB19</i>	ΔNB	2.4	2-8	3

<sup>a</sup> *trpE65*, *tyr*, and *his-4* are ochre (UAA) nonsense mutations; *leu* is an amber (UAG) nonsense mutation; *leuB19* is a missense mutation.

<sup>b</sup> The symbol Δ signifies that the nutrient (e.g., tryptophan, Casamino Acids, nutrient broth, leucine, tyrosine, or histidine) was the growth-limiting factor in the mutant-selection medium, except for a fraction of the inoculum that had reverted to prototrophy for the phenotype being studied.

<sup>c</sup> Mutant frequency response data were replotted (if necessary) on log-log coordinates and the slope was determined for a line visually fitted to at least 3 points. Data for similar strains were pooled to get a range for two slopes or an average for three or more slopes.

<sup>d</sup> The brace indicates that the UV radiation MFR was clearly biphasic; thus, two slopes were derived.

was consistent with a two-hit mechanism that began to have an effect only above  $\sim 3 \text{ J m}^{-2}$ . An analysis of both our own mutagenesis data and those of Doudney (19) led us to different conclusions.

The quadratic equations derived for the  $\text{Lac}^+$  and  $\text{Leu}^+$  data (see Results) define a close-fitting curve (data not shown) through all of each respective set of data (in the former case excluding the fluence range of  $\sim 1$  to  $3 \text{ J m}^{-2}$ ). Since a similar smooth curve can also be drawn through all of Doudney's data (19; excluding the 1DM region data points) (data not shown), we presume that the 1DM "bump" (Fig. 3) represents a third mutagenic process, and it operates only between UV radiation fluences of  $\sim 1$  to  $3 \text{ J m}^{-2}$  in these *uvr* strains. The independence of this presumed third mechanism is further suggested by its presence in the  $\text{Lac}$  but absence in the  $\text{Leu}$  reversion system (compare Fig. 3 and 4), whereas the aforementioned one-hit and two-hit mechanisms both function in the  $\text{Lac}$  and  $\text{Leu}$  reversion systems of strain SR250.

The following analysis also suggests that, unlike our linear mechanism, the 1DM mechanism does not operate at UV radiation fluences greater than  $\sim 3 \text{ J m}^{-2}$  in strains SR250 and WP2<sub>s</sub>. Subtraction of the assumed contribution of the linear process from the total MFR (*lacZ53*  $\rightarrow$   $\text{Lac}^+$ ) achieved the expected two-hit kinetics for UV radiation mutagenesis. It seemed reasonable that if our apparently linear 1DM region (Fig. 3) was also the result of a process that was linear between  $\sim 1$  and  $6 \text{ J m}^{-2}$ , then the subtraction of its assumed contribution from the total MFR should yield data fitting a line with a slope of 2.0 even better than after subtracting the effect of the other linear process. This subtraction procedure was also performed with Doudney's data for *E. coli* B/r *uvrA* (WP2<sub>s</sub>) (19). We calculated the resultant MFR data (for both strains) to fit a line with a slope of  $\sim 6.5$  (data not shown). This result suggested to us that, rather than postulating a 6.5-hit error-prone mechanism, it is more reasonable to believe that a 1DM (?-hit) process does not operate at the same rate, if at all, at fluences above  $\sim 3 \text{ J m}^{-2}$ . This conclusion was also reached by Witkin (43) to explain a very similar phenomenon, the fluence-range limitation for thermal enhancement of UV radiation mutagenesis in a *tif-1* strain.

**Three mechanisms of UV radiation mutagenesis in *E. coli*.** Since the three components of the UV radiation MFR appear to function independently, they can be resolved as shown in Fig. 7. The one-hit component was subtracted from the total UV radiation MFR

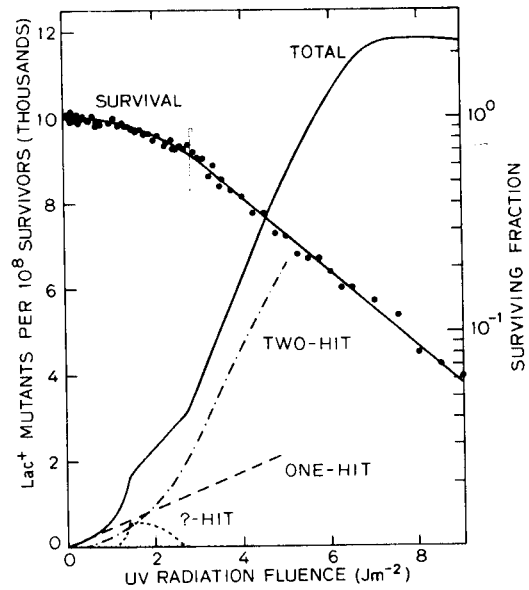


FIG. 7. UV radiation survival and mutagenesis to  $\text{Lac}^+$  of *E. coli* K-12 *uvrB5* (SR250) with presumed UV radiation MFR components. The "total" curve was taken from Fig. 3. The method of resolution of the one-hit, two-hit, and ?-hit components of the total UV radiation MFR curve is explained in the text.

curve (both taken from Fig. 3) to obtain coordinates for the two-hit component. A smooth curve was then drawn through these calculated points (excluding the data points for  $1.5$  to  $3.0 \text{ J m}^{-2}$ ). The ?-hit component was then plotted by using data obtained by subtracting the sum of the contribution from both the one-hit and the two-hit components from the total UV radiation MFR. Our resolution of these three proposed components indicates that the nonlinear nature of the  $\text{F}^2$  region (Fig. 3) appears to be largely a result of the contribution of the two-hit component.

We conclude that the UV radiation MFR in *E. coli* K-12 *uvrB5* (SR250), and perhaps other strains, is a result of three mechanisms, as depicted in Fig. 7: (i) a "one-hit" process that yields a previously undetected linear MFR that is readily observed at UV radiation fluences of  $< 0.5 \text{ J m}^{-2}$  (however, this process appears to operate at least up to  $6 \text{ J m}^{-2}$ ); (ii) a "two-hit" process that yields a fluence-squared MFR at fluences greater than  $\sim 0.5 \text{ J m}^{-2}$  (in part, approximating the 2DM region of Doudney [19]); (iii) a "?-hit" process that yields a MFR that does not appear to result from a one-hit or a two-hit process, but was initially designated by Doudney (19) as the 1DM region. This process is unusual in that it appears to initiate at  $\sim 1 \text{ J m}^{-2}$  and terminate at

$\sim 3 \text{ J m}^{-2}$  and is specific for nonsense reversion. This process may only occur in cells that have undergone a specific physiological change, e.g., involving the *tif* locus (41) or perhaps the blockage of DNA synthesis (19).

#### ACKNOWLEDGMENTS

We thank Richard C. Bockrath for valuable advice and discussion.

This investigation was supported by Public Health Service research grant CA-02896 and research program project grant CA-10372 from the National Cancer Institute.

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