DISCONTINUOUS DNA REPLICATION IN A lig-7 STRAIN OF Escherichia
COli IS NOT THE RESULT OF MISMATCH REPAIR, NUCLEOTIDE-EXCISION
REPAIR, OR THE BASE-EXCISION REPAIR OF DNA URACIL

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The question of whether discontinuous DNA replication operates only for the lagging strand or for both strands in <u>Escherichia coli</u> is still not resolved (10). Most <u>in vitro</u> data indicate that DNA replication is semi-discontinuous, i.e., continuous synthesis in the leading strand and discontinuous synthesis in the lagging strand (5, 13; see 6 for a review). In contrast, the <u>in vivo</u> data suggest that DNA replication is discontinuous in both strands (see 10). Evidence supporting discontinuous synthesis in both DNA strands <u>in vivo</u> comes mainly from studies with temperature-sensitive ligase (<u>lig</u>) mutants (4, 8, 9), and with DNA polymerase I (<u>polA</u>) mutants (5, 11, 14, 16), i.e., after pulse labeling these mutants with ³H-thymidine, virtually all of the radioactivity is found in short DNA chains. However, since ligase and DNA polymerase I are also required for the completion of several DNA repair processes (such as mismatch repair and excision repair), these results can also be interpretated

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to suggest that DNA replication is really continuous in the leading strand, but the observed strand interruptions result from some ongoing repair process. The inhibition of uracil-DNA glycosylase by an <u>ung</u> mutation did not eliminate the accumulation of short DNA chains in a <u>polA</u> strain (15), indicating that the excision of uracil residues in DNA plays little role in the observed discontinuous DNA synthesis in a <u>polA</u> strain.

It is not known, however, whether mismatch repair and other excision repair processes may account for the apparent discontinuous DNA replication observed in <u>polA</u> and <u>lig</u> mutants. In this communication, we examine the role of mismatch repair, nucleotide-excision repair, and the base-excision repair of DNA uracil in discontinuous DNA replication in a $\frac{1 + 7}{2}$ strain of $\frac{E}{2}$. $\frac{1 + 7}{2}$

The bacterial strains used in this work are listed in Table 1. The <u>mutL</u> and <u>mutS</u> mutants are deficient in mismatch repair (see 19), which removes mismatched bases from nascent DNA. The <u>uvrB5</u> mutant is deficient in the incision step of nucleotide-excision repair. The <u>ung-1</u> and <u>ung152</u>::Tn10

TABLE 1. \underline{E} . coli K-12 strains used^a

Strains	Genotype	Source or derivation (strain no.)
BD2328	Hfr KL16 ung152::Tn10 pheA97 nadB7	B. Duncan
SR292	F lig-7 proC hsp rpsL	K.B. Konrad (KS252)
SR294	F <u>uvrB5 lig-7 leuB19 metE70</u> <u>deo(C2?) lacZ53 malB45 rha-5</u> rpsL151 \(\lambda\)	D. Youngs
SR686	ung-l arghl ara-13 gal-6 lacYl malBl rha-7 xyl-7 thi-1 tonA2 rpsL9 supE44 \(\lambda^T\)	B. Duncan (BD1153)
SR 990	HfrH <u>pheAl8</u> ::Tn <u>l0</u> Δ(<u>qpt</u> - <u>lac</u>)5 thi relAl spoTl	N. Kleckner (NK6024)
SR1689	F mutS215::Tn10 thy metB1 lacY14	R. Fowler (ES1481)
SR1690	F mutl218::Tn10 trpA78 his leu arg thr	R. Fowler (KD1073)
SR1829	As SR294, also <u>pheAl8</u> ::Tn <u>10</u>	SR294 x Plvira [·] SR990, select Tc ^r
SR1830	As SR294	SR1829 x T4GT7 SR686, select Phe ⁺
SR1 83 1	As SR294, also <u>ung-l</u>	SR1829 x T4GT7 SR686, select Phe ⁺
SR1 832	As SR294, also <u>mutS215</u> ::Tn <u>10</u>	SR1830 x Plvira·SR1689 select Tc ^r
SR1833	As SR294, also <u>mutL218</u> ::Tn <u>10</u>	SR1830 x Plvira·SR1690 select Tc ^r
SR1 834	As SR294, also <u>ung-1</u> <u>mutS215</u> ::Tn <u>10</u>	SR1831 x Plvira·SR1689 select Tc ^r
SR1835	As SR294, also <u>ung-1 mutL218</u> ::Tn <u>10</u>	
SR2011	As SR294, also <u>ung152</u> ::Tn <u>10</u>	SR1830 x Plvira·BD2328 select Tc ^r

^aGenotype symbols are those used by Bachmann (1). Tc^r means tetracycline-resistance. Plvira was a reisolate of Plvir obtained from Dr. A.J. Clark.

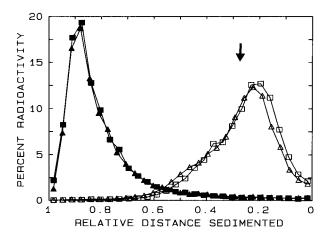


Figure 1. Effects of the uvrB5, ung and mutL(S) mutations on the size distribution of DNA synthesized at 42°C in a $\frac{1 \text{ig-7}}{1 \text{ig-7}}$ strain. Cells were grown in minimal medium (16) at 30°C . For prelabeling the DNA, [^{14}C]thymidine (51 Ci/mol) was added to logarithmic cultures at 1 μ Ci/ml, and the cultures were incubated at 30°C for 2 h before they were filter-washed and resuspended in the original volume of minimal medium. The cultures were grown to 5 x 10° cells per ml at 30°C , and then incubated at 42°C for 5 min before they were pulse-labeled with [^{3}H]thymidine (79.9 Ci/mmol) at 8.3 μ Ci/ml for 30 s. The pulses were terminated by the addition of an equal volume of an ice-cold solution composed of ethanol at 75%, phenol at 2%, sodium acetate (pH 5.3) at 20 mM and EDTA at 2 mM. Incorporation of [^{3}H]thymidine into DNA is about 5 x 10^{-4} cpm per cell. The resulting suspension was centrifuged, and the pellet was resuspended in 0.2 M NaOH containing EDTA at 10 mM. After incubation at 37°C for 1 h, the mixture was centrifuged to remove insoluble material. An aliquot (50 μ I) of the supernatant was layered on top of an alkaline sucrose gradient (5 to 20% in 0.1 N NaOH on top of a 0.5 ml cushion of 50% sucrose), and was centrifuged at 20 krpm for 16 h at 20°C . Gradients were collected and processed as previously described (17). Solid symbols are for prelabeled [^{14}C]DNA, while the open symbols are for [^{3}H]DNA. Squares (|||, and ||) are for uvrB |1iq-7 (SR1830) while triangles (|0, |4) are for uvrB5 |1iq-7 mutS215::Tn10, SR1833 (uvrB5, |1iq-7 mutL218::Tn10, and SR1834 (uvrB5 |1iq-7 mutS215::Tn10, SR1833 (uvrB5, |1iq-7 mutL218::Tn10, and SR1834 on and SR1835. The arrow indicates the position of a marker DNA of about 2,000 nucleotides in length, derived by digesting plasmid pACYC184 (2) with restriction endonucleases |EcoR1 and |Sa1I.

with earlier data on a single <u>liq-7</u> mutant (4, 8, 9). The presence of <u>unq-1</u>, ung152::Tn10, mutL(S), or a combination of the ung-1 and mutL(S) mutations in the <u>uvrB lig-7</u> strain had no effect on the size of newly-synthesized DNA (Fig. 1), and there was an absence of ³H-radioactivity in high-molecular-weight

If DNA replication is semidiscontinuous (i.e., continuous in the leading strand and discontinuous in the lagging strand), and there is no postreplicative repair processes operating on the nascent DNA strand, one would predict that about half of the ³H-radioactivity in newly-synthesized DNA should sediment in alkaline sucrose gradients as high-molecular-weight DNA, and half as short Okazaki fragments in a <u>liq</u> mutant. Since none of the pulse-labeled DNA from uvrB5 lig-7, uvrB5 lig-7 ung, uvrB5 lig-7 mutL(S), and uvrB liq-7 unq mutL(S) cells appeared in high-molecular-weight form, this indicates that the apparent discontinuous DNA synthesis observed in lig mutants is not the result of mismatch repair, nucleotide-excision repair, or the base-excision repair of DNA uracil.

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