**A DinB variant reveals diverse physiological consequences of incomplete TLS extension by a Y-family DNA polymerase**

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A DinB variant reveals diverse physiological consequences of incomplete TLS extension by a Y-family DNA polymerase

Daniel F. Jarosz, Susan E. Cohen, James C. Delaney, John M. Essigmann, and Graham C. Walker

The only Y-family DNA polymerase conserved among all domains of life, DinB and its mammalian ortholog pol κ, catalyzes proficient bypass of damaged DNA in translesion synthesis (TLS). Y-family DNA polymerases, including DinB, have been implicated in diverse biological phenomena ranging from adaptive mutagenesis in bacteria to several human cancers. Complete TLS requires dNTP insertion opposite a replication blocking lesion and subsequent extension with several dNTP additions. Here we report remarkably proficient TLS extension by DinB from Escherichia coli. We also describe a TLS DNA polymerase variant generated by mutation of an evolutionarily conserved tyrosine (Y79). This mutant DinB protein is capable of catalyzing dNTP insertion opposite a replication-blocking lesion, but cannot complete TLS, stalling three nucleotides after an N2-dG adduct. Strikingly, expression of this variant transforms a bacteriostatic DNA damaging agent into a bactericidal drug, resulting in profound toxicity even in a dinB* background. We find that this phenomenon is not exclusively due to a futile cycle of abortive TLS followed by exonucleolytic reversal. Rather, gene products with roles in cell death and metal homeostasis modulate the toxicity of DinB(Y79L) expression. Together, these results indicate that DinB is specialized to perform remarkably proficient insertion and extension on damaged DNA, and also expose unexpected connections between TLS and cell fate.

MazEF | proofreading | TonB

Y-family DNA polymerases are found in virtually all organisms and possess the remarkable ability to copy over lesions that otherwise stall DNA replication, a process termed translesion synthesis (TLS) (1). Such broadened substrate specificity comes at a mutagenic cost, however, as these enzymes display lower fidelities on undamaged DNA than their replicative counterparts (2–4). Organisms have therefore developed elaborate regulatory systems to restrict the access of Y-family DNA polymerases to appropriate primer termini (3–16). In E. coli, activity of both DinB (DNA pol IV) and UmuD2:C (DNA pol V) is strongly influenced by interactions with the β processivity clamp of DNA polymerase III (pol III) (10, 17, 18) and the umuD gene products, UmuD2 and UmuD’2 (5, 19–22). Other protein–protein interactions, notably with single stranded DNA binding protein (SSB) (19, 21), RecA (23–25), and RecFOR (26) also play critical roles in regulating TLS. In eukaryotes, TLS is similarly controlled by association with the PCNA processivity clamp (9, 13, 16, 27, 28), interaction with recombination proteins (29, 30), and by ubiquitylation of both PCNA and the polymerases themselves (7, 8, 13, 16, 27, 31, 32).

Several Y-family DNA polymerases display marked preference for catalysis on particular damaged substrates. Pol κ from yeast and humans preferentially replicates cyclobutane pyrimidine dimers (33–35), whereas E. coli DinB and its ortholog mouse DNA polymerase κ (pol κ) display strikingly elevated catalytic proficiency for dC insertion opposite N2-dG lesions (36). Diverse structural features contribute to these catalytic capabilities. Relatively accommodating active sites (37–39) and divergent C-terminal domains (40) facilitate TLS by several Y-family DNA polymerases. Specialized TLS function does not arise exclusively from open active sites, however. The active sites of both pol κ (41) and DinB (22) are somewhat closed under many conditions. This may occur at least in part through interaction with other proteins.

Although relatively little is known about the detailed molecular basis of intrinsic preference for replication of particular damaged substrates, specific active site residues in both pol κ and DinB are critical for TLS function. In E. coli DinB and yeast pol κ, mutation of F13 or F34, respectively, generates polymerase variants that are proficient for normal DNA synthesis but cannot catalyze TLS (36, 42). Similarly, mutation of Y52 in human pol κ profoundly reduces UV-induced mutagenesis, but does not alter catalysis of canonical DNA synthesis (43). Other such molecular determinants of TLS function assuredly exist (40). Some may be common to all Y-family DNA polymerases and others may be restricted to certain polymerases according to their distinct substrate specificities.

Complete TLS involves insertion of a nucleotide opposite an added base (i.e., lesion bypass) and extension by several subsequent additions. In eukaryotes these steps are often catalyzed by two distinct DNA polymerases (16). Replication by the TLS polymerase must continue beyond the DNA lesion, >5 nucleotides in the case of E. coli pol V, to avoid reversal by the proofreading activity of the replicative DNA polymerase (11). Consistent with a role in surveying the products of TLS, the E. coli dnaQ+ gene, which encodes the ρ processing subunit of pol III, affects several dinB+-dependent mutagenic phenomena (44–46). Thus, regulating the length of the products formed by TLS seems to be of critical importance. Those that are too small risk being removed by proofreading, and those that are too long carry undue mutagenic potential.

More broadly, recent studies hint that TLS may be connected to cellular stress response networks in unexpected ways (47–49). Lethality induced by hydroxyurea (HU)-mediated dNTP depletion can be abrogated by certain UmuC variants, and this requires dinB+ (47). Cytotoxicity from HU exposure also requires the toxin-antitoxin modules mazEF and relBE (47); in a wild-type (wt) background, deletion of these genes and tonB substantially prevents HU-induced cell death (50).

Here we report that DinB catalyzes strikingly proficient extension after dC incorporation opposite an N2-furfuryl-dG (N2-FG) DNA lesion. Preferential TLS extension of this magnitude has not previously been observed for any DNA polymerase. Moreover, a cluster of aromatic hydrophobic residues surrounding DinB’s steric gate dictate its function in TLS extension. Specifically, we demonstrate...
strate that Y79, which is invariant among DinB orthologs, critically influences the extension steps of DinB-catalyzed TLS. Expression of DinB(Y79) mutant proteins reveals profound toxicity that is mediated by DnaQ, MazEF, and the iron import protein TonB. Together, our data suggest that survival may be coupled to proper execution and completion of TLS through unexpected aspects of cellular physiology.

Results

DinB Catalyzes Preferential Extension on a Damaged DNA Template

We systematically analyzed DinB activity around a site-specific N2-furfuryl-dG lesion using staggered starting point primer extension assays. Primer termini initiated four base pairs before and ended four base pairs after the lesion (Table 1; primers described in Table S1 and Fig. S1). The apparent catalytic proficiency of DinB (Vmax/Km) on the damaged template is similar to an undamaged control for the first several additions we tested. As we previously reported, DinB is ~15-fold more proficient at catalyzing dC insertion opposite this lesion than opposite dG; this is largely due to a reduced Km for dCTP (36).

Strikingly, we found that DinB is even more proficient (~25-fold relative to an undamaged control) at extending from dC opposite the N2-furfuryl-dG lesion (Table 1). This effect arises primarily from a low Km for dATP addition. Subsequent extension steps proceed with comparable efficiencies on both damaged and undamaged templates. These observations reveal that both highly efficient insertion opposite an N2-furfuryl-dG lesion and highly efficient addition of the next nucleotide are specialized functions of DinB. Modest preferential extension activity has previously been observed for pol n nucleotide are specialized functions of DinB. Modest preferential activity of DinB (F13) is indispensable for its TLS function (36). This insight modulates its TLS function. (A) Structural model of conserved residues in the active site of DinB showing conserved residues (red), the N2-furfuryl moiety (yellow), and the incoming nucleotide (blue). (B) Mutation of Y79 eliminates the ability of DinB to complement NFZ sensitivity. Error bars, the standard deviation determined from three independent cultures.

Table 1. Steady state kinetic parameters for staggered primer extension assays

<table>
<thead>
<tr>
<th>Primer</th>
<th>Vmax, G</th>
<th>Vmax, N2-FG</th>
<th>Km, G</th>
<th>Km, N2-FG</th>
<th>Vmax/Km, G</th>
<th>Vmax/Km, N2-FG</th>
<th>N2-FG/G preference</th>
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<tbody>
<tr>
<td>G-5</td>
<td>557.8</td>
<td>668.9</td>
<td>83.2</td>
<td>27.9</td>
<td>6.7 × 10^6</td>
<td>2.4 × 10^5</td>
<td>3.6</td>
</tr>
<tr>
<td>G-4</td>
<td>755.9</td>
<td>2492.7</td>
<td>173.9</td>
<td>129.3</td>
<td>4.4 × 10^6</td>
<td>1.9 × 10^5</td>
<td>4.4</td>
</tr>
<tr>
<td>G-3</td>
<td>464.2</td>
<td>304.6</td>
<td>9.6</td>
<td>5.1</td>
<td>4.8 × 10^7</td>
<td>6.0 × 10^6</td>
<td>1.2</td>
</tr>
<tr>
<td>G-2</td>
<td>1081.7</td>
<td>1149.6</td>
<td>109.0</td>
<td>51.7</td>
<td>9.9 × 10^6</td>
<td>2.2 × 10^6</td>
<td>2.2</td>
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<tr>
<td>G-1</td>
<td>894.3</td>
<td>990.5</td>
<td>231.6</td>
<td>16.0</td>
<td>3.9 × 10^6</td>
<td>6.2 × 10^6</td>
<td>16.0</td>
</tr>
<tr>
<td>G + 1</td>
<td>619.8</td>
<td>886.3</td>
<td>42.2</td>
<td>2.35</td>
<td>1.5 × 10^7</td>
<td>3.8 × 10^6</td>
<td>25.7</td>
</tr>
<tr>
<td>G + 2</td>
<td>240.4</td>
<td>167</td>
<td>67.1</td>
<td>41.7</td>
<td>3.6 × 10^6</td>
<td>4.0 × 10^6</td>
<td>1.1</td>
</tr>
<tr>
<td>G + 3</td>
<td>188.2</td>
<td>150.3</td>
<td>24.9</td>
<td>8.4</td>
<td>7.6 × 10^6</td>
<td>1.8 × 10^6</td>
<td>4.4</td>
</tr>
<tr>
<td>G + 4</td>
<td>446.1</td>
<td>438.2</td>
<td>59.8</td>
<td>19.6</td>
<td>7.5 × 10^6</td>
<td>2.2 × 10^6</td>
<td>3.0</td>
</tr>
</tbody>
</table>

Vmax units are pmol min^-1 mg^-1; Km units are μM; Vmax/Km units are pmol min^-1 mg^-1 M^-1. Undamaged template designated G; N2-furfuryl-dG abbreviated as N2-FG.
DinB(Y79L) is proficient at both inserting a nucleotide opposite an \(N^2\)-FG lesion and adding the next nucleotide. DinB(Y79L) also has comparable activity to wt DinB on undamaged DNA (Fig. 2). However, products synthesized by DinB(Y79L) replicating a damaged template are shorter than those produced by wt-DinB. The majority arise from stalled synthesis three nucleotides after the lesion. At 5-nM enzyme concentration, the ratio of G + 3 stalled to full-length products is 4-fold higher for DinB(Y79L) than for wt DinB. However, this is insignificant relative to the same comparison on damaged DNA, where the ratio is 125-fold. As even wt DinB shows modest accumulation of this product at lower enzyme concentrations, this may arise from exacerbation of a natural pause site at the + 3 position. Notably, DinB has also been observed to stall three nucleotides following an \(N^2\)-dG DNA-protein cross-link in a different sequence context from the one we used (54). This suggests that such pausing may be an intrinsic property of DinB rather than an isolated effect of sequence context.

To examine the nature of DinB(Y79L)’s defect in TLS extension we examined its activity on primers synthetically elongated either two or three base pairs beyond the \(N^2\)-FG lesion. At the + 2 position, DinB(Y79L) showed similar activity to wt DinB on both undamaged (\(V_{\text{max}} = 654.8 \text{ pmol/min/mg}; K_M = 217.7 \mu\text{M}; V_{\text{max}}/K_M = 3.0 \times 10^6 \text{ pmol/min/mg/\muM}\)) and damaged templates (\(V_{\text{max}} = 442.9 \text{ pmol/min/mg}; K_M = 118.5 \mu\text{M}; V_{\text{max}}/K_M = 3.7 \times 10^6 \text{ pmol/min/mg/\muM}\)). In contrast, DinB(Y79L) showed a pronounced defect on the damaged template when extending from the primer synthetically elongated three base pairs beyond the \(N^2\)-FG lesion. Whereas DinB(Y79L) retains roughly half the activity of wt DinB for this addition on undamaged DNA, it is impaired by \(>20\)-fold on the damaged substrate (Table 2). Thus, the stalling behavior of DinB(Y79L) likely arises from communication between the already bypassed lesion and DinB’s active site, now at the + 3 position. There is an emerging precedent for such enzyme/template interactions. Catalysis of -1 frameshift mutagenesis in polyG regions by the archaeal DinB ortholog Dbh requires specific interactions between enzyme and template at the + 3 position to stabilize an extrahelical base (55). Similarly, contacts between enzyme and template allow replicative DNA polymerases to couple distal mismatch recognition to synthesis in the active site (56).

DinB(Y79L) expression does not increase the frequency of mutation to rifampicin resistance upon NFZ treatment (4.2 ± 2.0 \times 10^{-8} for pDinB(Y79L) vs. 5.5 ± 3.0 \times 10^{-8} for pDinB; average and standard deviation from five independent cultures), suggesting that it is relatively accurate. Thus, DinB(Y79L) is a type of DNA polymerase mutant that can catalyze formal lesion bypass but cannot finish the subsequent extension steps that are required to complete TLS. The strong toxicity of DinB(Y79L) expression indicates that the extension steps of TLS have at least as much physiological importance as lesion bypass itself.

Expression of DinB(Y79L) Changes NFZ from a Bacteriostatic to a Bactericidal Drug. Not only do DinB(Y79L) and DinB(F13V) confer NFZ hypersensitivity in a \(\Delta\text{dinB}\) background, but even more strikingly they do so in a \(\Delta\text{dinB}^+\) background (Fig. 3). In contrast, a catalytically deficient DinB mutant protein does not similarly increase NFZ sensitivity under these conditions (Fig. S4). We expressed wt DinB, DinB(Y79L), and DinB(F13V) from a low copy number plasmid (\(\sim5\) copies per cell) under the control of dinB’s native promoter (Plasmids described in Table S1). Such modest expression of \(\omega\text{DinB}\) does not result in the lethality that has been observed when it is overexpressed 30- to 140-fold in the AB1157 strain background (57) or when DinB is overexpressed to a lesser extent in the BW27786 strain background (58).

The extreme phenotypes arising from modest expression of DinB(Y79L) and DinB(F13V) led us to investigate the underlying cause of the increased NFZ sensitivity in greater detail.

### Table 2. Steady state kinetic parameters for extension from the G + 3 primer by DinB(Y79L)

<table>
<thead>
<tr>
<th>Template</th>
<th>Enzyme</th>
<th>(K_M) ((\mu\text{M}))</th>
<th>(V_{\text{max}})</th>
<th>(V_{\text{max}}/K_M)</th>
<th>Fold change</th>
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</thead>
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<tr>
<td>G-control/(G + 3)</td>
<td>WT DinB</td>
<td>59.8</td>
<td>446.1</td>
<td>7.5 \times 10^6</td>
<td>—</td>
</tr>
<tr>
<td>DinB(Y79L)</td>
<td>330.0</td>
<td>1072.0</td>
<td>3.2 \times 10^6</td>
<td>2.3</td>
<td></td>
</tr>
<tr>
<td>(N^2)-FG/(G + 3)</td>
<td>WT DinB</td>
<td>19.6</td>
<td>438.2</td>
<td>2.2 \times 10^7</td>
<td>—</td>
</tr>
<tr>
<td>DinB(Y79L)</td>
<td>1551.0</td>
<td>1416.0</td>
<td>0.9 \times 10^6</td>
<td>24.0</td>
<td></td>
</tr>
</tbody>
</table>

Units as in Table 1.
Consistent with the bacteriostatic rather than bactericidal mechanism of NFZ (59), we recovered an expected number of colony forming units from regions between colonies on NFZ agar plates for strains expressing DinB. In contrast, we were unable to recover any bacteria from strains expressing DinB(Y79L) or DinB(F13V), indicating that NFZ is transformed from a bacteriostatic into a bactericidal agent in the presence of these DinB mutants that are specifically unable to carry out normal TLS.

**Interaction between dinB and the e Proofreading Subunit of DNA Pol III.** These observations, along with the biochemical properties of DinB(Y79L) and DinB(F13V) raised the possibility that these mutant proteins may induce a futile cycle in which the immature TLS intermediates they produce are repeatedly destroyed by the proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III. A similar behavior has been observed for pol V (11), where extension of a TLS product by a proofreading activity of pol III.

We therefore examined DinB(Y79L) and DinB(F13V) expression in a \( \Delta\text{dnaQ} \) dinB \( \Delta^+ \) background. Deletion of \( \text{dnaQ} \) does not prevent DinB(Y79L) or DinB(F13V) expression from conferring NFZ sensitivity in a \( \Delta^+ \) background (Fig. 3 A and B). However, toxicity from DinB(Y79L) expression is partially reduced by \( \text{dnaQ} \) deletion (Fig. 3 A and B; Fig. S5A). Thus, NFZ killing brought about by DinB(Y79L), but not DinB(F13V), expression is at least partially due to a futile cycle of abortive TLS followed by proofreading. In *E. coli*, \( \text{dnaQ} \) deletion leads to suppressor mutations in \( \text{dnaE} \) (60, 61); these do not affect the phenotypes of any *dinB* allele used in this study.

Given the abundant reports of genetic interactions between *dnaQ* and TLS polymerases, including \( \Delta^+ \) (11, 44–46), we were surprised that \( \text{dnaQ} \) deletion had only a modest effect on NFZ sensitivity from DinB(Y79L) expression and none at all for DinB(F13V) expression. We therefore examined combinations of *dinB* deletion with a *dnaQ* deletion or *dnaQ903*, which encodes an e variant lacking an exonuclease domain and the C-terminal amino acids that mediate its interaction with pol III (61, 62). Both *dnaQ* alleles confer NFZ sensitivity, although the magnitude differs somewhat (Fig. S5B). In a *dnaQ903* mutant the N-terminal portion of DnaQ is present, providing a possible explanation for the differing NFZ sensitivities. This may point to additional DnaQ functions, other than proofreading, that are important for survival in NFZ. We observed an epistatic relationship with respect to NFZ sensitivity for each *dnaQ* allele and \( \Delta\text{dinB} \) (Fig. S5B) in which the double mutants behave most similarly to the *dnaQ* mutants alone. These observations confirm that *dnaQ* \( ^+ \) affects *dinB* function under conditions of NFZ exposure. However, this interaction does not entirely explain the NFZ sensitivity observed upon DinB(Y79L) or DinB(F13V) expression.

**Toxin-Antitoxin Pairs and Metal Homeostasis Modulate Toxicity of Abortive TLS.** We also examined the effects of DinB(F13V) and DinB(Y79L) expression in a variety of mutant backgrounds. The *mazEF* and *relBE* genes encode toxin-antitoxin modules that alter cellular physiology and metabolism in response to environmental stress, such as antibiotic exposure (63, 64). Inactivation of *mazEF* or *relBE* increases resistance to replication inhibition by HU (47). We considered whether toxin-antitoxin pairs might also mediate lethality associated with incomplete TLS. Strains bearing deletions of *mazEF*, *relBE*, or an alternative toxin-antitoxin pair *hipAB* are not themselves sensitive to NFZ (Fig. S6), and the effects of DinB(Y79L) and DinB(F13V) expression are unchanged in *relBE* and *hipAB* strains. However, DinB(Y79L) expression confers increased cell death in a *mazEF* strain at low NFZ doses (Fig. 4 A), suggesting that MazEF may protect the cell from abortive TLS intermediates. We do not observe this effect at higher doses of NFZ (Fig. 4 A), consistent with NFZ’s highly dose-dependent mode of action (59, 65–69). In contrast, there is no statistically significant difference in NFZ-mediated killing promoted by DinB(F13V) expression in a *mazEF* strain (Fig. S7), indicating that there is an important physiological difference between a failure to insert a lesion [DinB(F13V)] and a failure to sufficiently extend past a lesion [DinB(Y79L)].

We also examined the effect of *tonB* deletion on cytotoxicity from DinB(Y79L) and DinB(F13V) expression. The *tonB* gene encodes a ferric iron import protein that contributes to cellular lethality from oxidative stress (70) and HU (50), but not bactericidal drugs (71). At low NFZ doses *tonB* deletion completely suppresses lethality associated with DinB(F13V) expres-
sion and partially suppresses that associated with DinB(Y79L) expression (Fig. 4 B and C), indicating that incomplete TLS induces cellular toxicity linked to iron homeostasis. In contrast, at higher NFZ levels of DNA damage than on undamaged DNA. Preferential extension of this magnitude has not been reported for any Y-family DNA polymerase. In contrast to models for eukaryotic TLS that involve two DNA polymerases (16, 28, 72), E. coli DinB appears capable of catalyzing both insertion and extension with remarkable proficiency.

To explain these findings, we revisited our model of DinB encountering an N²-FG lesion. We noted that F12, F76, and Y79 along with F13 comprise a conserved core of aromatic residues. Each contributes to dinB⁺-dependent NFZ resistance. Mutation of F76 or F12 creates dinB variants that cannot complement the NFZ sensitivity of a ΔdinB strain. However, mutation of Y79 results in variants that confer NFZ hypersensitivity by as much as 50-fold. Based on similar behavior by dinB(F13V) in vivo, we anticipated that DinB(Y79L) would be unable to catalyze lesion bypass in vitro. Instead, we found that DinB(Y79L) is entirely proficient at dNTP insertion opposite an N²-FG adduct and three subsequent nucleotide additions. However, it is unable to catalyze the final extension steps of TLS. The striking toxicity of DinB(F13V) and DinB(Y79L) expression indicates that cellular survival is coupled to successful completion of TLS, and suggests that the extension steps of TLS are at least as physiologically important as dNTP insertion opposite an ad- duced base.

DinB(Y79L) or DinB(F13V) expression fails to complement the NFZ sensitivity of a ΔdinB strain and exerts a dominant effect on survival in dinB⁺ backgrounds. This effect is not seen with a catalytically deficient DinB variant under these conditions, and could be explained in part by the unique features of each mutant protein. The defect of a catalytically deficient DinB variant is manifested before dNTP insertion opposite a replication blocking lesion ever takes place. In contrast, both DinB(F13V) and DinB(Y79L) could participate in the initial steps of TLS that precede nucleotide insertion opposite a damaged base. The relatively late manifestation of their TLS deficiencies may restrict alternative mechanisms the cell can employ (Fig. S8). The inability of chromosomally expressed DinB to negate the effects of DinB(F13V) or DinB(Y79L) expression is especially unexpected. This finding suggests that, once TLS is initiated, dynamic exchange of DinB at the primer terminus may be considerably reduced, a commitment that may ne- cessitate increased regulation. Further investigation of this point may prove interesting, especially in light of recent studies regarding competition between DNA polymerases III and IV (57, 58).

Remarkably, expression of DinB(F13V) or DinB(Y79L) also trans- forms NFZ from a bacteriostatic into a bactericidal agent. Further investigation revealed complex genetic interactions that mediate the lethality of incomplete TLS. Loss of proofreading function partially suppresses the effects of DinB(Y79L) expression, but has no effect on toxicity induced by DinB(F13V) expression. Inactivation of the toxin-antitoxin pair mazEF enhances lethality from expression of DinB(Y79L) but not DinB(F13V), suggesting that it may serve to specifically protect cells from the consequences of incomplete TLS extension. Immature TLS intermediates produced by both DinB(Y79L) and DinB(F13V) lead to cell death through a mechanism involving the TonB iron import protein. Thus, the mechanisms of lethality differ somewhat depending on the nature of the abortive TLS, suggesting that these diverse cellular stress responses may be coupled to the precise execution of TLS at several stages.

How is lethality from abortive TLS related to other types of replication stress? Deletion of tonB partially mitigates killing due to replication arrest induced by HU (50). Similarly, the effects of DinB(F13V) and DinB(Y79L) expression are suppressed in a ΔtonB strain. We previously observed that ΔmazEF strains are strikingly resistant to HU (47). In contrast, deletion of mazEF increases NFZ sensitivity upon DinB(Y79L), but not DinB(F13V) expression. Thus, although common factors govern cellular responses to these different replication stresses, their precise roles differ considerably.

Together, our data point to the critical importance of the extension phase of TLS. DinB itself is especially proficient at dNTP addition immediately following an N²-FG lesion. Subsequent TLS extension requires communication between the bypassed lesion and the active site that proceeds through an evolutionarily conserved tyrosine. Failure to complete further extensions results in pronounced lethality upon NFZ exposure, suggesting that TLS extension is as physiologically important as lesion bypass itself. Our observations strongly indicate that TLS is far more nuanced than mere insertion of a dNTP opposite a damaged base and subsequent extension. Indeed, the precise execution of TLS appears to be connected to a variety of cellular processes with roles extending well beyond DNA metabolism. DinB’s exceptional catalytic proficiency, extreme cellular abundance (73), and elaborate regulation point to its critical and conserved function in TLS over ubiquitous DNA lesions.

Materials and Methods

Bacterial Strains and Plasmids. Strains, plasmids, and primers used in this study are described in Table S1. Plasmid borne dinB variants were produced either from a low-copy number plasmid containing dinB⁺ under its own promoter (74) or from a DinB expression plasmid (36) using site-directed mutagenesis. Plasmids were maintained with ampicillin (100 μg/mL).

Sensitivity to DNA damaging agents was determined as described in refs. 36 and 75. Saturated cultures were diluted 1,000-fold, grown to exponential phase in LB medium, and plated on LB agar containing 0–20 μM NFZ or 4-NQO. Survival was determined relative to growth in the absence of DNA damaging agent. Mutation frequency was measured by reversion to rifampicin resistance as described in refs. 36 and 75. Procedures for assessing bacteriostatic vs. bactericidal behavior are described in the SI Text accompanying this article.

Oligonucleotide Synthesis. Synthesis of oligonucleotides used as templates is described in detail in ref. 36. Nested primers for extension assays were purified by gel electrophoresis before use and are described in Table S1.

Protein Purification and Primer Extension Assays. Purification of wt DinB and DinB(Y79L) was performed as previously (75), and is described in detail in SI Text accompanying this manuscript. Primer extension assays were performed as described in ref. 36, using equivalent concentrations of wt DinB and DinB(Y79L) (1, 5, and 50 nM) as indicated in the figure legends. Running start assays were performed in 10-μL volumes with 10 nM primer/template and 250 μM dNTPs. Reactions were carried out in 50 mM Hepes (pH 7.5), 100 mM KCl, 7.5 mM MgCl₂, 5% glycerol, and 0.1% BSA. Starting-end experiments were performed in triplicate with 5 mM DinB and 0-, 1000 μM dNTP (Fig. S1). Reactions were quenched with formamide after 15 min. Products were separated by 16% denaturation polyacrylamide gel and quantified using a phosphorimager. When nucleotide addition resulted in multiple products, the sum of all products was used to calculate an apparent V_max and K_m.

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Rajosz et al.