Intragenic and Extragenic Suppressors of Temperature Sensitive Mutations in the Replication Initiation Genes dnaD and dnaB of Bacillus subtilis

The MIT Faculty has made this article openly available. Please share how this access benefits you. Your story matters.

Citation

As Published
http://dx.doi.org/10.1371/journal.pone.0006774

Publisher
Public Library of Science

Version
Final published version

Accessed
Thu Jan 03 16:32:59 EST 2019

Citable Link
http://hdl.handle.net/1721.1/52512

Terms of Use
Creative Commons Attribution

Detailed Terms
http://creativecommons.org/licenses/by/2.5/
Intragenic and Extragenic Suppressors of Temperature Sensitive Mutations in the Replication Initiation Genes dnaD and dnaB of Bacillus subtilis

Megan E. Rokop, Alan D. Grossman*

Department of Biology, Massachusetts Institute of Technology, Cambridge, Massachusetts, United States of America

Abstract

Background: The Bacillus subtilis genes dnaD and dnaB are essential for the initiation of DNA replication and are required for loading of the replicative helicase at the chromosomal origin of replication oriC. Wild type DnaD and DnaB interact weakly in vitro and this interaction has not been detected in vivo or in yeast two-hybrid assays.

Methodology/Principal Findings: We isolated second site suppressors of the temperature sensitive phenotypes caused by one dnaD mutation and two different dnaB mutations. Five different intragenic suppressors of the dnaD23ts mutation were identified. One intragenic suppressor was a deletion of two amino acids in DnaD. This deletion caused increased and detectable interaction between the mutant DnaD and wild type DnaB in a yeast two-hybrid assay, similar to the increased interaction caused by a missense mutation in dnaB that is an extragenic suppressor of dnaD23ts. We isolated both intragenic and extragenic suppressors of the two dnaBts alleles. Some of the extragenic suppressors were informational suppressors (missense suppressors) in tRNA genes. These suppressor mutations caused a change in the anticodon of an alanine tRNA so that it would recognize the mutant codon (threonine) in dnaB and likely insert the wild type amino acid (alanine).

Conclusions/Significance: The intragenic suppressors should provide insights into structure-function relationships in DnaD and DnaB, and interactions between DnaD and DnaB. The extragenic suppressors in the tRNA genes have important implications regarding the amount of wild type DnaB needed in the cell. Since missense suppressors are typically inefficient, these findings indicate that production of a small amount of wild type DnaB, in combination with the mutant protein, is sufficient to restore some DnaB function.


Editor: Ramy K Aziz, Cairo University, Egypt

Received June 22, 2009; Accepted July 30, 2009; Published August 26, 2009

Copyright: © 2009 Rokop, Grossman. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Funding: This work was supported by an HHMI Predoctoral Fellowship to MER and by NIH grant GM41934 to ADG. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

* E-mail: adg@mit.edu

Introduction

Initiation of DNA replication is an important event in the cell cycle. In bacteria, several proteins are required for initiation, but not elongation, of replication. DnaA is the most highly conserved replication initiation protein and is found in virtually all bacteria [1–3]. It binds to sequences in the chromosomal origin of replication, oriC, and causes melting of an AT-rich region in oriC creating an open complex. In addition to DnaA, the proteins needed to load the replicative helicase at the origin are also needed for replication initiation. In Bacillus subtilis, these include DnaD, DnaB (not to be confused with the E. coli replicative helicase DnaB), and DnaI. These proteins are conserved in low GC content Gram-positive bacteria and in some cases are known to be required for replication initiation [e.g., {4,5}]. In B. subtilis, all are needed to load the helicase (DnaC in B. subtilis) at oriC [6,7]. They are also needed to load helicase at stalled replication forks [8] in a process that normally requires the restart protein PriA [8–10]. Mutations that bypass the need for priA in replication restart have been described in both E. coli [11,12] and B. subtilis [8]. In E. coli, these mutations are typically in the gene for the helicase loader (E. coli dnaC) [11,12]. In B. subtilis, these mutations are in dnaB, part of the helicase loading machinery [6–8].

The dnaD and dnaB gene products are both essential proteins that interact with each other in vitro [13] and apparently in vivo [6]. DnaD also interacts with DnaA [14] and PriA [8–10]. In a growing population of cells, DnaB, but not DnaD, is normally found in membrane fractions of B. subtilis and dnaB is needed for enrichment of the oriC region in membrane fractions [6,15–17]. Temperature sensitive mutations in dnaD and dnaB cause a block in replication initiation at the non-permissive temperatures. Four temperature sensitive mutations in B. subtilis dnaB have been described: dnaB134ts (also called dnaB37ts), dnaB1ts, dnaB27ts, and dnaB19ts [17]. One temperature sensitive mutation in B. subtilis dnaD, dnaD23ts, has been described [18].

Previously, we described the isolation and characterization of suppressors (temperature resistant revertants) of the temperature sensitive phenotypes caused by dnaD23ts and dnaB134ts [6]. In both selections for temperature resistant revertants, we isolated the same missense mutation in dnaB, dnaBS371P, that causes a serine
to proline change at amino acid 371. That is, dnaBS371P is an extragenic suppressor of the temperature sensitive phenotype of dnaD23ts cells, and an intragenic suppressor of the temperature sensitive phenotype of dnaB134ts cells [6], dnaBS371P, also called dnaB37, had been isolated previously based in its ability to bypass the need for FtsA in replication restart [8]. It was isolated a third time, independently, based on its ability to suppress dnaD23ts [13]. The dnaBS371P mutant protein has increased affinity for DNA in vitro [7,8]. It also detectably interacts with DnaD in a yeast two-hybrid assay [6], in contrast to the lack of detectable interaction between wild type DnaB and DnaD [6,14,19]. The DnaBS371P mutant protein also recruits DnaD to the membrane fraction of B. subtilis cells, indicating an increased interaction between these proteins in vivo [6].

In addition to the extragenic suppressor of the dnaD23ts mutation, three different intragenic suppressors have been described [13]. Here we describe additional intragenic suppressors of the dnaD23ts mutation. We found that one of the intragenic suppressors caused increased interaction between the mutant DnaD and wild type DnaB in a yeast two-hybrid assay, similar to the increased interaction between wild type DnaD and the mutant DnaBS371P [6].

We also isolated suppressors of two different dnaBts mutations, dnaB19ts and dnaB37ts. In both cases, intragenic and extragenic suppressors were isolated. None of the extragenic suppressors were in replication genes and most appeared to be informational suppressors.

### Materials and Methods

**Media and growth conditions**

Briefly, rich medium (LB) was used for routine growth and maintenance of E. coli and B. subtilis. Transformations were done using standard procedures [20,21]. Antibiotics were used at the following concentrations: ampicillin (100 µg/ml); spectinomycin (100 µg/ml); chloramphenicol (5 µg/ml); and erythromycin (0.5 µg/ml) with lincomycin (12.5 µg/ml) to select for the mls marker.

**Strains and alleles**

E. coli strains used for cloning and procedures used for strain constructions were as previously described [6]. B. subtilis strains are listed in Table 1, and are derivatives of JH642 (AG174) that contain the trpC and pheA mutations. Suppressor strains are listed in Tables 2-4. dnaB and dnaD alleles discussed here are listed in Table 5.

### Table 1. B. subtilis strains used.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Relevant genotype</th>
<th>(notes)</th>
</tr>
</thead>
<tbody>
<tr>
<td>BB302</td>
<td>Tn917DHU162:ptv212A</td>
<td>(cat) this Tn917 insertion is linked to dnaA</td>
</tr>
<tr>
<td>K1346</td>
<td>zhb83::Tn917:pTV212A</td>
<td>(cat) this Tn917 insertion is linked to dnaB</td>
</tr>
<tr>
<td>K696</td>
<td>dnaB134ts-zhb83::Tn917 (mls)</td>
<td></td>
</tr>
<tr>
<td>KPL73</td>
<td>dnaD23ts-Tn917::XHU151 (mls)</td>
<td></td>
</tr>
<tr>
<td>KPL154</td>
<td>Tn917DHU151::ptv212A (cat) this Tn917 insertion is linked to dnaD</td>
<td></td>
</tr>
<tr>
<td>KPL314</td>
<td>dnaC-myc (spc)</td>
<td></td>
</tr>
<tr>
<td>MER271</td>
<td>dnaB19ts-zhb83::Tn917 (mls)</td>
<td></td>
</tr>
</tbody>
</table>

1. All strains are derived from JH642 and contain trpC pheA mutations. doi:10.1371/journal.pone.0006774.t001

### Table 2. Mutations that suppress the temperature sensitive phenotype caused by dnaDA166S (dnaD23ts).

<table>
<thead>
<tr>
<th>Suppressor mutation</th>
<th>Representative strain (#isolates)</th>
</tr>
</thead>
<tbody>
<tr>
<td>dnaBS371P</td>
<td>MER372 (5)</td>
</tr>
<tr>
<td>dnaD.154-155</td>
<td>MER373 (5)</td>
</tr>
<tr>
<td>dnaDA138G</td>
<td>MER369 (3)</td>
</tr>
<tr>
<td>dnaD7148M</td>
<td>MER383 (1)</td>
</tr>
<tr>
<td>dnaDA166S</td>
<td>MER370 (1)</td>
</tr>
<tr>
<td>dnaDW188L</td>
<td>MER382 (1)</td>
</tr>
</tbody>
</table>

1. All strains are derived from KPL73, and except for the dnaDA166S mutant, all contain the indicated mutation, dnaD23ts (dnaDA166T) and the linked Tn917DHU151.
2. One representative strain is indicated, along with the total number of independent isolates that were sequenced.

### Table 3. Mutations that suppress the temperature sensitive phenotype caused by dnaBK85E (dnaB134ts).

<table>
<thead>
<tr>
<th>Suppressor mutation</th>
<th>Representative strain (#isolates sequenced; total @in group)</th>
</tr>
</thead>
<tbody>
<tr>
<td>dnaBS371P</td>
<td>MER505 (5; 6)</td>
</tr>
<tr>
<td>dnaBK66S</td>
<td>MER512 (5; 1)</td>
</tr>
<tr>
<td>dnaBS151P</td>
<td>MER524 (1; 6)</td>
</tr>
<tr>
<td>dnaBA164V</td>
<td>MER510 (2; 6)</td>
</tr>
<tr>
<td>dnaBE288K</td>
<td>MER517 (3; 6)</td>
</tr>
<tr>
<td>likely in rrnO</td>
<td>MER498 (2)</td>
</tr>
</tbody>
</table>

1. All strains are derived from KPL69 and contain the indicated suppressor, dnaB134ts (dnaBK85E) and the linked Tn8833:Tn917 (mls).
2. One representative strain is indicated, along with the total number of independent isolates that were sequenced. In addition, the second number in parentheses indicates the total number of mutants with a phenotype indistinguishable from that of the sequenced representatives.

### EMS mutagenesis

We also isolated suppressors of dnaB19ts following mutagenesis with ethyl methanesulfonate (EMS). For the mutagenesis, dnaB19ts cells are grown at 30°C. The suppressors found were wild type, indicating that the mutation, at least the one cloned, is most likely in an rRNA gene in the rrn operon.
(MER271) cells were grown in LB medium at 30°C to an OD$_{600}$ = 0.4. Cells were washed twice with LB and resuspended to an OD$_{600}$ = 1.0. Seven independent pools of cells were mutagenized in LB with 1.2% EMS (Sigma) for 30 minutes at 30°C, and then washed twice with LB. Cells were grown for four generations at 30°C in LB without mutagen for recovery, and plated on LB at 45°C or 48°C for selection of temperature resistant suppressors.

Classification and mapping of suppressor mutations
Suppressor mutations were classified and mapped essentially as described [6]. Briefly, colonies of suppressor strains were purified three times and grouped by growth phenotypes on LB plates described [6]. Briefly, colonies of suppressor strains were purified three times and grouped by growth phenotypes on LB plates.

### Table 4. Mutations that suppress the temperature sensitive phenotype caused by dnaBA379T (dnaB19ts).

<table>
<thead>
<tr>
<th>Suppressor mutation</th>
<th>Representative strain (#isolates sequenced; total # in group)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>dnaBT355I MER284 (1; 7)</td>
</tr>
<tr>
<td>2</td>
<td>dnaBT366N MER281 (1; 5)</td>
</tr>
<tr>
<td>3</td>
<td>trnO-ala anticodon MER280 (1; 8)</td>
</tr>
<tr>
<td>4</td>
<td>trnA-ala anticodon MER274 (2; 4)</td>
</tr>
<tr>
<td>5</td>
<td>trnB-ala anticodon MER283 (1; 1)</td>
</tr>
</tbody>
</table>

1 All strains are derived from MER271 and contain the indicated suppressor, dnaB19ts (dnaBA379T) and the linked zhb83::Tn917 (mhs).
2 One representative strain is indicated, along with the total number of independent isolates that were sequenced. In addition, the second number in parentheses indicates the total number of mutants with a phenotype indistinguishable from that of the sequenced representative.

Two-hybrid analysis

DNA alleles dnaD23A154-155, dnaD23W188L, dnaD23T148M, and dnaD23A138G were amplified by PCR from the appropriate chromosomal DNA and inserted into the vector pGBDU-C3 to create in frame fusions of DnaD23A154-155, DnaD23W188L, DnaD23T148M, and DnaD23A138G to the DNA binding domain (DBD) of the Gal4 transcription factor [26]. The resulting plasmids, pMR81 (encoding DBD-DnaD23A154-155), pMR82 (encoding DBD-DnaD23W188L), pMR83 (encoding DBD-DnaD23T148M), and pMR80 (encoding DBD-DnaD23A138G) were individually co-transformed with pMR58 (encoding AD-DnaB) into the yeast strain DWY112, and the yeast two-hybrid analysis was performed as described previously [6].

### Table 5. Summary of dnaB and dnaD mutations discussed in this work.

<table>
<thead>
<tr>
<th>Allele (other names)</th>
<th>Comments/phenotype</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>dnaDA166T (dnaD23)</td>
<td>temperature sensitive</td>
<td>[18]</td>
</tr>
<tr>
<td>dnaD154-155A166T</td>
<td>$\Delta$154-155 suppresses A166T (DnaD23)</td>
<td>this work</td>
</tr>
<tr>
<td>dnaDA138G A166T</td>
<td>A138G suppresses A166T</td>
<td>this work</td>
</tr>
<tr>
<td>dnaDT148MA166T</td>
<td>Y148M suppresses A166T</td>
<td>this work</td>
</tr>
<tr>
<td>dnaDA166S</td>
<td>A166S isolated as a suppressor of A166T</td>
<td>this work</td>
</tr>
<tr>
<td>dnaDA166T W188L</td>
<td>W188L suppresses A166T</td>
<td>this work</td>
</tr>
<tr>
<td>dnaDA166TL193I (dnaD235)</td>
<td>L193I suppresses A166T</td>
<td>[13]</td>
</tr>
<tr>
<td>dnaD155-156A166T</td>
<td>$\Delta$155-156 suppresses A166T</td>
<td>[13]</td>
</tr>
<tr>
<td>dnaRA3279T (dnaB19)</td>
<td>temperature sensitive</td>
<td>[17]</td>
</tr>
<tr>
<td>dnaRA8KSE (dnaB134; dnaB37)</td>
<td>temperature sensitive</td>
<td>[17]</td>
</tr>
<tr>
<td>dnaBS371P (dnaB75)</td>
<td>suppresses: dnaDA166T (dnaD23), dnaBK85E (dnaB134)</td>
<td>[6,8,18]</td>
</tr>
<tr>
<td>dnaBH65K8SE</td>
<td>H65Y suppresses K85E (DnaB134)</td>
<td>this work</td>
</tr>
<tr>
<td>dnaBK85E151P</td>
<td>S151P suppresses K85E</td>
<td>this work</td>
</tr>
<tr>
<td>dnaBK85E A164V</td>
<td>A164V suppresses K85E</td>
<td>this work</td>
</tr>
<tr>
<td>dnaBK85E288K</td>
<td>E288K suppresses K85E</td>
<td>this work</td>
</tr>
<tr>
<td>dnaBK85E371P</td>
<td>S371P suppresses K85E</td>
<td>this work</td>
</tr>
<tr>
<td>dnaRT355A379T</td>
<td>T355I suppresses A379T (DnaB19)</td>
<td>this work</td>
</tr>
<tr>
<td>dnaRT366NA379T</td>
<td>T366N suppresses A379T</td>
<td>this work</td>
</tr>
</tbody>
</table>

1 The mutant allele is named using the convention indicating the wild type amino acid, the codon number and the mutant amino acid. Intragenic suppressors contain the original mutation (dnaBK85E, dnaBA379T, or dnaDA166T) as indicated.

doi:10.1371/journal.pone.0006774.t005
**Rationale**

DnaD and DnaB are involved in multiple protein and DNA interactions. The existence of mutations in dnaB that cause altered interaction between DnaB and DnaD indicate that these proteins are likely targets for regulatory factors. One approach to study DnaB and DnaD, and to possibly identify regulators of their functions, is to identify second site mutations that suppress phenotypes caused by dnaB and dnaD mutations. In the case of intragenic second site suppressors, this approach also has the potential to provide structure-function insights. To these ends, we isolated and characterized second site suppressors of a temperature sensitive mutation in dnaD and two different temperature sensitive mutations in dnaD. Temperature resistant revertants were isolated and characterized phenotypically to determine which were most likely to be second site suppressors and not simple back mutations. Isolates that were more temperature resistant than the original mutant, but also more temperature sensitive than the true wild type were chosen for further analyses. Most of the second site suppressors were intragenic and the dnaD and dnaB alleles discussed in this work are listed in Table 5.

**Isolation of suppressors of the temperature sensitive phenotype caused by dnaD23ts**

We isolated 25 independent spontaneous suppressors (temperature revertants) of the temperature sensitive phenotype caused by the dnaD23ts mutation (summarized in Table 2). The dnaD23ts allele (dnaDA166T) causes an alanine to threonine change at amino acid 166 of DnaD [18]. Five of the 25 suppressors were extragenic and all contained the dnaBS371P mutation (Table 2, line 1) described previously [6,13].

The remaining 20 apparently intragenic suppressor mutants fell into six classes based on differences in growth and colony phenotypes on LB plates at a series of temperatures. The phenotypes of one group of 9 independent revertants were indistinguishable from those of wild type dnaD cells. They grew as well as wild-type through the full range of temperatures at which wild-type grows. We chose not to characterize these because it was not clear that they represented second site suppressors.

The remaining 11 suppressor mutants fell into 5 groups. All of these suppressor mutations were sequenced and found to be in dnaD (Table 2). They include: dnaDT148M and dnaDW188L, each isolated once and dnaDA138G isolated three times independently. Another group of intragenic suppressors consisted of one isolate, which contained the suppressor mutation dnaDA166S. The original dnaD23ts mutation causes an alanine to threonine change at amino acid 166 [18], and thus this suppressor mutation, which causes an alanine to serine change at amino acid 166, suppresses the temperature sensitivity caused by dnaD23ts by changing the threonine at position 166 of the mutant DnaD23 to a serine.

The final group of dnaD23ts suppressors consisted of five isolates, all of which contained the identical intragenic suppressor mutation. This mutation is a deletion of six base pairs from a region that contains a repeat of the five base pair sequence 5'-CAGGA. This six base pair deletion (between the repeated sequence) leads to deletion of two amino acids in DnaD, amino acids 154 (asp) and 155 (gln). We refer to the allele of dnaD that contains both this deletion and the original mutation that causes the temperature sensitivity as dnaD23A154-155 (Table 2, line 2).

Three intragenic suppressors of dnaD23ts were described previously [13]. These include: dnaD321 causing a leucine to valine change at codon 193 (dnaDL193V), dnaD325 causing a leucine to isoleucine change also at amino acid 193 (dnaDL193I), and dnaD326 causing a deletion of glutamine and aspartate at amino acids 155 and 156 (dnaDA155-156). All three of these suppressors are different from the alleles described here, although the 2 amino acid deletions are remarkably similar. That we isolated different alleles in our experiments indicates that none of the selections have been saturated.

**dnaD23A154-155 allows for the detection of the physical interaction between DnaD and DnaB**

We previously found that the only extragenic suppressor isolated in the dnaDts selection, dnaBS371P, allowed for detection of an interaction between DnaB and DnaD in a yeast two-hybrid assay [6]. Just as dnaBS371P is located at the region of DnaB that is similar to a family of phage replication proteins [6], the five intragenic suppressors of dnaDts were also located in the phage homology region of DnaD. We used yeast two-hybrid analysis [26] to test whether any of the dnaDts intragenic suppressors allowed for a detectable interaction between mutant DnaD and wild-type DnaB.

We found that DnaD23A154-155 and DnaB interact in the yeast two-hybrid assay. We fused DnaB to the activation domain (AD) and DnaD23A154-155 to the DNA binding domain (DBD) of the yeast transcription factor Gal4. In this system, a physical interaction between the Gal4 AD and DBD domains will drive expression of ADE2, thereby allowing for growth of the yeast on medium lacking adenine [26]. We found that yeast expressing AD-DnaB and DBD-DnaD23A154-155 grew on medium lacking adenine, indicating that DnaD23A154-155 and DnaB physically interact (Figure 1). Although we have not tested this directly, we suspect that in *B. subtilis*, the dnaD23A154-155 mutation allows for increased or unregulated interactions to occur between DnaB and DnaD, just as dnaBS371P does [6].

In contrast to the yeast two-hybrid results indicating increased interaction between DnaD23A154-155 and DnaB, we did not detect physical interactions between the other mutant forms of DnaD and DnaB. Wild-type DnaB did not detectably interact in

![Image of yeast two-hybrid results](https://example.com/image.png)

**Figure 1. DnaD23A154-155 interacts with DnaB.** Yeast two-hybrid analysis was used to examine physical interactions between DnaB fused to the activation domain (AD) and wild-type and mutant forms of DnaD fused to the DNA binding domain (DBD) from the Gal4 transcription factor. A physical interaction activates the expression of ADE2, allowing for growth on medium lacking adenine. Plate section 1, upper right (AD-DnaB, DBD-DnaD23A154-155), shows that DnaB and DnaD23A154-155 interact. Plate section 2, lower right (AD-DnaB, DBD-DnaD), confirms previous results that DnaB and DnaD do not detectably interact in the two-hybrid assay. Plate sections 3, lower left (AD-DnaB, DBD-DnaD23W188L), and section 4, upper left (AD-DnaB, DBD-DnaD23T148M), show that DnaB does not detectably interact with DnaD23W188L or DnaD23T148M in this assay. doi:10.1371/journal.pone.0006774.g001
the two-hybrid assay with either DnaD23T148M or DnaD23W188L (Figure 1). The intragenic suppressor dnaB23A158G did not yield reproducible results, and the intragenic suppressor dnaD1166S was not tested.

Possible mechanisms of intragenic suppression of dnaD23ts

There are multiple mechanisms by which intragenic suppressors could partly restore function to the DnaDA166T (DnaD23ts) mutant protein. Wild type DnaD is an oligomer [27,28], binds to and can remodel DNA [9,13,28-32], and forms a scaffold on DNA [28,29]. It also interacts with DnaA [14] and DnaB [6,9,13]. DnaD has two domains with different functions. The N-terminal domain (amino acids 1-128) has oligomerization activity and the C-terminal domain (aa 129-232) has DNA binding activity and DNA-induced oligomerization activity [28 activities].

The DnaDA166T (DnaD23ts) mutant protein has decreased binding to ssDNA in vitro, and decreased cooperativity of binding [9,13]. The mutation is in the C-terminal DNA binding domain of DnaD. In vivo, the mutant protein is unstable, but this instability does not seem to be the primary cause of the temperature sensitive phenotype [13]. This conclusion is based on the finding that increased amounts of the mutant protein expressed from a plasmid do not suppress the temperature sensitive phenotype and the previously described intragenic suppressors did not seem to function simply by increasing stability of the mutant protein [13].

One of the intragenic suppressors, DnaD23A154-155, caused increased interaction with DnaB, possibly contributing to the mechanism of suppression. The loss of these two residues likely uncovers an otherwise hidden DnaB binding site. This phenotype is similar to that caused by the extragenic suppressor of dnaD23ts that is in dnaB. This extragenic suppressor, dnaBS371P, causes increased interaction with DnaD [6]. It also causes DnaB to have increased affinity for DNA [7,8]. It is not yet known if the DnaDA154-155 mutant has increased DNA binding, but the mutation is in the domain that binds DNA. It is possible that the other intragenic suppressors of dnaD23ts restore the normally cooperative DNA binding and/or cause increased interaction with DnaB, although any potential increase in interaction with DnaB was not detected in a yeast two-hybrid assay.

It is also possible, although probably less likely, that the suppressors compensate for the defect caused by dnaDA166T (dnaD23ts) by altering some other aspect of DnaD function. For example, the suppressors could alter the oligomeric state of DnaD, affect interaction with DnaA, or possibly make DnaD less sensitive to uncharacterized negative regulatory factors affecting replication initiation. The suppressors are not in the N-terminal region of DnaD that contains the main oligomerization activity (aa 1-128) [20]. However, the C-terminal domain of DnaD has a DNA-stimulated oligomerization activity [28], making a possible effect on oligomerization plausible. Likewise, the suppressor mutations are not in the region of DnaD (aa 1-140) that is known to interact with DnaA [14]. However, it is not known if the C-terminal region (aa 141-232) contributes to the interaction with DnaA nor is it known if there are residues in this region that normally reduce the interaction between DnaD and DnaA. Of course, these possibilities are not mutually exclusive and the mechanisms of suppression could involve multiple activities of DnaD and be different for different alleles.

Intragenic suppressors of dnaB134ts and dnaB19ts mutations

We isolated 41 independent spontaneous suppressors of dnaB134ts (dnaBk83E). In addition, we isolated a total of 31 independent suppressors of dnaB19ts (dnaBa379T), some spontaneous and some following EMS mutagenesis (Materials and Methods). Suppressor strains were grouped based on growth and colony phenotypes at different temperatures and representatives of each phenotypic group were tested for linkage to different replication genes, as described above. Then, representative suppressor alleles from different linkage and phenotypic groups were sequenced (Tables 3, 4). There were 6 suppressors of dnaB19ts that were phenotypically indistinguishable from wild type. One of these was sequenced and was a back mutation restoring dnaB+ and the others were not characterized further. There were 5 suppressors of dnaB134ts that were phenotypically indistinguishable from wild type. Since it was not clear that these were second site suppressors, none were characterized further.

dnaBS371P suppresses dnaB134ts. As reported previously, dnaBS371P is an intragenic suppressor of dnaB134ts (dnaBk83E) [6]. This suppressor allele was present in five independent isolates that were sequenced. A sixth suppressor strain isolated in this selection had the same phenotype as these five and likely also contains this same mutation (Table 3, line 1).

Other intragenic suppressors of dnaB134ts. There remaining intragenic suppressors of dnaB134ts fell into four groups based on growth and colony phenotypes at a series of temperatures. All groups contained members that were linked to dnaB and the sequence of at least one representative from each group was determined (Table 3, lines 2–5). One class contained six isolates, two of which were sequenced and each had the suppression mutation, dnaBA164V. Another group contained five isolates, one of which was sequenced and had the suppression mutation dnaBH653Y. Another group contained six isolates, three of which were sequenced. Each had the suppression mutation dnaBE288K. The final group contained six isolates, one of which was sequenced and found to contain the suppressor mutation dnaBS151P.

Intragenic suppressors of dnaB19ts. There were two groups of intragenic suppressors of dnaB19ts (dnaBk83E) (Table 4, lines 1–2). One group contained five isolates, one of which was sequenced and found to contain the suppressor mutation dnaBT366N. The other group contained seven isolates, one of which was sequenced and found to contain the suppressor mutation dnaBT353L. dnaBS371P was not isolated as a suppressor of dnaB19ts.

Possible mechanisms of intragenic suppression of dnaB134ts and dnaB19ts

As with dnaD, there are multiple mechanisms by which the intragenic suppressors could partly restore function to DnaBk83E (DnaB134ts) or DnaBa379T (DnaB19ts). Little is known about the mechanismic defects caused by these dnaB mutations, so it is difficult to know if the suppressors restore normal function or compensate for decreased function by increasing some other aspect of DnaB function. Wild type DnaB is found in membrane fractions of cells and is involved in the enrichment of oriC in membrane fractions [6,15–17], although it is not itself an integral membrane protein as shown. DnaB is a tetramer [9,31,33] and binds to and remodels DNA [31]. In addition, it interacts with DnaD [6,13] and DnaI [7]. Presumably, most, if not all, of these properties are important for DnaB function in replication initiation. The intragenic suppressors could stimulate one or more of these functions or an as yet uncharacterized property of DnaB. Since dnaBS371P (DnaB75) has increased DNA binding [7] and increased interaction with DnaD [6,13], and is an intragenic suppressor of dnaB134ts, it is plausible that some of the other intragenic suppressors could work similarly.
Extragenic suppressors of dnaB19ts and dnaB134ts mutations

Informational suppressors of dnaB19ts. Three classes of suppressors of dnaB19ts were extragenic, as they were not linked to dnaB. All of these mutations caused allele-specific suppression and the mutants formed very small colonies on LB plates. Cells appeared normal in phase contrast microscopy (data not shown). Suppressors from one of these groups were linked to Tn917ΔH163 (near dnaA), but did not appear to be in dnaA. A ribosomal RNA and rRNA gene cluster (rrnO) is also linked to this transposon, and based on the growth phenotype and linkage, we suspected that the suppressors might be informational. We PCR-amplified and sequenced trnO-ala from the rrnO operon of one of the suppressor mutants and found a mutation in the rrnO-ala gene that changes the anti-codon from recognizing an alanine codon to one that will recognize a threonine codon (Table 4, line 5). That is, the mutant rRNA-ala gene contained the exact missense mutation that should allow the alanine tRNA to read the mutant codon in the dnaB19ts mRNA and insert the wild type alanine in place of the mutant threonine.

Based on the finding that a mutation in trnO-ala suppressed the temperature sensitive phenotype caused by dnaBA379T, we decided to sequence the rrnO-ala genes from at least one representative of the other two groups of suppressors with similar phenotypes. There are six tRNA-ala genes (including trnO-ala). We found that, in the three additional mutants that were characterized, each had a mutation that changes the anti-codon from recognizing an alanine codon to recognizing a threonine codon. In total, two sequenced isolates were in trnA-ala, and one each was in trnB-ala and trnO-ala (Table 4, lines 3–5).

Extragenic suppressors of dnaB134ts are probably in rRNA or tRNA genes. Two groups of the dnaB134ts (dnaB835E) suppressors were not linked to dnaB and thus were extragenic. These caused phenotypes similar to those of the suppressors of dnaB19ts that were in tRNA genes. That is, all of the extragenic suppressors of dnaB134ts were allele-specific and caused slow growth. One group of suppressors (Table 3, line 6) contained a mutation that was linked to Tn917ΔH163 (near the rrnO–rrn operon) and suppressors in the other group were not linked to the rrnO operon and were not characterized further.

We cloned the rrnO operon from one suppressor mutant into the integration vector pGEMcat. When integrated into the chromosome of a dnaB134ts (dnaB835E) mutant, this clone was able to suppress the temperature sensitive phenotype, indicating that it contained the suppressor mutation. We sequenced the two tRNA genes in the rrnO operon, trnO-ala and trnO-ile, from all four suppressors in this class, i.e., the cloned rrnO operon and the other three that were not cloned. In all four suppressors, trnO-ala and trnO-ile were wild type. This was not completely surprising since the mutation in dnaB134ts is in a lysine codon (changing it to glutamate) and not in an alanine or isoleucine codon.

These extragenic suppressors of dnaB134ts were not likely to be in any regulatory factor affecting replication initiation. Rather, we suspect that, while not in trnO-ala or trnO-ile, they might still be informational suppressors, and at least the one we cloned is likely to be in one of the rRNA genes of the rrn operon (Table 3, line 6). Informational suppressors are most common in tRNA genes and the most widely known are nonsense suppressors. However, mutations in ribosomal components that affect translational fidelity and cause informational suppression have been known for a long time [34–36]. These can be in ribosomal protein genes or in rRNA genes [37,38]. We suspect that the suppressor of dnaB134ts that appears to be in the rrnO cluster, but that is not in either of the tRNA genes in the rrn operon, is in the 16S rRNA gene and might be causing translational misreading, thereby allowing for synthesis of some wild type DnaB protein.

Perspectives

The isolation of temperature resistant revertants of dnaDs and dnaB19ts mutants did not result in the identification of new regulators of DNA replication. Most of the revertants were intragenic and some were allele-specific informational suppressors. The nature of these mutations have functional implications for DnaB and DnaD.

The isolation of mutations in tRNA-ala genes that are informational suppressors of the temperature sensitive phenotype caused by the dnaB19ts mutation has some interesting implications regarding DnaB function. The efficiency of suppressor tRNAs that suppress missense mutations is generally very low [39]. This low frequency would result in only a small amount of wild type DnaB in the cell, and most of the protein would still be the mutant DnaBA379T (dnaB19ts). The finding that alanine tRNA mutations are able to suppress the temperature sensitivity of dnaB19ts cells implies that the amount of wild-type DnaB necessary for the cell is much lower than the amount of DnaB found in wild-type cells. It may be that there is excess DnaB in wild-type cells, and thus decreasing the concentration of functional DnaB is not harmful to cells. In addition, since DnaB is a tetramer, it is possible that mixed tetramers are functional and perhaps only a single wild type protein in a tetramer is sufficient for function and restoration of temperature resistant growth to dnaB19ts cells. We have not tested these possibilities.

Intragenic suppressors of dnaD23ts that increase interaction with DnaB, and mutations in dnaB that increase interaction with DnaD and suppress dnaD23ts, together indicate that increased interaction between these proteins might be an important part of suppression. Perhaps DnaB and DnaD naturally interact in vivo, as indicated by weak interactions in vitro. The mutations that increase this interaction could either strengthen the interaction or increase the frequency of interaction, perhaps by bypassing a normal regulatory step. The increased interaction could restore a function defective in the mutant protein or enhance a different function, thereby compensating for the defect in the mutant protein. The mechanisms by which these mutations affect DnaD and DnaB should become clearer with more structural analyses of these essential replication initiation proteins.

Acknowledgments

We thank Bill Burkholder, Jenny Auchtung, and Soni Laceyfield Shimoda for reagents and helpful advice.

Author Contributions

Conceived and designed the experiments: MER ADG. Performed the experiments: MER. Analyzed the data: MER ADG. Contributed reagents/materials/analysis tools: MER. Wrote the paper: MER ADG.

References


