Limits to the Role of Palindromy in Deletion Formation

KATHLEEN WESTON-HAFER1 AND DOUGLAS E. BERG1,2*

Departments of Molecular Microbiology1 and Genetics,2 Box 8230, Washington University School of Medicine, St. Louis, Missouri 63110

Received 2 July 1990/Accepted 16 October 1990

We tested the effect of palindromy on deletion formation. This involved a study of reversion of insertion mutations in the pBR322 amp gene at a site where deletions end either in 9-bp direct repeats or in adjoining 4-bp direct repeats. Inserts of palindromic DNAs ranging from 10 to more than 26 bp and related nonpalindromic DNAs were compared. The frequency of deletions (selected as Ampr revertants) was stimulated by palindromy only at lengths greater than 26 bp. The 4-bp direct repeats, one component of which is located in the palindromic insert, were used preferentially as deletion endpoints with palindromes of at least 18 bp but not of 16 or 10 bp. We interpret these results with a model of slippage during DNA replication. Because deletion frequency and deletion endpoint location depend differently on palindrom length, we propose that different factors commit a molecule to undergo deletion and determine exactly where deletion endpoints will be.

Short repeated sequences are commonplace in bacterial DNAs. They specify important structural features in rRNAs and tRNAs, often serve as sites of regulation of gene expression, and may also help maintain the overall organization of DNA domains in the bacterial nucleoid (8, 9, 12, 18). Repetitive sequences can also cause instability, however. DNA sequencing showed that the endpoints of spontaneous deletions occur preferentially in short direct repeats (1, 6, 17). In addition, many deletions are associated with palindromic DNAs, and it has been tempting to imagine that even inverted repeats of just a few base pairs can provoke deletion events (1, 7, 14).

Tests based on the reversion of insertion mutations have been used to examine deletion formation more closely. We found that deletion frequencies increased with palindrome length in the range of 22 to 90 bp, up to 18,000-fold at some sites, as little as 8-fold at others (5). These outcomes indicated that both palindromy and other subtle features of DNA sequence affect the deletion process. Palindromes may stimulate deletion events by allowing hairpin structures to form in single-stranded DNAs that then provoke slippage errors during DNA synthesis (Fig. 1). Given the abundance and importance of short or imperfect inverted repeats in bacterial DNAs, it became interesting to test directly the effects of palindrom length on deletion events.

We exploited a set of insertions at a site in the pBR322 amp gene. Here we report that changes in palindrome size from 10 to 22 bp did not significantly affect deletion frequencies, measured as the formation of Ampr revertants. Deletions at this site can end in 9-bp direct repeats of amp sequence that bracket the insert or in 4-bp repeats, one copy of which is in the insert (Fig. 2). Here we report that the 4-bp repeat is used preferentially for palindromes of at least 18 bp but not for palindromes of 16 or 10 bp. This implies different thresholds for effects of palindromy on the local probability of deletion and the exact location of deletion endpoints.

MATERIALS AND METHODS

General procedures. Media, bacterial growth, plasmid DNA extractions, recombinant DNA cloning, and restriction endonuclease analyses have been described elsewhere (10, 11). DNA sequences were determined by the chain termination method (13) adapted for double-stranded DNA (19). The primer used to sequence new insertion mutant alleles (near pBR322 positions 3730 to 3740) and representative revertant alleles corresponds to pBR322 positions 3677 to 3693 (5'-GGCGAGTTACATGATCC). Synthetic oligonucleotides were made on an Applied Biosystems 380A DNA synthesizer.

Bacterial strains. Escherichia coli K-12 derivative MC1061 (4) was the host for both plasmid constructions and reversion tests; GM119 (Dam-) (2) was used for DNAs to be digested with BclI. All plasmids used are derivatives of pBR322 (Amp' Tet').

Amp' insertion mutant alleles. Palindromes of 18 and 20 bp at site A10 were made as follows. Plasmid DNA containing inserts of a segment consisting of 45-bp inverted repeats bracketing the kan gene from Tn5 at site A10 was digested with BclI and either 2 or 4 bp were removed by digestion with mung bean nuclease prior to religation to generate palindromes of 20 and 18 bp, respectively (16).

The 12-bp palindrome at site A10 was made by oligonucleotide mutagenesis. pBR322 DNA was digested with PvuI (pBR322 position 3735) and religated with complementary oligonucleotides designed to create a 12-bp palindrome

\[
5'\quad \text{CGCCTCGTTAGACGAGTCCGAT} \\
\text{TAGCGACAGTCTGCGAGGC}
\]

(XbaI site underlined). The 16-bp palindrome was made by digesting the 12-bp palindrome with XbaI and filling in with the Klenow fragment of DNA polymerase I before religation. To make the 10-bp palindrome at site A10, the 12-bp palindrome was digested with XbaI, followed by limited digestion with mung bean nuclease and religation. All new palindromic inserts were confirmed by DNA sequencing.

The 10-bp nonpalindromic inserts at site A10 were made by oligonucleotide mutagenesis as described for the 12-bp palindrome. pBR322 DNA was digested with PvuI and ligated to the double-stranded oligonucleotide

\[
5'\quad \text{CGCCTCGTTNNNCTCGGAT} \\
\text{TAGCGACAGNNNNNGAGGC}
\]

where N represents an equimolar mixture of G, A, T, and C.

* Corresponding author.
Amp<sup>+</sup> alleles were sequenced, and three different nonpalindromic inserts were recovered (see Table 2).

Reversion tests. Amp<sup>+</sup> revertant frequencies were measured in clones grown in L broth for about 32 cell doublings from the founding cell prior to plating on L agar with ampicillin (250 μg/ml) as described previously (5, 16). Each frequency reported represents the median of determinations with at least five separate single-cell clones and counts of 100 to 300 revertant colonies from each clone. The frequencies generally varied by less than a factor of three in repeated determinations.

Analysis of Amp<sup>+</sup> revertants. Amp<sup>+</sup> revertants formed by deletion at site A10 (changes at position 3740) were analyzed by colony hybridization. Two types of revertants (T/A or C/G at position 3740) were obtained and were distinguished with complementary oligonucleotide probes, one containing T and the other containing C at the critical position (16). The sequences of the probes used are 5'-CTCCGATCGTTGT CAG (T probe) and 5'-CTCCGATCGCTGTCAG (C probe).

RESULTS AND DISCUSSION

Palindrome length affects deletion frequency and endpoint location. To study deletion formation, we constructed a series of insertions at the A10 site in the pBR322 amp gene and then measured the frequency of reversion from Amp<sup>+</sup> to Amp<sup>+</sup> (Table 1). The effect of moderate-sized palindromes on deletion frequency at this site is illustrated by the 100-fold
difference in stability of the 32- versus 22-bp palindromic sequence was also investigated. The data in Table 1 also showed that the distribution of deletion endpoints between the 9- and 4-bp direct repeats was strongly affected by palindromic length, when less than 26 bp. In particular, with palindromes of 22, 20, and 18 bp, two-thirds of deletion endpoints were in the 4-bp repeats, whereas with palindromes of 16 or 10 bp, only one-sixth of deletion endpoints were in the 4-bp repeats. Thus, the placement of deletion endpoints was markedly more sensitive to differences in the length of short palindromes than is the frequency of deletion.

Deletion of short nonpalindromic inserts. To test the idea that for very short palindromes the inverted repeat structure per se is not important as a determinant of either the frequency of deletion or the location of deletion endpoints, we constructed three nonpalindromic variants of the 10-bp insert, differing only in the second set of 5 bp (Table 2, column 1). We found a 50-fold variation in reversion frequency among the four alleles at this site (Table 2); the palindromic insert was actually less deletion prone than the other three alleles. In addition, the use of the 4-bp direct repeats as deletion endpoints ranged from 5 to 17%, independent of palindromy (Table 2). Thus, for deletions of 10-bp inserts, palindromy does not significantly influence the frequency of deletion or the precise location of deletion endpoints.

TABLE 1. Effect of palindromic length on deletion formation

<table>
<thead>
<tr>
<th>Palindrome length (bp)</th>
<th>Amp⁰ reversion frequency</th>
<th>Fraction of endpoints in 4-bp repeats</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>5.5 × 10⁻⁷</td>
<td>10/58 (0.17)</td>
</tr>
<tr>
<td>16</td>
<td>7.2 × 10⁻⁷</td>
<td>12/71 (0.17)</td>
</tr>
<tr>
<td>18</td>
<td>9.4 × 10⁻⁷</td>
<td>63/98 (0.64)</td>
</tr>
<tr>
<td>20</td>
<td>1.2 × 10⁻⁶</td>
<td>66/95 (0.69)</td>
</tr>
<tr>
<td>22⁻</td>
<td>9.5 × 10⁻⁷</td>
<td>51/78 (0.65)</td>
</tr>
<tr>
<td>26⁻</td>
<td>1.5 × 10⁻⁶</td>
<td>33/35 (0.94)</td>
</tr>
<tr>
<td>32⁻</td>
<td>1.1 × 10⁻⁴</td>
<td>67/72 (0.93)</td>
</tr>
</tbody>
</table>

* Palindrome sequences are as follows:
  10 bp, cgtgacagctggg
  16 bp, cgtgcttgagccccgc
  18 bp, cgtgcTCTGGagccccgc
  20 bp, cgtgctcttgagccccgc
  22 bp, cgtgctcttgtaTctagagccccgc
  26 bp, cgtgctcttgatccTCTGGagccccgc
  32 bp, cgtgctcttgatccTCTGGagccccgc

b From Weston-Hafer and Berg (16).

Differences in the frequency of deletion of the same palindromic sequence from different locations had been explained by nonrandom pausing and loss of processivity by DNA polymerases, as seen in vitro (3, 15). We propose that such a sequence- and conformation-dependent effect is reflected in the distribution of endpoints seen here: the preferential use of the 4-bp repeats during deletion of 18-bp and larger palindromes versus the preferential use of the 9-bp repeats during deletion of 16- and 10-bp palindromes and of nonpalindromic DNA. Given this threshold (18 bp versus 16 bp), the finding that palindromic length affects deletion frequency only with palindromes longer than 26 bp implies that the local frequency of DNA synthesis errors and their exact locations are controlled differently. One interesting possibility is that deletion events are provoked by local perturbations in the balance of replication proteins, for example, an undersupply of single-stranded DNA-binding protein (Ssb) and that the chance of such an imbalance is also sequence and conformation dependent. Thus, the local probability of slippage could be increased by palindromy only with palindromes longer than 26 bp, while the chance that DNA lacking Ssb protein provokes slippage after copying the first 4 bp becomes significant with hairpin structures of at least 16 bp.

ACKNOWLEDGMENTS

We thank L. Henry for skilled technical assistance.

This research was supported by National Science Foundation grant DMB-8608193, Public Health Service grant GM-37138 from the National Institutes of Health, and Department of Energy grant DEFG02-89ER60862 to D.E.B.

REFERENCES