Cleavage of a DNA–RNA–DNA/DNA chimeric substrate containing a single ribonucleotide at the DNA–RNA junction with prokaryotic RNases HII

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Abstract We have analyzed the cleavage specificities of various prokaryotic Type 2 ribonucleases H (RNases H) on chimeric DNA–RNA–DNA/DNA substrates containing one to four ribonucleotides. RNases HII from Bacillus subtilis and Thermococcus kodakaraensis cleaved all of these substrates to produce a DNA segment with a 5′-monoribonucleotide. Consequently, these enzymes cleaved even the chimeric substrate containing a single ribonucleotide at the DNA–RNA junction (5′-side of the single ribonucleotide). In contrast, Escherichia coli RNase HII and B. subtilis RNase HIII did not cleave the chimeric substrate containing a single ribonucleotide. These results suggest that bacterial and archaeal RNases HIII are involved in excision of a single ribonucleotide misincorporated into DNA.

Key words: Type 2 ribonuclease H; DNA–RNA–DNA/DNA heteroduplex; DNA–RNA junction; Bacillus subtilis; Thermococcus kodakaraensis

1. Introduction

Ribonuclease H (RNase H) degrades only the RNA strand of an RNA/DNA heteroduplex [1]. The enzyme is ubiquitously present in various organisms. Single bacterial and eukaryotic cells often contain two different RNases H, which show little sequence similarity with each other [2,3]. Based on the difference in the amino acid sequences, RNases H are classified into two major families, Type I and Type II RNases H [2,3]. Type 1 enzymes include bacterial RNases H1, eukaryotic RNases H1, and the RNase H domains of reverse transcriptases. Type 2 enzymes include bacterial RNases HII and IIII, archaeal RNases HIII, and eukaryotic RNases HII. According to this classification, mammalian RNases H are classified into RNases H1 and H2. However, they have been classified into Class I (RNase H1) and Class II (RNase HII) RNases H, based on the difference in the biochemical properties of the enzymes purified from the cells [4]. Class I RNase H from calf thymus (RNase H1) has recently been shown to consist of two subunits with molecular masses of 32 kDa and 21 kDa [5]. This 32 kDa subunit is equivalent to RNase H2 and is enzymatically active as judged by renaturation gel assay.

It has been suggested that mammalian RNases H1 are involved in the removal of Okazaki fragments together with flap endonuclease-1 (FEN-1) [6,7]. These mammalian enzymes specifically recognize an RNA–DNA junction region and cleave RNA–DNA/DNA heteroduplex to produce a DNA segment with a 5′-monoribonucleotide, which is then digested by FEN-1. In addition to these mammalian enzymes, yeast RNase H(35) [8], which is a Type 2 RNase H [9], archaeal RNases HIII [10–12], and bacterial RNase HII [2] exhibit similar cleavage specificity on RNA–DNA/DNA or DNA–RNA–DNA/ DNA substrates. Coordination of Type 2 RNase H with FEN-1 in Okazaki fragment removal has also been proposed for yeast RNase H(35) [8] and archaeal RNase HIII [10,12]. A yeast strain lacking both of the RNase H(35) and FEN-1 genes has been shown to exhibit lethal phenotype [8]. In bacteria, which lack FEN-1, Okazaki fragments are removed by RNase H and the 3′→5′ exonuclease activity of DNA polymerase I [13].

The major RNase H purified from K562 human erythro-leukemia cells hydrolyzes a DNA–RNA–DNA/DNA substrate containing a single ribonucleotide at the DNA–RNA junction (5′-side of the single ribonucleotide), suggesting that it is involved in ribonucleotide excision from genomic DNA during DNA replication [14]. This RNase H has been designated as RNase H(1) (terminology is altered from RNase H1 to avoid confusion in this report). It remained to be determined whether human RNase H(1) is related to RNase H1 or H2. However, its enzymatic properties and subunit structure are similar to those of calf thymus RNase H1, suggesting that it is related to RNase H2. Therefore, an ability to cleave DNA–RNA junction excision from genomic DNA during DNA replication may be one of the characteristics common to Type 2 RNases H. However, it remained to be determined whether prokaryotic Type 2 RNases H cleave a DNA–RNA junction as well.

Several prokaryotic Type 2 RNases H, such as Escherichia coli RNase HII [15,16], Bacillus subtilis RNases HII and IIII [2], and RNases HII from hyperthermophilic archaea Thermococcus kodakaraensis KOD1 [11] and Archaeoglobus fulgidus [10,12], have been overproduced in E. coli, purified, and biochemically characterized. In this report, we analyzed cleavage specificities of B. subtilis RNase HIII, B. subtilis RNase HIII, and T. kodakaraensis RNase HIII in comparison with that of E. coli RNase H1 using chimeric DNA–RNA–DNA/DNA
heteroduplexes containing one to four ribonucleotides as substrates.

2. Materials and methods

2.1. Materials

[4′-32P]ATP (> 5000 Cimnmol) was obtained from Amer sham. Cro- tobacter durians phosphodiesterase was from Boehringer Mannheim. DNA–RNA–DNA chimeric oligonucleotides (5′-CGTCCC[rA]nCCGTGC-3′) and their complementary DNA oligonucleotides were chemically synthesized by Fasmac Co.

2.2. Enzyme preparation

E. coli RNase HI [17], T. kodakaraensis RNase HII [11], and B. subtilis RNases HIII and HIII [2] were overproduced in E. coli and purified as reported previously. The concentrations of these proteins were determined from the UV absorption on the basis that the absorbance at 280 nm of a 0.1% solution is 2.0 for BSA, and 0.62 for B. subtilis RNase HIII. These values, except that of E. coli RNase HI which has been experimentally determined [18], were calculated by using ε of 1576 M⁻¹ cm⁻¹ for Tyr and 5225 M⁻¹ cm⁻¹ for Trp at 280 nm [19].

2.3. Cleavage of DNA–RNA–DNA/DNA heteroduplexes

The DNA–RNA–DNA strands were 32P-labeled at the 5′-end. These 32P-labeled DNA–RNA–DNA strands (1.0 μM) were hybridized with 1.5 molar equivalents of the complementary DNA strands to produce hybrid duplexes. These duplexes are designated as [rA]ₙ substrates, in which n represents the number of adenosines. Hydrolysis of the substrate was carried out at 30°C for 15 min in 10 mM Tris–HCl (pH 8.0) containing 50 mM NaCl, 1 mM 2-mercaptoethanol, 0.1 mg/ml bovine serum albumin (BSA), and 10 mM MgCl₂ (for E. coli RNase HI and T. kodakaraensis RNase HIII), 10 mM Tris–HCl (pH 8.0) containing 50 mM KCl, 1 mM 2-mercaptoethanol, 0.1 mg/ml BSA, and 10 mM MnCl₂ (for B. subtilis RNase HIII), or 10 mM Tris–HCl (pH 8.5) containing 100 mM NaCl, 1 mM 2-mercaptoethanol, 0.1 mg/ml BSA, and 50 mM MgCl₂ (for B. subtilis RNase HIII).

The hydrolysates were separated on a 20% polyacrylamide gel containing 7 M urea as described in Section 2. The concentration of the substrate is 1.0 μM. These hydrolysates were identified by comparing their migrations on the gel with those of the oligonucleotides generated by the partial digestion of the 32P-labeled DNA–RNA–DNA with snake venom phosphodiesterase [20].

For the determination of the kinetic parameters, the concentrations of the substrate were varied from 0.1 to 1.0 μM. The amount of enzyme was controlled such that the ratio of the hydrolyzed substrate did not exceed 30% of the total. The hydrolysis of the substrate with the enzyme follows Michaelis–Menten kinetics, and the kinetic parameters, Kₘ and Vₘₐₓ, were determined from the Lineweaver–Burk plot.

3. Results

It has previously been shown that E. coli RNase HI, which represents Type 1 RNases H, cleaves the 20 bp chimeric DNA–RNA–DNA/DNA substrate containing four ribonucleotides (adenosines) (dT₈–rA₄–dT₃–dT₄–dT₈–dT₄–dT₄) exclusively at the phosphodiester bond between the third and fourth adenosines [21]. However, its cleavage efficiency dramatically decreased as the number of adenosines in the chimeric substrates decreased below three. As a result, E. coli RNase HI could not cleave the chimeric substrate containing one or two adenosines. In contrast, human RNase H(I), which may represent mammalian Type 2 RNases H, cleaved the dT₈–rA₂–dT₃–dA₅–dT₈–dT₄ exclusively at the phosphodiester bond between the third and fourth adenosines [14]. In addition, it cleaved even the chimeric substrate containing single adenosine at the 5′-side of this adenosine. To examine whether bacterial and archaeal Type 2 RNases H show similar substrate specificity to that of human RNase H(I), a series of chimeric DNA–RNA–DNA (5′-CGTCC-
HII cleaved the [rA]1 substrate less effectively than T. kodakaraensis RNase HII cleaved these substrates in a similar manner as described in the legend for Fig. 1. HII is shown in Fig. 2A and summarized in Fig. 2B. RNA junction. In addition, B. subtilis is at least 10 times larger than that of T. kodakaraensis RNase HII, because the amount of RNase HII required for complete cleavage of this substrate karaensis RNase HII, because the amount of B. subtilis RNase HII are at least twice as much as that of B. subtilis RNase HII. B. subtilis RNase HII less effectively cleaved even the [rA]1 substrate than B. subtilis RNase HII.

Cleavage of the [rA]1–4 substrates with E. coli RNase HI is shown in Fig. 4A and summarized in Fig. 4B. E. coli RNase HI cleaved the [rA]1 substrate almost exclusively at the middle of the tetra-adenosine. It cleaved the [rA]3 substrate at the phosphodiester bond between the first and second adenosines.

It also cleaved the [rA]1 substrate exclusively at the DNA–RNA junction.

Cleavage of the [rA]1–4 substrates with B. subtilis RNase HII is shown in Fig. 2A and summarized in Fig. 2B. B. subtilis RNase HII cleaved these substrates in a similar manner as did T. kodakaraensis RNase HII. However, B. subtilis RNase HII cleaved the [rA]1 substrate less effectively than T. kodakaraensis RNase HII, because the amount of B. subtilis RNase HII required for complete cleavage of this substrate is at least 10 times larger than that of T. kodakaraensis RNase HII. In addition, B. subtilis RNase HII cleaved the [rA]1–4 substrates less site-selectively than T. kodakaraensis RNase HII. Both enzymes cleaved these substrates at minor sites as well, which include the DNA–RNA junction and all possible RNA–RNA linkages. However, B. subtilis RNase HII cleaved at these minor sites more efficiently than T. kodakaraensis RNase HII.

Cleavage of the [rA]1–4 substrates with B. subtilis RNase HII is shown in Fig. 3A and summarized in Fig. 3B. B. subtilis RNase HII cleaved the [rA]4 substrate at the phosphodiester bonds between the first and second, the second and third, and the third and fourth adenosines to similar extents. It has previously been shown that B. subtilis RNase HII cleaves the 29 bp DNA–RNA–DNA/DNA substrate preferentially at the phosphodiester bond between the second and third adenosines, and less preferentially at those between the first and second, and the third and fourth adenosines [2]. This disagreement might be due to the difference in the length and/or sequence of the DNAs flanking both sides of tetra-adenosine. B. subtilis RNase HII cleaved the [rA]1 substrate at the phosphodiester bonds between the first and second, and the second and third adenosines, but with much less efficiency. It cleaved the [rA]2 substrate quite poorly at the phosphodiester bond between the first and second adenosines, and did not cleave the [rA]3 substrate. Because the amount of B. subtilis RNase HIII required for complete cleavage of the [rA]4 substrate is at least twice as much as that of B. subtilis RNase HIII, B. subtilis RNase HIII less effectively cleaved even the [rA]1 substrate than B. subtilis RNase HIII.

Cleavage of the [rA]1–4 substrates with E. coli RNase HI is shown in Fig. 4A and summarized in Fig. 4B. E. coli RNase HI cleaved the [rA]1 substrate almost exclusively at the middle of the tetra-adenosine. It cleaved the [rA]3 substrate at the phosphodiester bond between the first and second adenosines.

Fig. 2. Cleavage of DNA–RNA–DNA heteroduplexes by B. subtilis RNase HII. A: Hydrolysis of the 5’-end-labeled DNA–RNA–DNA containing four (a), three (b), two (c), or one (d) adenosine(s) hybridized to the complementary DNA with B. subtilis RNase HII and separation of the hydrolysates were carried out as described in the legend for Fig. 1. B: Cleavage sites of each DNA–RNA–DNA heteroduplex with B. subtilis RNase HII are shown as described in the legend for Fig. 1.

Fig. 3. Cleavage of DNA–RNA–DNA heteroduplexes by B. subtilis RNase HII. A: Hydrolysis of the 5’-end-labeled DNA–RNA–DNA containing four (a), three (b), two (c), or one (d) adenosine(s) hybridized to the complementary DNA with B. subtilis RNase HII and separation of the hydrolysates were carried out as described in the legend for Fig. 1. B: Cleavage sites of each DNA–RNA–DNA heteroduplex with B. subtilis RNase HII are shown as described in the legend for Fig. 1.
with much less efficiency, and did not cleave the [rA]$_1$ and [rA]$_4$ substrates. These results agree with those obtained using the 20 bp DNA–RNA–DNA/DNA substrate [21].

The kinetic parameters of *T. kodakaraensis* RNase HII and *B. subtilis* RNase HII for hydrolysis of the [rA]$_1$ and [rA]$_4$ substrates are summarized in Table 1. The $K_m$ and $k_{cat}$ values of these enzymes for hydrolysis of the [rA]$_1$ substrate are comparable to those for hydrolysis of the [rA]$_4$ substrate. These results suggest that reduction in the number of ribonucleotides in the chimeric substrate from four to one seriously affects neither the binding affinity nor the hydrolysis rate.

When the kinetic parameters of *T. kodakaraensis* RNase HII are compared with those of *B. subtilis* RNase HII, the $K_m$ value of the former enzyme is comparable to that of the latter, whereas the $k_{cat}$ value of the former enzyme is higher than that of the latter by roughly 20-fold, whatever the substrate is. Hence, these two enzymes differ mainly in the hydrolysis rate.

### 4. Discussion

In this study, we showed that *T. kodakaraensis* RNase HII and *B. subtilis* RNase HII cleaved even the [rA]$_1$ substrate at the DNA/RNA junction. In contrast, *E. coli* RNase HI and *B. subtilis* RNase HIII did not cleave this substrate. These results suggest that this cleavage specificity is a characteristic common to bacterial RNase HIII, archaeal RNases HII, and eukaryotic RNases H2. In addition, the current results, as well as the previous ones [2,10–12], indicate that bacterial RNase HII, archaeal RNases HII, and eukaryotic RNases H2 cleave RNA–DNA/DNA and DNA–RNA–DNA/DNA substrates containing multiple ribonucleotides to produce a DNA segment with a single ribonucleotide at the 5'-terminus whereas *E. coli* RNase HI and *B. subtilis* RNase HIII do not. Thus, Type 2 RNases H, except for bacterial RNases HIII, are clearly distinct from Type 1 RNases H in substrate specificities.

The kinetic studies indicate that *T. kodakaraensis* RNase HII, as well as *B. subtilis* RNase HII, interact with the [rA]$_1$ and [rA]$_4$ substrates with similar affinities and cleave these substrates with similar hydrolysis rates. In contrast, the kinetic studies of *E. coli* RNase HI using the dT$_7$-(rA)$_n$-dT$_7$ol dA$_7$-(rA)$_n$ substrates have previously shown that reduction in the number of ribonucleotides in the chimeric substrate from four to three does not seriously affect the binding affinity, but seriously affects the hydrolysis rate [21]. These results suggest that the [rA]$_1$ substrate binds to *T. kodakaraensis* RNase HII and *B. subtilis* RNase HII such that the RNA/DNA hybrid region can contact the active-sites of these enzymes, whereas it binds to *E. coli* RNase HI such that the RNA/DNA hybrid region cannot contact the active site of the enzyme. This difference may be ascribed to the structural difference in the substrate-binding sites of these enzymes.

Comparison of the crystal structures of *E. coli* RNase HI [24,25] and *T. kodakaraensis* RNase HII [23], which represent those of Type 1 and Type 2 RNases H, revealed that these two enzymes share a main chain fold consisting of a five-stranded β-sheet and two α-helices. In addition, steric configurations of the four acidic active-site residues are conserved in these two structures. These results suggest that Type 1 and Type 2 RNases H hydrolyze substrates by a similar mechanism. However, *E. coli* RNase HI and *T. kodakaraensis* RNase HII differ in the location of the substrate-binding domain. The former contains it as an internal domain termed basic protrusion, whereas the latter contains it as an extra C-terminal domain. According to the model for a complex between DNA/RNA hybrid and *E. coli* RNase HI [26] or *T. kodakaraensis* RNase HII [23], the length of the substrate covered by *T. kodakaraensis* RNase HIII is shorter than that covered by *E. coli* RNase HI. Therefore, *T. kodakaraensis* RNase HIII may interact with a substrate less strictly than does *E. coli* RNase HI and thereby accommodate a variety of substrates. This may be the reason why *T. kodakaraensis* RNase HIII recognizes and cleaves even the chimeric substrate containing a single ribonucleotide.

### Table 1

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Substrate</th>
<th>$K_m$ (μM)</th>
<th>$k_{cat}$ (min$^{-1}$)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>T. kodakaraensis</em> RNase HII</td>
<td>[rA]$_1$</td>
<td>0.58</td>
<td>11.5</td>
</tr>
<tr>
<td></td>
<td>[rA]$_4$</td>
<td>0.56</td>
<td>8.0</td>
</tr>
<tr>
<td><em>B. subtilis</em> RNase HII</td>
<td>[rA]$_1$</td>
<td>0.43</td>
<td>0.52</td>
</tr>
<tr>
<td></td>
<td>[rA]$_4$</td>
<td>0.21</td>
<td>0.34</td>
</tr>
</tbody>
</table>

Hydrolyses of the substrates were carried out at 30°C for 15 min as described in Section 2. Errors, which represent the 67% confidence limits, are all at or below ±20% of the values reported.
**B. subtilis** RNase HIII lacks either an internal or C-terminal substrate-binding domain. Instead, it has a long N-terminal extension, which has been suggested to form an alternative substrate-binding domain [27]. Because *B. subtilis* RNase HIII cleaves the chimeric substrate containing a single ribonucleotide as well, the length of the substrate covered by this enzyme may be similar to that covered by *T. kodakaraensis* RNase HIII.

*B. subtilis* RNase HIII is a member of Type 2 RNases H. Nevertheless, its behavior on the \([\text{A}]-1\) substrate was different from those of other Type 2 enzymes, but similar to that of *E. coli* RNase HIII. Consistent results have been reported previously [2]. The reason as to why this enzyme functionally resembles a Type 1 enzyme, instead of a Type 2 enzyme, remains to be determined.

The physiological roles of RNases H still remain unclear, although they are thought to be involved in DNA replication and repair [28]. The observation that *T. kodakaraensis* RNase HIII and *B. subtilis* RNase HIII cleaved the DNA–RNA–DNA/DNA substrate with a single ribonucleotide suggests that bacterial and archael RNases HIII, as well as eukaryotic Type 2 RNases H, are involved in excision of a single ribonucleotide misincorporated into DNA. Most of the bacteria and eukaryotes, such as *E. coli*, yeast, and human, contain both Type 1 and Type 2 RNases H within a single cell [3]. Whether their in vivo functions are cooperative, complementary, or independent is of great interest.

Takara Bio Inc. has developed a novel DNA amplification method using DNA–RNA chimeric primers, RNase H, and strand-exchanging DNA polymerase (International Publication Numbers WO 00/56877, 2000 and WO 02/16639, 2002). In this method, named ‘Isothermal and Chimeric primer-Ini-
tiated Amplifica-
tion Numbers’ (ICAN®), RNase H introduces a nick in the extended product at the RNA derived from the chimeric primers. The strand-exchanging DNA polymerase synthesizes the complementary strand from the nick. The dispensability of the denaturation–hybridization step of primer in this method enables isothermal amplification of DNA. However, *E. coli* RNase HIII, which cannot cleave the DNA–RNA junction, is used for this method, resulting in ribonucleotides left in the amplified DNA. Therefore, Type 2 enzymes with an ability to cleave the DNA–RNA junction, such as *T. kodakaraensis* RNase HIII and *B. subtilis* RNase HIII, may be more useful for this method than *E. coli* RNase HIII.

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**References**


