Conformational Stability Is a Determinant of Ribonuclease A Cytotoxicity*

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Onconase™, a homolog of bovine pancreatic ribonuclease A (RNase A) with high conformational stability, is cytotoxic and has efficacy as a cancer chemotherapeutic agent. Unlike wild-type RNase A, the G88R variant is toxic to cancer cells. Here, variants in which disulfide bonds were removed from or added to G88R RNase A were used to probe the relationship between conformational stability and cytotoxicity in a methodical manner. The conformational stability of the C40A/G88R/C95A and C65A/C72A/G88R variants is less than that of G88R RNase A. In contrast, a new disulfide bond that links the N and C termini (residues 4 and 118) increases the conformational stability of G88R RNase A and C65A/C72A/G88R RNase A. These changes have little effect on the ribonucleolytic activity of the enzyme or on its ability to evade the cytosolic ribonuclease inhibitor protein. The changes do, however, have a substantial effect on toxicity toward human erythroleukemia cells. Specifically, conformational stability correlates directly with cytotoxicity as well as with resistance to proteolysis. These data indicate that conformational stability is a key determinant of RNase A cytotoxicity and suggest that cytotoxicity relies on avoiding proteolysis. This finding suggests a means to produce new cancer chemotherapeutic agents based on mammalian ribonucleases.

The free energy difference between the native and unfolded states of a protein is small—typically 5–15 kcal/mol (1, 2). In their native state, many proteins are less susceptible to proteolytic degradation than when unfolded (3). In the unfolded state, the steric protection of peptide bonds provided by the compact native state is lost (4). For example, bovine pancreatic ribonuclease A (RNase A)1 (EC 3.1.27.5 (5, 6)) is degraded more readily by proteases in the presence of denaturants or elevated temperatures (7–10) and less readily when glycosylated (11). The rates of intracellular protein turnover vary by 10^3-fold (12). Apparently, some proteins are better able to thwart the proteolytic machinery (13, 14). These proteins remain intact and retain activity longer within the cell. A correlation between the conformational stability of a protein and its catabolism was reported over 20 years ago (15). Since then, studies using unrelated proteins have either supported (16) or contradicted (14, 17) this correlation. Drawing conclusions from these studies is problematic because the proteins were divergent in characteristics that have been implicated in metabolic turnover. In contrast, variants of a single protein, the N-terminal domain of the represor protein from bacteriophage λ, have been used to demonstrate a definite link between conformational stability and metabolic turnover (18). More recently, the conformational stability of bovine pancreatic trypsin inhibitor variants was shown to correlate with the yield of intact protein produced in a heterologous system (19).

RNase A homologs elicit diverse biological activities, including specific toxicity to cancer cells (20, 21). Onconase™, which is a homolog of RNase A in the Northern leopard frog, is now in Phase III clinical trials for the treatment of malignant mesothelioma. It has been shown that the ribonucleolytic activity of ribonucleases is essential to their cytotoxicity (49). Nonetheless, ribonucleolytic activity is not the only requirement for a ribonuclease to be a cytotoxin. For example, relative to Onconase, RNase A is a 500-fold more effective catalyst of RNA cleavage (51), yet RNase A is not toxic to cancer cells. Still, the high ribonucleolytic activity of RNase A can engender a potent cytotoxin. Indeed, substitutions at Gly^{88} enable RNase A to mimic the ability of Onconase to evade the endogenous ribonuclease inhibitor (RI) protein and become cytotoxic (22). Still, no RNase A homolog is as cytotoxic as Onconase.

Onconase and RNase A differ substantially in another property—conformational stability. The value of $T_m$ (which is the temperature at the midpoint of the thermal transition) for Onconase ($T_m = 90$ °C) is much greater than that of RNase A ($T_m = 63$ °C) (22). Is conformational stability a determinant of ribonuclease cytotoxicity? Answering this question requires a means to increase or decrease conformational stability without altering other important properties of the enzyme. We suspected that adding or removing disulfide bonds would provide such a subtle means.

RNase A contains four disulfide bonds (Cys{sup 26}–Cys{sup 84}, Cys{sup 40}–Cys{sup 95}, Cys{sup 58}–Cys{sup 110}, and Cys{sup 65}–Cys{sup 72}; Fig. 1). Previously, we dissected the contribution of each disulfide bond to conformational stability by replacing each cystine with a pair of alanine residues (23). Of the four disulfide bonds, the Cys{sup 40}–Cys{sup 95} and Cys{sup 65}–Cys{sup 72} cross-links are the least important to conformational stability (23, 24). Removing these disulfide bonds leads to RNase A variants that have $T_m$ values below that of the wild-type enzyme but above physiological temperature.

Here, we investigate the relationship between the conformational stability and cytotoxicity of RNase A. Specifically, we construct G88R RNase A variants that are missing the Cys{sup 40}–Cys{sup 95} or Cys{sup 65}–Cys{sup 72} disulfide bonds. We also introduce a new disulfide bond into G88R RNase A and a variant missing the Cys{sup 65}–Cys{sup 72} disulfide bond. We find that the $T_m$ values for G88R RNase A and its four disulfide variants vary by nearly...
Ribonuclease A: Conformational Stability and Cytotoxicity

EXPERIMENTAL PROCEDURES

Materials—Encherichia coli strain BL21(DE3) was from Novagen (Madison, WI). E. coli strain DH5α, RPMI medium, fetal bovine serum, proteinase K, penicillin, and streptomycin were from Life Technologies, Inc. E. coli strain C356 and helper phage M13K07 were from Bio-Rad (Richmond, CA). A plasmid encoding G88R was a generous gift of P. A. Leland (22). All enzymes for the manipulation of recombinant DNA were from Promega (Madison, WI). E. coli strain CJ236 and helper phage M13K07 were from Bio-Rad (Richmond, CA). A plasmid encoding G88R RNase A was a generous gift of P. A. Leland (22). All enzymes for the manipulation of recombinant DNA were from Promega (Madison, WI). E. coli strain CJ236 (30). To produce plasmids encoding the C40A/G88R/C95A and C65A/C72A/G88R variants, the ggc codon for Gly was replaced in DNA encoding the C40A/G88R/C95A and C65A/C72A/G88R variants using the oligodeoxyribonucleotide TTTGGACTAACCCGTCCT-CAGC (reverse complement in boldface). To produce plasmids encoding the A4C/G88R/V118C and A4C/C65A/C72A/G88R/V118C variants, the GCA codon for Ala was replaced in DNA encoding the G88R and C65A/C72A/G88R variants using the oligodeoxyribonucleotide GCTGCAAGTTCTTTGTC (reverse complement in boldface), and the GTC codon for Val was replaced using the oligodeoxyribonucleotide GCATCAAGGTCGACATACGGTCTC (reverse complement in boldface).

Wild-type RNase A and its variants were produced and purified by methods described previously (29, 31) except for minor modifications in the conditions for oxidative folding (22, 23). The purity of each protein was assessed by SDS-polyacrylamide gel electrophoresis. Adding or removing a disulfide bond is expected to alter the extinction coefficient of RNase A by ~1% (32, 33). Hence, the concentrations of wild-type RNase A and the disulfide variants were determined by using ε = 0.72 mg m⁻¹ cm⁻¹ at 277.5 nm (34).

Assays of Conformational Stability—Differential scanning calorimetry was used to determine the conformational stability of each RNase A variant. Differential scanning calorimetry experiments were performed as described (23), with the following modifications. Protein solutions (0.98–5.6 mg/ml) were dialyzed exhaustively against phosphate-buffered saline and then centrifuged at 15,300 × g for 30 min to remove particulate matter. Data were collected with the program ORIGIN (MicroCal Software, Northampton, MA). The unfolding of wild-type RNase A and each of the variants was 90% reversible, as demonstrated by reheating of the protein samples (data not shown).

Assays of Cytotoxicity—The cytotoxicity of the RNase A variants was assessed using the continuous human erythroleukemia cell line K-562 as described (22). Briefly, K-562 cells were grown at 37 °C in RPMI medium supplemented with fetal bovine serum (10% v/v) with penicillin (100 units/ml) and streptomycin (100 μg/ml) in the presence of wild-type RNase A, a variant, or a phosphate-buffered saline control for 44 h, followed by a 4-h pulse with [methyl-3H]thymidine (0.20 μCi per well). Each experiment is the average of triplicate determinations for each ribonuclease concentration. The standard error of the values from each protein concentration is ±20%. The IC₅₀ value is the concentration of an RNase A variant that kills 50% of the K-562 cells.

Assays of Ribonucleolytic Activity—A fluorogenic substrate, 6-FAM-(dA)r(U)dA₂−6-TAMRA, was used to determine the values of k₅'/K₅ for each RNase A variant (25). A large increase in fluorescence corresponding to the cleavage of the FAM²⁺ bond on the single ribonucleotide residue embedded within this substrate (25). Assays were performed with stirring in 2.0 ml of 0.10 M MES-NaOH buffer (pH 6.0) containing NaCl (0.10 μM), 6-FAM/(dA)r(U)dA₂−6-TAMRA (60 nM), and enzyme (5 ps to 50.50 nM). Fluorescence was monitored at 515 nm.
Conformational stability, cytotoxicity, ribonucleolytic activity, inhibition by ribonuclease inhibitor, and protease susceptibility of wild-type ribonuclease A and disulfide variants

<table>
<thead>
<tr>
<th>Ribonuclease A</th>
<th>Tm&lt;sup&gt;a&lt;/sup&gt; °C</th>
<th>IC&lt;sub&gt;50&lt;/sub&gt;&lt;sup&gt;b&lt;/sup&gt; µM</th>
<th>k&lt;sub&gt;cat&lt;/sub&gt;/K&lt;sub&gt;m&lt;/sub&gt;&lt;sup&gt;c&lt;/sup&gt;</th>
<th>K&lt;sub&gt;i&lt;/sub&gt;&lt;sup&gt;d&lt;/sup&gt;</th>
<th>t&lt;sub&gt;90&lt;/sub&gt;&lt;sup&gt;e&lt;/sup&gt;proteinase K&lt;sup&gt;f&lt;/sup&gt;</th>
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<tbody>
<tr>
<td>A4C/G88R/V118C</td>
<td>68.8 ± 0.1</td>
<td>3</td>
<td>49 ± 6</td>
<td>0.65 ± 0.11</td>
<td>6.9</td>
</tr>
<tr>
<td>G88R</td>
<td>64.0 ± 0.1</td>
<td>9</td>
<td>150 ± 30</td>
<td>0.24 ± 0.05</td>
<td>5.3</td>
</tr>
<tr>
<td>Wild-type</td>
<td>63.2 ± 0.1</td>
<td>&gt;100</td>
<td>360 ± 40°</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>A4C/C65A/C72A/G88R/V118C</td>
<td>50.4 ± 0.1</td>
<td>17</td>
<td>4.0 ± 0.7</td>
<td>3.9 ± 0.3</td>
<td>5.3</td>
</tr>
<tr>
<td>C65A/C72A/G88R</td>
<td>45.9 ± 0.1</td>
<td>26</td>
<td>36 ± 2</td>
<td>0.78 ± 0.16</td>
<td>4.1</td>
</tr>
<tr>
<td>C40A/G88R/C95A</td>
<td>40.4 ± 0.2</td>
<td>25</td>
<td>76 ± 1</td>
<td>0.35 ± 0.05</td>
<td>2.4</td>
</tr>
</tbody>
</table>

* Values (± S.E.) from differential scanning calorimetry are for tryplicate experiments performed in protein-buffered saline. Determine errors for T<sub>m</sub> values are approximately 1%.  
Values (± S.E.) from cleavage of 6-FAM-(dA)rU(dA)<sub>2</sub>-6-TAMRA are for tryplicate experiments at 25 °C in 0.10 M MES-NaOH buffer (pH 6.0) containing NaCl (0.10 M) and dithiothreitol (8.0 mM).

**Results**

**Conformational Stability**

The reversible thermal transitions of wild-type RNase A and the G88R, A4C/G88R/V118C, C40A/G88R/C95A, C65A/C72A/G88R, and A4C/C65A/C72A/G88R/V118C variants were fitted to equations describing a two-state model for unfolding: 

\( n = \frac{n_c}{n_c + [E]} \)

where \( n_c \) is the native state and \( U \) is the unfolded state. Removing a native disulfide bond in RNase A decreases the stability significantly (24, 23). The C65A/C72A/G88R and C40A/G88R/C95A variants are approximately 90 and 60% folded at 37 °C, respectively (data not shown). Compared with G88R RNase A, the T<sub>m</sub> values for the C65A/C72A/G88R and C40A/G88R/C95A variants are decreased by 18.1 and 23.6 °C, respectively. In contrast to these variants, wild-type RNase A and the G88R, A4C/G88R/V118C, and A4C/C65A/C72A/G88R/V118C variants are >99% folded at 37 °C. The T<sub>m</sub> values of wild-type RNase A and G88R RNase A are 63.2 and 64.0 °C, respectively (Table I).

**Cytotoxicity**

The cytotoxicity of wild-type RNase A and the G88R, A4C/G88R/V118C, C40A/G88R/C95A, C65A/C72A/G88R, and A4C/C65A/C72A/G88R/V118C variants was assessed by measuring the incorporation of [methyld-<sup>3</sup>H]thymidine into cellular DNA after a 44-h incubation with K-562 cells. Wild-type RNase A is not cytotoxic to K-562 cells at the concentrations used in this assay (Table I). The IC<sub>50</sub> value of 9 µM for G88R RNase A agrees closely with those reported previously (22, 38). Most significantly, adding the disulfide bond between residues 4 and 118 decreases the IC<sub>50</sub> value for A4C/G88R/V118C RNase A by 3-fold (IC<sub>50</sub> = 3 µM). Although still cytotoxic, each of the remaining variants is less cytotoxic than is G88R RNase A. The IC<sub>50</sub> values for the C40A/G88R/C95A, C65A/C72A/G88R, and A4C/C65A/C72A/G88R/V118C variants are 25, 26, and 17 µM, respectively.

**Ribonucleolytic Activity**

A highly sensitive fluorometric assay was used to assay ribonucleolytic activity. The values of k<sub>cat</sub>/K<sub>m</sub> for wild-type RNase A and variants are the average of three independent assays. Each variant is a potent catalyst of RNA cleavage. At 25 °C, the values of k<sub>cat</sub>/K<sub>m</sub> for the variants are 2.4–90-fold lower than that of the wild-type enzyme (Table I).

**Inhibition by Ribonuclease Inhibitor**

Inhibition of the ribonuclease-catalyzed cleavage of 6-FAM-(dA)rU(dA)<sub>2</sub>-6-TAMRA by dithiothreitol (8.0 mM).
RI was assessed in a continuous assay. The effect of RI concentration on the ribonuclease activity of each variant is reported as $K_i$ (Table I). The value of $K_i = 0.24$ nM for G88R RNase A agrees closely with those reported previously (22, 38). Removing or adding a disulfide bond to G88R RNase A affects only slightly its affinity for RI. The $K_i$ values for the A4C/G88R/V118C, C40A/G88R/C95A, C65A/C72A/G88R, and A4C/C65A/C72A/G88R/V118C variants are 0.65, 0.35, 0.78, and 3.9 nM, respectively.

Protease Susceptibility—The proteolytic susceptibility of each of the RNase A variants was assessed by monitoring ribonuclease activity after exposure to proteinase K. The C40A/G88R/C95A and C65A/C72A/G88R variants are the most susceptible to proteinase K digestion. Furthermore, the addition of the Cys$^1$–Cys$^{118}$ disulfide bond decreased the proteinase K susceptibility of A4C/G88R/V118C RNase A and A4C/C65A/C72A/G88R/V118C RNase A relative to the G88R and C65A/C72A/G88R variants. The values of $t_{50\text{proteinase}}$ for the A4C/G88R/V118C, G88R, A4C/C65A/C72A/G88R/V118C, C65A/C72A/G88R, and C40A/G88R/C95A variants are 6.9, 5.3, 5.3, 4.1, and 2.4 h$^{-1}$, respectively (Table I).

**DISCUSSION**

Disulfide bonds contribute to protein stability primarily by limiting the flexibility of the unfolded polypeptide chain and thereby destabilizing the unfolded state relative to the native state (26). The loss of entropy in the unfolded state is not, however, the only effect of disulfide bonds on conformational stability. A disulfide bond can enhance (39–41) or diminish (42–45) interactions in the folded state that contribute to conformational stability. Thus, predicting the precise contribution of a particular native or nonnative disulfide bond to conformational stability is difficult. Still, we find that replacing a cystine with a pair of alanine residues is a superb means of altering conformational stability without affecting severely the other attributes of a protein. Moreover, the judicious addition of a new cystine to a protein expands the range of accessible stabilities.

Conformational Stability—RNase A contains four disulfide bonds that are important to its conformational stability (23). Substitutions at Gly$^{88}$ have little effect on conformational stability but endow RNase A with cytotoxic activity (22). We constructed four disulfide variants of G88R RNase A that are mostly folded at physiological temperature, which is the temperature of the cytotoxicity assays. The $T_m$ values of the C65A/C72A/G88R and C40A/G88R/C95A variants are 18.1 and 23.6 °C lower, respectively, than that of G88R RNase A (Table I). These decreases in conformational stability are similar to those suffered by the analogous disulfide variants of wild-type RNase A (23). The other two variants have a new disulfide bond. A4C/G88R/V118C RNase A is the only known disulfide variant of RNase A with greater conformational stability than the wild-type enzyme. Moreover, conformational stability lost by removing the native Cys$^65$–Cys$^{72}$ disulfide bond is recovered by adding the nonnative Cys$^1$–Cys$^{118}$ disulfide bond. The $T_m$ values of the A4C/G88R/V118C and A4C/C65A/C72A/G88R/V118C variants are 4.8 and 4.5 °C higher, respectively, than that of the G88R and C65A/C72A/G88R variants (Table I). Thus, the $T_m$ values of the RNase A variants studied herein range from 40.4 to 68.8 °C.

Within the G88R RNase A variants, cytotoxicity correlates well with conformational stability (Fig. 2). For example, A4C/G88R/V118C RNase A has the highest $T_m$ value of the five enzymes and is the most potent cytotoxin. In contrast, the C40A/G88R/C95A and C65A/C72A/G88R variants have the lowest $T_m$ values and the highest $IC_{50}$ values. The G88R and A4C/C65A/C72A/G88R/V118C variants have intermediate $T_m$ values and intermediate $IC_{50}$ values. These data are consistent with a model in which conformational stability is a determinant of cytotoxicity.

This model ignores the low thermodynamic stability of disulfide bonds in the reducing environment of the cytosol (46). The four disulfide bonds in wild-type RNase A are virtually inaccessible to solvent (23) and have considerable kinetic stability in a highly reducing environment (47). Indeed, the $t_{50}$ of RNase A in the cytosol is $>44$ h (48), which is the incubation time of our cytotoxicity assays. Hence, we suspect that the disulfide bonds of RNase A are not susceptible to reduction in the cytosol within the time course of our assays.

Ribonuclease Activity—RNase A must retain ribonuclease activity to be toxic to cells (49). We determined the values of $k_{cat}/K_m$ for the cleavage of 6-FAM–(dA)+(dU)+dA)–6-TAMRA to determine whether differences in cytotoxicity were caused by differences in ribonuclease activity. Each of the disulfide variants is a somewhat less efficient catalyst of RNA cleavage than is G88R RNase A (Table I). Ribonuclease activity does not, however, correlate with cytotoxicity. For example, G88R RNase A has a 3-fold larger $k_{cat}/K_m$ value than does A4C/G88R/V118C RNase A but is less cytotoxic. Furthermore, the C65A/C72A/G88R and C40A/G88R/C95A variants are 9- and 19-fold more efficient catalysts of RNA cleavage but are less cytotoxic than is A4C/C65A/C72A/G88R/V118C RNase A.

Inhibition by Ribonuclease Inhibitor—Cytosolic ribonuclease activity is controlled by the presence of RI (37). RI is a 50-kDa scavenger of pancreatic-type ribonucleases and forms a tight noncovalent complex with wild-type RNase A ($K_d = 4 \times 10^{-14}$ M (36)). Hence, wild-type RNase A has low cytotoxicity. Still, large quantities of RNase A in the cytosol can overwhelm the sentry. For example, microinjection of RNase A greatly increases its cytotoxicity (50).

Ribonucleases that are capable of evading cytosolic RI are cytotoxic at much lower concentrations than is RNase A (51, 52). Indeed, Onconase has $>10^6$-fold lower affinity for RI than does RNase A (53). Variations at Gly$^{88}$, which is an important contact point within the RI-RNase A complex, allows RNase A to evade RI binding more effectively and increases its cytotoxicity (22, 54).

Each of the G88R disulfide variants has slightly less affinity for RI than does G88R RNase A (Table I). The $K_i$ values of the disulfide variants are between 1.5- and 16-fold lower than that of G88R RNase A. Nonetheless, the affinity of RI for the G88R disulfide variants does not correlate with their cytotoxicity (Table I). For example, A4C/C65A/C72A/G88R/V118C RNase A has a 16-fold lower affinity for RI than does G88R RNase A but is less cytotoxic.

Proteinase K Susceptibility—Proteolytic susceptibility is greater in misfolded or unfolded proteins, relative to folded...
proteins (3, 10). Steric hindrance of the peptide bonds in a folded protein blocks possible protease cleavage sites. Indeed, simple glycosylation can slow proteolysis (11). A protein with low conformational stability will exist in an unfolded state to a greater extent than a protein with high conformational stability, increasing proteolytic susceptibility (18).

Is the conformational stability of a ribonuclease linked to its cytotoxicity via its proteolytic susceptibility? C40A/G88R/C95A RNase A and C65S/C72A/G88R RNase A have the lowest conformational stability and the highest IC$_{50}$ values and are also the most susceptible to inactivation by proteinase K digestion (Table I). In contrast, A4C/G88R/V118C RNase A has the highest $T_m$ value, is the most cytotoxic, and is the least susceptible to inactivation by proteinase K digestion. The addition of the Cys$^4$–Cys$^{119}$ disulfide bond increases the $T_m$ value and decreases both the IC$_{50}$ value and the $t_{1/2}$proteinase K value of two different enzymes. Thus, high conformational stability is linked to both high cytotoxicity and low proteolytic susceptibility.

**Implications for the Mechanism of Cytotoxicity**—The cytotoxicity of ribonucleases is manifested in the cytosol. To gain access to the cytosol, an extracellular ribonuclease must cross a cellular membrane. Protein traffic through membranes is thought to require unfolding prior to translocation (55, 56). For example, the translocation of barnase variants across the mitochondrial membrane decreases with increasing disulfide cross-links and conformational stability (62). Our data are in apparent conflict with this model, as the disulfide variants with greater conformational stability are more cytotoxic (Table I). An explanation of this discrepancy is that the translocation of RNase A and its variants could be relatively rapid and another step, such as cytosolic proteolysis, could limit cytotoxicity. Indeed, protease inhibitors are known to increase the cytotoxicity of other protein cytotoxins (57). Similarly, the addition of proteolytic degradation signals can decrease protein cytotoxicity (58). Finally, it is noteworthy that protein toxins such as diphtheria toxin, enterotoxin, and aubrin II have $T_m$ values near that of RNase A (59–61). Increasing the conformational stability of these protein toxins could increase their cytotoxicity, as we have shown with G88R RNase A.

**Relevance to Cancer Chemotherapy**—Onconase, which is an alfamycin, is on the verge of approval as a human cancer chemotherapeutic agent. We find that enhanced conformational stability can increase the toxicity of a mammalian homolog of Onconase toward cancer cells. This finding suggests a means to produce new cancer chemotherapeutic agents based on mammalian ribonucleases.

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**REFERENCES**