Cleavage of an Inaccessible Site by the Maxizyme with Two Independent Binding Arms: An Alternative Approach to the Recruitment of RNA Helicases

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To overcome obstacles to target site selection, we recently created a novel hybrid ribozyme that could access any chosen site by the recruitment of intracellular RNA helicases [Warashina et al. (2001) Proc. Natl. Acad. Sci. USA 98, 5572-5577; Kawasaki et al. (2002) Nat. Biotech. 20, 376-380]. We also demonstrated previously that pol III-driven maxizymes with two substrate-binding arms that were directed against two different sites within a target mRNA formed very active heterodimers in vivo [Kuwabara, et al. (2000) Trends Biotechnol. 18, 462-468; Tanabe et al. (2001) Nature 406, 473-474]. Despite the complicated dimerization process, all the maxizymes that we tested in cultured cells had greater catalytic activity than the parental ribozymes. To investigate the action of maxizymes in cells, we designed a specific maxizyme with two substrate-binding arms that was directed against endogenously expressed LTR-luciferase chimeric mRNA, where LTR refers to the long terminal repeat of HIV-1. One substrate-binding arm of the maxizyme was designed to bind to a site within HIV-1 TAR RNA that is known to form a stable stem structure that normally prevents binding of a ribozyme. The other substrate-binding arm was directed against a relatively accessible site within the luciferase gene. As expected, the conventional ribozyme failed to cleave the TAR region in vivo because of the latter's stable secondary structure. However, to our surprise, the maxizyme cleaved the TAR region within the stem with high efficiency in vivo. The enhanced cleavage in vivo by the maxizyme might have resulted from an entropically favorable, intramolecular, second binding process that occurred during the breathing of the stem structure of the target mRNA. Importantly, our data suggest that this maxizyme technology might be used as an alternative approach to the recruitment of RNA helicases in cleaving sites previously found to be inaccessible.

Key words: HIV-1 TAR, maxizymes, ribozymes, substrate-binding.

Hammerhead ribozymes are small and versatile catalytic RNAs that can cleave target RNAs at specific sites (Fig. 1A) (1-15). In studies directed towards the development of therapeutic applications and potentially useful tools *in vivo*, various ribozymes have been designed and tested *in vivo* (16-32). During attempts to shorten a hammerhead ribozyme, we developed the maxizyme, which functions as a dimer (5, 33-43). Kinetic and NMR analyses indicated that the shortened ribozyme was essentially inactive as a monomer but exhibited strong catalytic activity as a dimer (Fig. 1B) (5, 34). We also designed a heterodimer composed of two different monomers, designated maxizyme left (MzL) and maxizyme right (MzR) (Fig. 1C) (5). Such a heterodimer has two substrate-binding arms and two catalytic cores and the substrate is cleaved only when MzL and MzR

form a dimer. The heterodimeric maxizyme simultaneously cleaved HIV-1 tat mRNA at two independent sites both *in vitro* and in cultured cells (33, 37). The catalytic activity of heterodimeric maxizymes depends on a complex dimerization process, and inactive homodimers are formed in addition to the complex of heterodimers with the target (Fig. 1C) (37–39). Because of the mixed populations of dimeric forms generated *in vitro*, the cleavage activities of heterodimeric maxizymes examined previously were lower than those of parental hammerhead ribozymes and of the homodimeric maxizyme (35–43). Nonetheless, the intracellular activities of heterodimeric maxizymes were as high as those of homodimeric maxizymes and higher than those of parental ribozymes that targeted the two independent cleavage sites.

Successful gene inactivation by ribozymes *in vivo* depends strongly on the design of the expression vector. The design can determine both the level of expression and the half-life of the expressed ribozyme (25). In previous studies we found that pol III-mediated expression of ribozymes as tRNA fusions resulted in highly expressed stable ribozymes (27-43). However, even these improved ribozymes were

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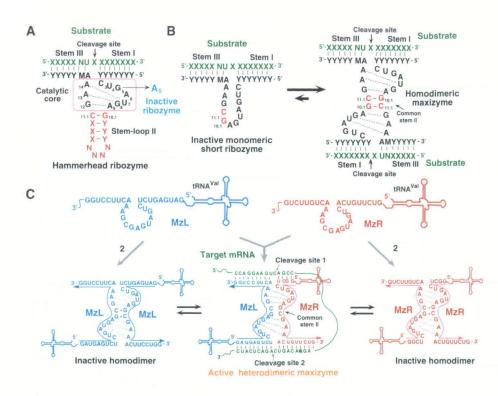


Fig. 1. Secondary structures of ribozyme and maxizyme. (A) Secondary structures of the wild-type hammerhead ribozyme. (B) Secondary structures of the inactive monomeric short ribozyme (left) that is capable of forming a homodimeric maxizyme (right). (C) Secondary structures of the heterodimeric maxizyme that can cleave an mRNA at two sites simultaneously. The active heterodimeric and inactive homodimeric forms of dimeric maxizymes under the control of a human $tRNA^{Val}$ -promoter are shown at the bottom.

sometimes ineffective, probably because the ribozyme was unable to locate its target. One potential explanation for this ineffectiveness is that the rate-limiting step in vivo for the cleavage of phosphodiester bonds is the annealing/association of the ribozyme with its target site (28). To overcome the problem of accessibility, we reasoned that it would be useful to design a ribozyme that could recruit a protein that could, in turn, relieve any interfering secondary structure, thereby making any site accessible to the ribozyme. To accomplish this, we linked a ribozyme to an RNA helicase(s), proteins demonstrated to have nonspecific RNA binding, sliding and unwinding activities (27, 44-47). The introduction of an RNA motif, the constitutive transport element (CTE), that appears to interact with RNA helicases in vitro and in vivo (48-54) led to cleavage in vivo at any chosen target site regardless of the local RNA secondary or tertiary structure (27).

In this study, we examine the features of the maxizyme in greater detail. Our present analysis indicates that, once a maxizyme has been anchored at a more accessible site, its activity *in vivo* can be improved significantly by permitting cleavage of sites previously found to be inaccessible. We suggest that the enhanced cleavage *in vivo* by the maxizyme resulted from an entropically favorable, intramolecular, second binding process that occurred during the breathing of the stem structure of the target mRNA. Importantly, the improved efficacy as a result of anchoring by one of the binding arms of the maxizyme makes it even more suitable for a wide range of applications in the post-genome era.

MATERIALS AND METHODS

Kinetic Analysis—Kinetic measurements of reactions catalyzed by tRNA^{Val}-driven ribozymes (tRNA-Rz) and tRNA^{Val}-driven maxizymes (tRNA-Mz) were performed with 2 nM 5'-³²P–labeled LTR-Luc RNA as substrate. Reaction rates were measured, in 10 mM MgCl₂ and 50 mM Tris-HCl (pH 8.0), under single-turnover conditions with high concentrations of tRNA-Mz and tRNA-Rz (5 μ M) at 37°C. The extent of cleavage was determined by quantitation of radioactivity in the bands of substrate and product with a Bio-Image Analyzer (BA2000; Fuji Film, Tokyo).

Cell Culture and Luciferase Assay-Methods for cell culture were described previously (25, 37, 55). Luciferase activity was monitored basically as described elsewhere (37). LTR-Luc HeLa cells were plated at 80% confluence in twelve-well plates and incubated at 37°C in a CO₂ incubator. The cells were washed twice with phosphate-buffered saline (PBS) before (co-)transfection. Four µg of each ribozyme-expression plasmid and 150 ng of Tat-expressing plasmid (pCD-SRa/tat) (55, 56) were mixed with 4 µl of Lipofectin reagent (Gibco-BRL, Rockville, MD) in 400 µl of serum-reduced medium (OPTI-MEM I; Gibco-BRL) and incubated for 30 min at room temperature, as described in the user's bulletin from Gibco-BRL. Then the mixture was gently added to cells. After 12 h, the medium was replaced by growth medium (DMEM) supplemented with 10% fetal calf serum and cells were cultured for another 24 h. Luciferase activity was measured with a PicaGene kit (Toyoinki, Tokyo) as described elsewhere (25, 37, 55). To normalize the efficiency of transfection by reference to β-galactosidase activity, cells were co-transfected with 200 ng of the pSV-β-galactosidase control vector (Promega, Madison, WI) and the chemiluminescent signal due to the activity of β galactosidase was determined with a luminescent b-galactosidase Genetic Reporter System (Clontech, Palo Alto, CA), as described elsewhere (55).

RESULTS

Design of Maxizyme with Two Independent Binding Arms—Heterodimeric maxizymes have two substrate-binding arms and can bind to two different sites on a target mRNA simultaneously (29–32). We wondered what would happen when the apparent accessibility of the respective binding sites differed significantly. We postulated that, even if one of the maxizyme-binding sites were hidden within the stable stem of an mRNA, the maxizyme might still be able to access and cleave the site provided that the other site were accessible to the maxizyme. We reasoned that, if the maxizyme can bind to a substrate with one accessible site, the binding to the second but less accessible site should become an intramolecular interaction, which should be entropically favored. To analyze the effect of such double binding of a maxizyme to its substrate on intracellular cleavage activity, we designed a maxizyme that was specifically targeted against endogenously expressed chimeric LTR-luciferase mRNA (where LTR is the long terminal repeat of HIV-1). Figure 2A shows the secondary structure of the target mRNA (as predicted by the MulFold program). One substrate-binding region of the maxizyme was targeted to an apparently inaccessible site within HIV-1 TAR RNA. This site is known to be located within a tight stem structure that prevents a normal ribozyme from binding (27). The other substrate-binding region was directed against a site that is considered to be relatively accessible within the luciferase gene (Fig. 2A). Using such a maxizyme with binding arms directed against two sites with different accessibilities, we hoped to gain some insight into

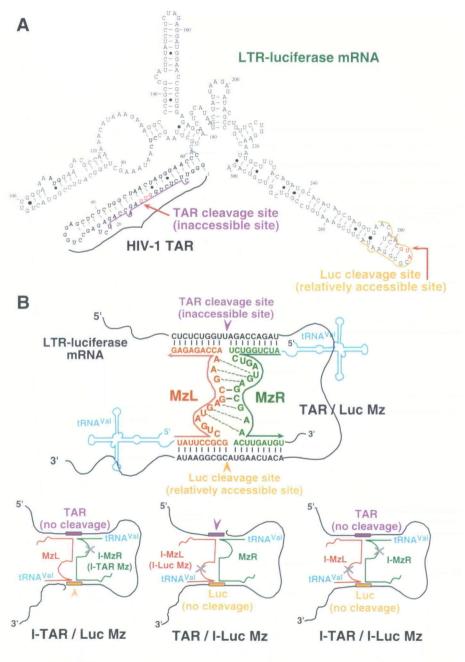


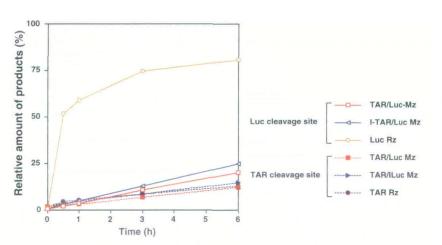
Fig. 2. Design of heterodimeric maxizymes directed against chimeric LTR-Luc mRNA. (A) Predicted secondary structure, based on calculations with the Mul-Fold program (Biocomputing Office, Biology Department, Indiana University, IN, USA), of the target LTR-Luc mRNA. (B) Various combinations of maxizymes for targeting the TAR cleavage site and/or the Luc cleavage site in LTR-Luc mRNA. X indicates in activation by a point mutation (G5 to A5) within respective catalytic cores. I indicates an inactivated monomer. Thus, I-MzR indicates inactivated MzR. the molecular mechanism of action of the maxizyme in vivo.

To ensure efficient formation of dimers in cells, we expressed maxizymes under the control of the promoter of a human gene for tRNA^{Val} which is recognized by RNA polymerase III (25) The sequences of the monomers of the maxizyme were inserted downstream of a modified gene for tRNA^{Val}, and the expression cassettes of the monomer units were subcloned into one vector (TAR/Luc Mz) as described elsewhere (34, 35, 37). For comparisons of activity, we prepared plasmids that encoded wild-type ribozymes directed against the two individual sites (TAR Rz and Luc Rz). We also prepared plasmids that encoded inactive maxizymes with a point mutation (G5 to A5 in Fig. 1A) within the catalytic core specific for each cleavage site (TAR/I-Luc Mz and I-TAR/Luc Mz; Fig. 2B, bottom).

Characterization of Cleavage Activity In Vitro and In Vivo—We first examined the cleavage activities and the accessibilities of maxizymes and ribozymes and the extent to which they were able to interact with or gain access to the substrate RNA in vitro. The cleavage activities of the various maxizymes and ribozymes in vitro are shown in Table I. The time courses of reactions are plotted in Fig. 3. As we had anticipated, the tRNA-ribozyme directed against the accessible Luc cleavage site (Luc Rz) was two orders of magnitude more active than the tRNA-ribozyme directed against the inaccessible TAR cleavage site (TAR Rz). Apparently, access to the target had determined the cleavage activity of each ribozyme. In the reactions with maxizymes. as observed previously, in the absence of facilitators such as cetyltrimethylammonium bromide (CTAB) (38, 39), the majority of all maxizymes were basically trapped in their inactive forms, which included homodimers, at least under the reaction conditions that we used in vitro.

It should be emphasized here that our recent studies demonstrated that no relationships were found between the activities of catalytic RNAs in cultured cells and the kinetic parameters of their respective chemical cleavage reactions *in vitro*, indicating that in no case was chemical cleavage the rate-limiting step *in vivo* (28). Therefore, in order to gain insight into the molecular mechanism of action of the maxizyme *in vivo*, analysis must be carried out *in vivo*.

Accordingly, we next evaluated the intracellular activities of the ribozymes and maxizymes in HeLa cells that expressed LTR-Luc (Fig. 4). The target chimeric gene was



stably expressed and consisted of the long terminal repeat (LTR) of HIV-1 and a gene for luciferase. The expression of this reporter is Tat-dependent and, therefore, an expression plasmid for Tat was co-transfected and transiently expressed together with each ribozyme-expression vector (Fig. 4A) (*55, 56*). As anticipated, Luc Rz reduced the expression of the reporter (lane 3; Fig. 4B) while TAR Rz had no effect on the activity of the luciferase reporter (lane 2).

In contrast to the results in vitro (Fig. 1, Table I), when maxizymes were expressed in HeLa cells, the maxizyme that had been designed to cleave both the TAR and the Luc cleavage sites (TAR/Luc Mz) had higher activity than the corresponding ribozymes (lane 7; Fig. 4B). The maxizymes, whose active dimeric form is in equilibrium with many inactive forms (34-41), must have been converted preferentially to the active form by endogenous intracellular facilitators, since only the active heterodimeric maxizyme is stabilized when its two binding arms anneal to the target regions (Fig. 1C, bottom) (37). The individual maxizyme monomers (MzL and MzR, lanes 5 and 6) by themselves were ineffective. In addition, the completely inactive maxizyme (I-TAR/I-Luc Mz) with double point-mutations (G5 to A5) within the two catalytic cores was also ineffective (lane 10). These results clearly indicated that, in cells, the active maxizyme was a heterodimer and, furthermore, that it was cleavage by the maxizyme, not an antisense effect, that was responsible for the specific suppression of expression of LTR-Luc mRNA.

Both half-inactive maxizymes, in which just one catalytic core had a point mutation (G5 to A5), namely, TAR/I-Luc

 $\ensuremath{\mathsf{TABLE}}$ I. Kinetic parameters of cleavage of the LTR-Luc RNA substrate.

	$K_{ m obs} imes 10^{-2} \ ({ m min}^{-1})$
Cleavage at the Luc cleavage si	te
TAR/Luc Mz	0.060
I-TAR/Luc Mz	0.076
Luc Rz	2.4
Cleavage at the TAR cleavage s	ite
TAR/Luc Mz	0.032
TAR/I-Luc Mz	0.037
TAR Rz	0.028

Rate constants were measured in 50 mM Tris-HCl (pH 8.0) and 10 mM MgCl₂ under enzyme-saturating conditions (5 μ M ribozyme or maxizyme and less than 2 nM substrate) at 37°C.

Fig. 3. Time courses of reactions catalyzed by tRNA^{Val}-ribozymes and maxizymes *in vitro*. Reactions were carried out in 10 mM MgCl₂ and 50 mM Tris-HCl (pH 8.0) under single-turnover conditions with high concentrations of tRNA-Mz and tRNA-Rz (5 μ M) at 37°C. Reaction conditions and the rate constants obtained are summarized in Table I.

1RN

LTR-Luc

HeLa cells

LTB Luc LTR-luciferase gen

Measurement of luciferase activity

Maxizyme

tRNA-Mz

(tRNA-Bz

Luciferase activity

B

120

100

80

60

40

20

0

TAR PL + LICE

TARIAL control

TARILICAN

4

1

TARIHLUC MA FARILUCHE FTARILLICHE

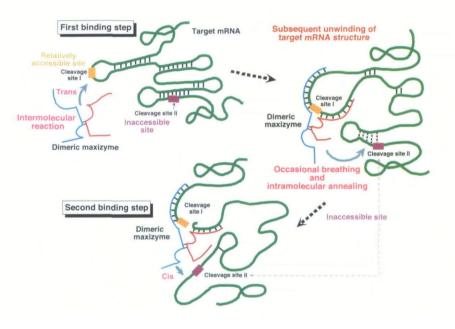
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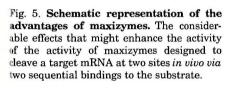
A

HTLVITE Tat CDNA

pCD-SBa/ta

Fig. 4. Intracellular activities of tR-NA^{Val}-enzymes in HeLa cells that stably expressed LTR-Luc. (A) Assay system for measurement of the activities of tRNA^{Val-} enzymes in LTR-Luc HeLa cells. (B) The effects of tRNA^{Val}-enzymes on the Tat-mediated transcription of the chimeric LTR-Luc gene. The results shown are the averages of results from three sets of experiments. Luciferase activity was normalized by reference to the efficiency of transfection, which was determined by monitoring the activity of β-galactosidase encoded by a co-transfected gene.





Mz and I-TAR/Luc Mz (Fig. 2B, bottom), cleaved the substrate with remarkable efficiency (lanes 8 and 9). In fact, the activity of the half-inactive I-TAR/Luc Mz maxizyme was higher (80% reduction in luciferase activity) than that of the wild-type ribozyme, Luc Rz (50% reduction). The activity was actually equal to that of the normal maxizyme (lane 7), indicating the potential advantage of any maxizyme with an additional binding arm.

In general, the rate-limiting step in vivo of a reaction mediated by a catalytic RNA, such as a ribozyme, has been considered to be the substrate-binding step (28, 57-62). Our present analysis further strengthens this hypothesis, since the efficacy of our maxizymes in vivo apparently reflected enhanced accessibility to the substrate. It is also noteworthy that TAR/I-Luc Mz, which was designed to cleave only the inaccessible TAR cleavage site (lane 8), suppressed the expression of the LTR-luciferase gene to the same extent as the normal heterodimeric maxizyme. The binding arm of the maxizyme has to gain access to the TAR region prior to

cleavage of the target mRNA. Once one binding arm of the maxizyme has bound to the more accessible Luc cleavage site (TAR/I-Luc Mz cannot cleave the Luc cleavage site but can bind to this site with the same affinity as the normal maxizyme), binding of the other arm to the TAR cleavage site becomes an entropically favorable intramolecular interaction that can occur during the breathing of mRNA, which is most probably the result of the action of some endogenous RNA helicase(s) (27, 44-47). Even within the tight structure of the TAR region, the stem structure can be disrupted by interactions with cellular factors and the maxizyme, having already bound via the Luc cleavage site, should be able to bind efficiently to the disrupted region. The additional binding arm appears to allow the maxizyme to attack efficiently even at an otherwise inaccessible target site.

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DISCUSSION

Under conditions where the rate-limiting step is the substrate-binding step, once the maxizyme with two binding arms has bound to the more accessible target site via one of its binding arms, the second binding step at the second site becomes an intramolecular interaction (Fig. 5). This intramolecular annealing process is much more favorable entropically than the intermolecular annealing process that must occur when independent standard ribozymes are involved. Figure 5 summarizes the considerable effects that might enhance the activity of maxizymes in vivo specifically via the two sequential bindings to the target mRNA. As a result of the advantage of the intramolecular interactions in the second binding step, as described above, the maxizyme can gain access to a structured region in the target RNA by increasing the chance of an encounter, once the structured region has been disrupted by cellular factors (yellow panel in Fig. 5). Structural changes in the target RNA caused by the initial binding of the maxizyme might also trigger the second binding/cleavage reaction. The enhancement of the intracellular activity of the present maxizymes is reflected by the results of several earlier successful studies in vivo (34-41). Maxizymes, which can easily be designed (40), should be useful as tools in molecular biology, with potential utility in vivo and in a clinical setting.

Our present studies suggest that, once a maxizyme has been anchored at a more accessible site, its activity *in vivo* can be improved significantly. Our present maxizyme technology should complement the hybrid ribozyme technology that uses endogenous RNA helicases (27, 63–65). It may be possible to devise a universal anchor, for example, an anchor that binds to the poly(A) tails of mRNAs to create universally active maxizymes *in vivo*. Such an anchoring strategy might not be limited to maxizymes exclusively but might also apply to parental ribozymes. Such possibilities are currently being investigated in our laboratory.

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