

## Accelerated Publications

### Metal Coordination Sites That Contribute to Structure and Catalysis in the Group I Intron from *Tetrahymena*<sup>†</sup>

Eric L. Christian and Michael Yarus\*

Department of Molecular, Cellular, and Developmental Biology, University of Colorado, Boulder, Colorado 80309-0347

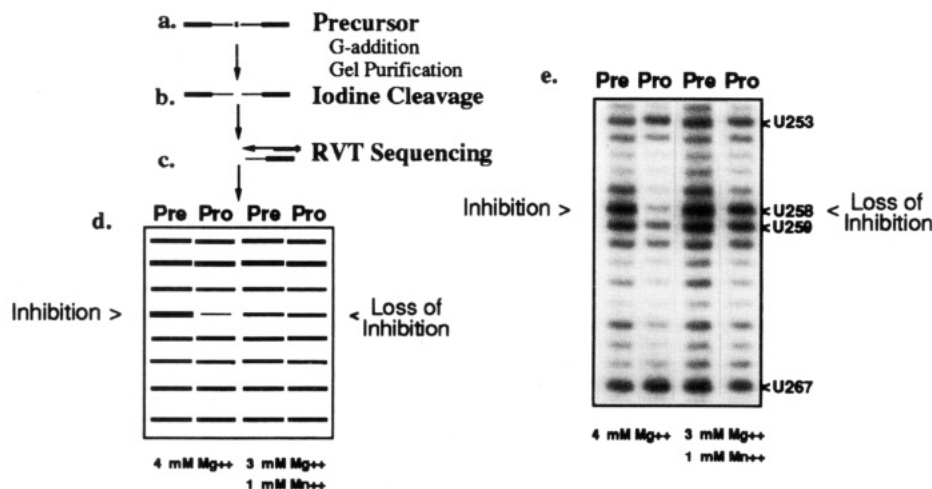
Received December 21, 1992; Revised Manuscript Received February 22, 1993

**ABSTRACT:** We have used nucleoside phosphorothioates (NTP $\alpha$ S) and a substitution-interference method to identify phosphate oxygens that appear to be important to guanosine cofactor addition in the self-splicing group I intron from *Tetrahymena thermophila*. For the majority of these phosphate oxygens, however, the effect of NTP $\alpha$ S substitution is significantly reduced in reactions containing the added presence of manganese ion (Mn<sup>2+</sup>) relative to magnesium ion (Mg<sup>2+</sup>) alone. The observed "rescue" of the NTP $\alpha$ S effect at these positions is thought to be due to the larger affinity of Mn<sup>2+</sup> for sulfur. These data suggest the direct coordination of divalent metal ions within the highly conserved catalytic core of the *Tetrahymena* intron. Because many of these metal binding sites appear to be in positions of close backbone-backbone approach, and adjacent to the guanosine binding site the splice junction, we suggest roles for the corresponding ions in stabilizing tertiary structure and substrate recognition and as participants in catalysis.

Metal ions in RNA are not only important in determining tertiary structure but they can also provide reactive groups for RNA catalysis (Saenger, 1984; Yarus, 1993). In crystals of tRNA<sup>Phe</sup> at least three magnesium ions are bound to the RNA, predominately coordinating nonbridging phosphate oxygens (Holbrook et al., 1977; Jack et al., 1977; Quigley et al., 1978). These metal ions join disparate parts of the RNA sequence and stabilize sharp bends in the sugar-phosphate backbone. Other studies have shown that the binding of lead(II) to one of the positions of Mg<sup>2+</sup> coordination can catalyze the cleavage of an adjacent phosphodiester bond (Werner et al., 1976; Brown et al., 1985). Divalent metal ions are also required for the activity of a number of catalytic RNAs (Dange et al., 1990; Dahm & Uhlenbeck, 1991; Guerrier-Takada et al., 1986; Pan & Uhlenbeck, 1992; Piccirilli et al., 1993). In particular, the activity of the group I intron from *Tetrahymena* is completely dependent upon the presence of magnesium (Mg<sup>2+</sup>) or manganese (Mn<sup>2+</sup>) ions which are likely to play an important structural and catalytic role (Grosshans & Cech, 1989; Celander & Cech, 1991).

Substitution interference studies with phosphorothioates in the *Tetrahymena* intron have identified a number of phosphate oxygens within the intron that appear to be important to enzymatic activity. Phosphorothioates (NTP $\alpha$ S) are nucleotide analogs that contain sulfur in place of a nonbridging phosphate oxygen (Eckstein, 1985). When these structural probes are incorporated into RNA (strictly in the *pro-R<sub>p</sub>* configuration), they are thought to perturb the formation of hydrogen bonds and the coordination of Mg<sup>2+</sup> without a significant disruption of the secondary structure (Eckstein, 1985; Jaffe & Cohn, 1978; Pecoraro, 1984; Frey & Sammons, 1985). RNAs with multiple NTP $\alpha$ S substitutions (>13 NTP $\alpha$ S/molecule) have been used to identify five phosphate oxygens important to the attack of the CU dinucleotide at the 3' splice site (CU addition, an analog of exon ligation) (Waring, 1989). A more sensitive approach which quantitated the effects of individual NTP $\alpha$ S substitution at all positions identified 44 phosphate oxygens that alter the rate of 3' splice site hydrolysis (Christian & Yarus, 1992). In both of these studies the strongest NTP $\alpha$ S effects are found in regions of close backbone to backbone apposition as judged

<sup>†</sup> This work was supported by the NIH and the W. M. Keck Foundation.



**FIGURE 1:** Substitution interference. Precursor RNAs containing low levels of NTP $\alpha$ S (see Materials and Methods) are allowed to splice in the presence of excess guanosine until 20% of the initial precursor is consumed. Splicing products are gel purified and pooled into two fractions, precursor versus all reaction products, so that reaction rate changes are only detected in the first step of splicing, G-addition. The backbone at the phosphorothioate linkage is cleaved by incubation in the presence of iodine (Schatz et al., 1991) (Figure 1b) and the position of cleavage identified by reverse transcriptase sequencing with  $^{32}$ P end-labeled primers (Figure 1c). cDNA products are resolved on a sequencing gel where each band is representative of the level of precursor or products containing NTP $\alpha$ S at a specific position (Figure 1d). Comparison of single bands in precursor (Pre) and product (Pro) sequencing lanes indicates positions sensitive to NTP $\alpha$ S substitution. Inhibition is indicated in reactions carried out in  $Mg^{2+}$  alone by an enhancement of a specific band in the precursor lane and a corresponding reduction of the sequencing band in the same position in the product lane (Figure 1d, left lanes). The position-specific loss of inhibition in reactions carried out with the added presence of  $Mn^{2+}$  suggests a position of metal ion coordination (Figure 1d, right lanes). An example of “ $Mn^{2+}$  rescue” at positions  $U_{258}$  and  $U_{259}$  can be seen in Figure 1e. Bands observed between positions of predicted NTP $\alpha$ S substitution reflect experimental background due to stopping of reverse transcriptase. This background signal is subtracted when the level of the NTP $\alpha$ S effect is calculated (Christian & Yarus, 1992).

from the three-dimensional model of the catalytic core of the *Tetrahymena* intron proposed by Michel and Westhof (Christian & Yarus, 1992; Michel & Westhof, 1990). Our interpretation is that these NTP $\alpha$ S effects may indicate the position of metal ions that determine tertiary structure in the *Tetrahymena* intron. Moreover, a number of strong NTP $\alpha$ S effects appear to be adjacent to the guanosine binding domain and the splice junction and, therefore, could indicate ions involved in catalysis (Christian & Yarus, 1992).

In this paper, we use phosphorothioate substitution to identify structural and catalytically important  $Mg^{2+}$  binding sites throughout the phylogenetically conserved core of the group I intron from *Tetrahymena*. Specifically, we have measured the effect of NTP $\alpha$ S substitution on the first step of the splicing reaction, guanosine (G) addition, extending methods described previously (Christian & Yarus, 1992) and outlined in Figure 1. Positions of metal ion coordination were inferred from a comparison of modification interference studies performed with  $Mg^{2+}$  alone with those performed with the addition of  $Mn^{2+}$ . This experimental strategy takes advantage of the relative abilities of the two metal ions to coordinate oxygen and sulfur. While  $Mg^{2+}$  has been shown to have a much stronger affinity for the coordination of oxygen than sulfur [by ( $>3 \times 10^4$ )-fold in ATP $\beta$ S], the difference in the affinity of  $Mn^{2+}$  for oxygen and sulfur is much smaller ( $<200$ -fold) (Pecoraro, 1984). Thus, substitutions found inhibitory to splicing in the presence of magnesium but not in the added presence of manganese ion ( $Mn^{2+}$  rescue) imply coordination of magnesium to a specific phosphate oxygen (Figure 1d). Since this technique is sensitive to changes in the rate of reaction, metal ions detected in this way directly or indirectly affect the ability to attain the transition state. We find phosphate oxygens that appear to be universally important to *Tetrahymena* RNA-based reactions as well as oxygens specifically important to G-addition. In addition, we find that the strongest NTP $\alpha$ S effects coincide with positions of  $Mn^{2+}$  rescue. Some of these positions of implied metal coordination

appear sufficiently close to reactive bonds at the 5' splice site to participate directly in catalysis.

## MATERIALS AND METHODS

**Transcription and Purification.** Precursor RNAs containing the entire intron sequence from *Tetrahymena thermophila* (413 nt) and 5' and 3' exon sequences (42 and 82 nt, respectively) were transcribed and purified as described previously (Christian & Yarus, 1992). Briefly, 2  $\mu$ g of plasmid pTT1A3 was cut with *Eco*RI and transcribed for 1–2 h in a reaction mixture (100  $\mu$ L) containing 40 mM Tris-HCl, pH 8.0, 6 mM  $MgCl_2$ , 0.01% Triton X-100, and 5 mM dithiothreitol (DTT). In addition, reactions contained 1 mM each of ATP, CTP, GTP, and UTP and either ATP $\alpha$ S, CTP $\alpha$ S, GTP $\alpha$ S, or UTP $\alpha$ S at a level that yielded an average of two NTP $\alpha$ S incorporations per precursor. This level of incorporation minimizes multiple inhibitory substitutions while providing a sufficient experimental signal. Precursor RNAs were isolated on a 20-cm 5% polyacrylamide–8 M urea gel in 1  $\times$  TBE and eluted from the gel in 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl, and 0.01% SDS overnight at 4  $^{\circ}$ C. The supernatant was precipitated twice in 2 M  $NH_4$ -OAc and 3 volumes of distilled ethanol (EtOH), resuspended in distilled  $H_2O$ , and stored at  $-70$   $^{\circ}$ C.

**Reaction Conditions.** Precursor RNAs (300 nM) were renatured before splicing by heating in the presence of reaction buffer (50 mM CHES, pH 6.0, 0.2 mM EDTA,) for 3 min at 95  $^{\circ}$ C and cooled immediately on ice for at least 2 min. Metal ions (4 mM  $MgCl_2$ , or 3 mM  $MgCl_2$  and 1 mM  $MnCl_2$  final concentration) were added to reaction mixtures that were then preincubated at 37  $^{\circ}$ C for 5 min prior to reaction. Reactions were initiated by adding a molar excess of guanosine (100  $\mu$ M final) and incubating until approximately 20% of the initial precursor had been consumed. Reactions were stopped by the addition of EDTA (50 mM final) and the splicing products purified as described above. Acidic conditions were used to minimize side reactions due to hydrolysis

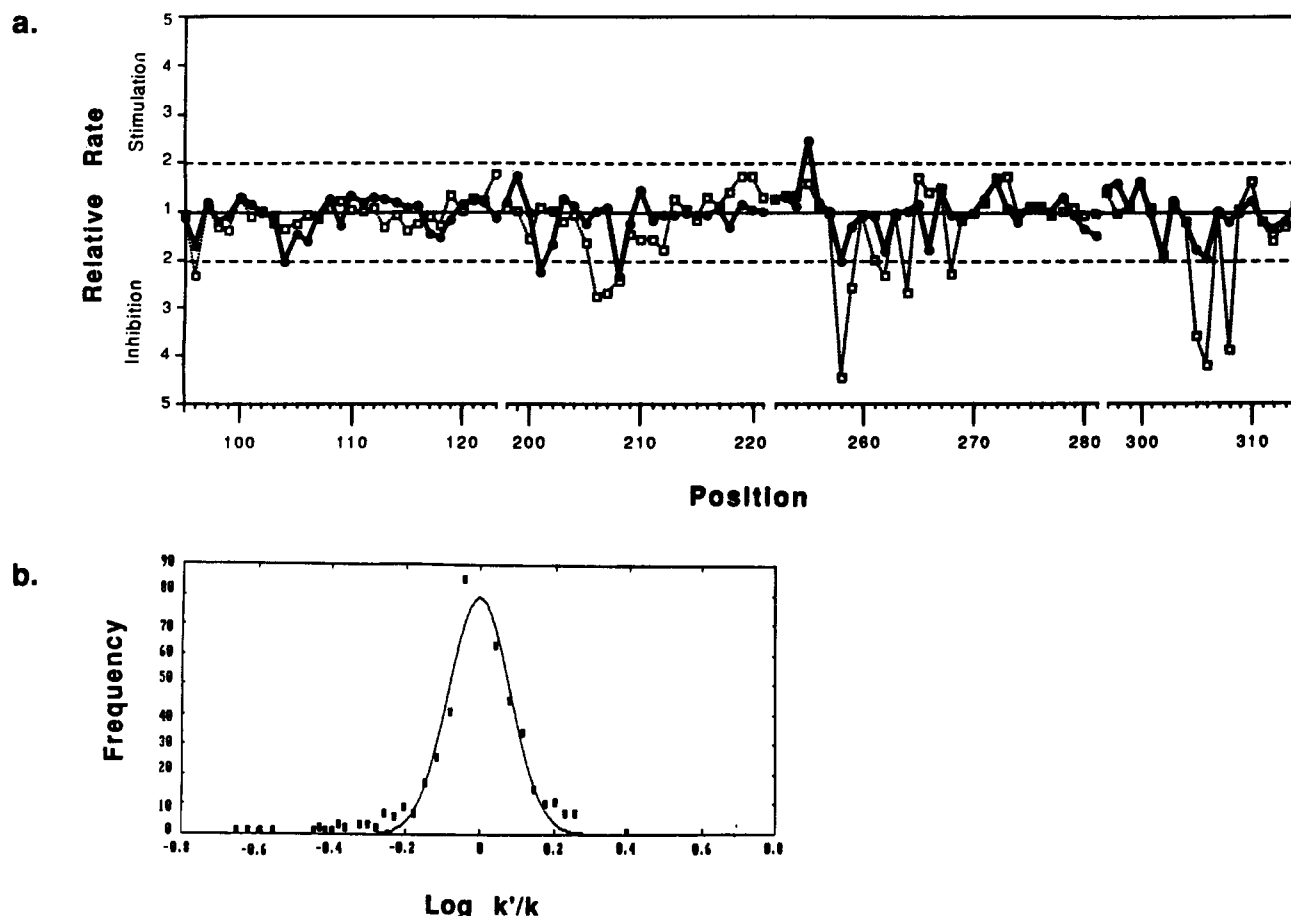


FIGURE 2: Effect of NTP $\alpha$ S substitution on G-addition. (a) Plot of the change in the observed rate of G-addition due to NTP $\alpha$ S substitution at different positions within the *Tetrahymena* intron (see below). The value 1 (dark line) indicates no change in rate, values  $>1$  reflect  $x$ -fold stimulation, and values  $<1$  reflect  $x$ -fold inhibition. Squares indicate reactions performed in 4 mM  $Mg^{2+}$ , and filled circles reflect reactions performed in 3 mM  $Mg^{2+}$  and 1 mM  $Mn^{2+}$ . (b) Distribution of the log of NTP $\alpha$ S effects. The significance of a NTP $\alpha$ S effect is determined from the radioactivity in sequencing bands (Figure 1d) by using an AMBIS two-dimensional radioanalytic scanner (Christian & Yarus, 1992). Since the fraction of positions strongly affected by NTP $\alpha$ S substitution is small (less than 10%), most band intensities in a given lane can be used to estimate the signal for an uninhibited control. The ratio of the observed band intensity at a given position to the calculated signal for an uninhibited reaction at the same position can be related directly to the change in the rate of the reaction due to NTP $\alpha$ S substitution at that position (Christian & Yarus, 1992). We express this change in rate as  $k'/k$  or the observed pseudo-first-order rate constant for NTP $\alpha$ S substitution at a single position ( $k'$ ) over the expected rate constant for an uninhibited reaction ( $k$ ). To simplify discussion (a) plots  $k'/k$  values for NTP $\alpha$ S effects observed to stimulate the rate of G-addition and  $(k'/k)^{-1}$  for effects observed to inhibit the rate of G-addition. NTP $\alpha$ S substitutions considered to have significant effects on the rate of G-addition are those whose values ( $\text{Log } k'/k$ ) lie outside the normal distribution of effects (b) and in excess of the number predicted to be more than two standard deviations ( $P = 0.05$ ) from the average effect of NTP $\alpha$ S substitution. Similarly, we define positions of metal ion coordination as those whose  $\text{Log } k'/k$  values ( $Mg^{2+}$  vs  $Mg^{2+}$  and  $Mn^{2+}$ ) differ by more than 4 standard errors.

at the splice junctions. Partial rather than complete substitution of  $Mn^{2+}$  for  $Mg^{2+}$  was chosen to minimize structural effects due to  $Mn^{2+}$  binding at positions other than those containing NTP $\alpha$ S.

**Analysis of Reaction Products.** The identification of phosphate oxygens that alter the rate of reactions noted above was derived from a method described previously (Christian & Yarus, 1992). In short, purified precursor and pooled reaction products were cleaved at the position of NTP $\alpha$ S incorporation by incubation in the presence of 100  $\mu$ M molecular iodine at 95  $^{\circ}\text{C}$  for 5 min, cooled on ice, and precipitated in 2 M  $NH_4OAc$  and 3 volumes of EtOH at  $-70^{\circ}\text{C}$  for at least 2 h. Cleaved splicing products were resuspended in distilled  $H_2O$  and stored at  $-70^{\circ}\text{C}$ . Sequencing reactions to determine the position of iodine-induced cleavage contained 0.5 pmol of iodine-cut precursor or splicing products and 2 pmol of 5'- $^{32}\text{P}$  end-labeled sequencing primer in 9  $\mu$ L of reverse transcriptase (RT) buffer (50 mM Tris-HCl, pH 8.3, 60 mM NaCl, 1 mM DTT). This mixture was heated for 3 min at 65  $^{\circ}\text{C}$  before addition of 1  $\mu$ L of RT buffer containing 36 mM  $MgCl_2$  and cooled on ice. Annealed primers were then

extended with 1 unit of avian myeloblastosis virus (AMV) reverse transcriptase in the presence of 1 mM dNTPs for 5 min at 37  $^{\circ}\text{C}$ . The resulting reaction products were separated on a 40-cm 8% polyacrylamide-8 M urea sequencing gel alongside dideoxynucleotide sequencing reactions of the original pTT1A3 plasmid which served to determine the positions of iodine-induced termination of primer extension. Interpretation of sequencing banding patterns is outlined in Figures 1 and 2.

## RESULTS

The effect of NTP $\alpha$ S substitution on G-addition in the presence of 4 mM  $Mg^{2+}$ , or 3 mM  $Mg^{2+}$  and 1 mM  $Mn^{2+}$ , is shown in Figure 2a. For reactions in the presence of  $Mg^{2+}$  alone, NTP $\alpha$ S substitution at most positions has little effect on G-addition, but a few positions show significant changes in rate. A plot of the log of these effects (representative of the change in free energy) vs the frequency of their occurrence (Figure 2b) demonstrates that a number of positions lie outside the normal distribution of NTP $\alpha$ S effects. We identify 28 positions as significant, that is, in excess of the number that

should be more than 2 standard deviations from the center of the normal distribution of effects (Figure 2b). However, half of these significant effects change the rate of G-addition by less than 2-fold. In fact, even more subtle kinetic and structural information may be contained within the data shown in Figure 2a where we reproducibly observe regions of slight enhancement or inhibition. In this initial analysis, however, we restrict discussion to the most significant NTP $\alpha$ S effects: those having a 2-fold effect or greater on the observed rate constant for reactions with G (dashed lines Figure 2a). These positions are G<sub>96</sub>, A<sub>206</sub>, A<sub>207</sub>, C<sub>208</sub> U<sub>258</sub>, U<sub>259</sub>, A<sub>261</sub> C<sub>262</sub>, G<sub>264</sub>, A<sub>268</sub>, U<sub>305</sub>, A<sub>306</sub>, and A<sub>308</sub>.

At positions of metal ion coordination, we expect the added presence of Mn<sup>2+</sup> ion to generally reduce the level of the NTP $\alpha$ S effect observed in the presence Mg<sup>2+</sup> alone. Indeed, this is observed for the majority of these larger NTP $\alpha$ S effects (9/13) at positions A<sub>206</sub>, A<sub>207</sub>, U<sub>258</sub>, U<sub>259</sub>, G<sub>264</sub>, A<sub>268</sub>, U<sub>305</sub>, A<sub>306</sub>, and A<sub>308</sub> (Figure 2). Position A<sub>261</sub> is also likely to be a position of metal rescue. Although this position shows complete rescue on gels, the level of inhibition in the presence of Mg<sup>2+</sup> is small and thus can only be considered significant with a 90% probability that this value is distinct from the normal distribution of NTP $\alpha$ S effects. At one position outside the catalytic core, G<sub>201</sub>, the presence of Mn<sup>2+</sup> ion causes inhibition that is not observed in the presence of Mg<sup>2+</sup> alone. The presence of "Mn<sup>2+</sup> inhibition" is not unexpected since Mn<sup>2+</sup> may coordinate a different subset of atoms in RNA than Mg<sup>2+</sup> (Holbrook et al., 1977). Thus, the Mn<sup>2+</sup> inhibition may be due to altered RNA structure near this one site.

Within the catalytic core, however, NTP $\alpha$ S and Mn<sup>2+</sup> rescue effects appear to be attributable to the inhibition of Mg<sup>2+</sup> binding at the site of sulfur substitution. If Mg<sup>2+</sup> binding is inhibited, then higher levels of Mg<sup>2+</sup> ion should compensate for the ion's reduced affinity for sulfur. Higher levels of Mg<sup>2+</sup> in these reactions do, in fact, rescue smaller NTP $\alpha$ S effects (data not shown). Mn<sup>2+</sup>, like Mg<sup>2+</sup>, can assume an octahedral coordination geometry (Gray, 1973), is active in G-addition and other reactions of the *Tetrahymena* intron, and is likely to occupy Mg<sup>2+</sup> binding sites and to employ phosphate oxygens in its coordination sphere (Grosshans & Cech, 1989). Although the exact coordination of Mn<sup>2+</sup> can be somewhat different from Mg<sup>2+</sup> (Jack et al., 1977), our results are consistent with the reestablishment of direct (inner sphere) metal ion coordination by Mn<sup>2+</sup> at sites of sulfur substitution.

## DISCUSSION

The positions of significant NTP $\alpha$ S effects on G-addition as well as the inferred positions of direct metal coordination are shown on the two-dimensional model of the *Tetrahymena* intron in Figure 3. Positions of NTP $\alpha$ S effects and Mn<sup>2+</sup> rescue occur within the highly conserved sequences in the group I core. Very strong NTP $\alpha$ S and Mn<sup>2+</sup> effects can be seen adjacent to bases A<sub>308</sub> (in helix P7) and A<sub>306</sub> (in the adjacent single-stranded region, J8/7), nucleotides that are more than 90% conserved among known group I introns (Michel & Westhof, 1990). Positions of NTP $\alpha$ S effects and Mn<sup>2+</sup> rescue are also seen adjacent to the universally conserved G<sub>264</sub>, which constitutes a portion of the guanosine binding site (Michel et al., 1989; Yarus et al., 1991a,b). In addition, these sites are seen adjacent to the universally conserved bases A<sub>261</sub>, in the single-stranded region connecting helices 6 and 7 (J6/7), and A<sub>207</sub> in loop L4, whose functions in splicing remain unknown (Michel & Westhof, 1990). The clustering of NTP $\alpha$ S effects and the positions of metal ion coordination are particularly evident when these effects are viewed on the

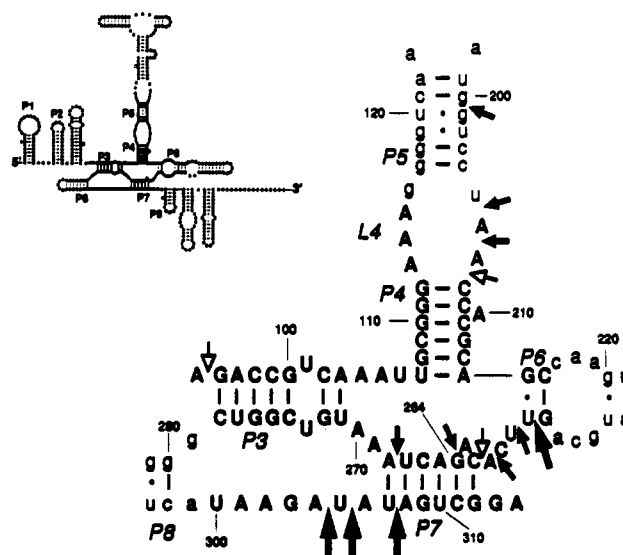


FIGURE 3: Positions of NTP $\alpha$ S effects and implied positions of metal ion coordination on the two-dimensional model of the *Tetrahymena* intron. The small drawing represents the complete *Tetrahymena* intron. The darkened region indicates the location of the expanded region shown to the right. Upper-case letters reflect nucleotides of the phylogenetically conserved core. All arrows indicate positions of NTP $\alpha$ S effects that change the observed rate of G-addition by 2-fold more. Larger arrows indicate rate changes of 3-fold or more. Filled arrows indicate positions of implied metal ion coordination.

three-dimensional model of the *Tetrahymena* core developed by Michel and Westhof (1990) (Figure 4). Both NTP $\alpha$ S effects and positions of implied metal coordination are particularly concentrated near the guanosine binding domain and the splice junction.

A number of these NTP $\alpha$ S positions have been detected in all reactions studied by the substitution interference method. In particular, clear NTP $\alpha$ S effects are seen at positions U<sub>305</sub>, A<sub>306</sub>, and A<sub>308</sub> for G-addition, CU-addition to the 3' splice site (Waring, 1989), and 3' splice site hydrolysis (Christian & Yarus, 1992). In addition, NTP $\alpha$ S substitution at U<sub>258</sub>, U<sub>259</sub>, and G<sub>264</sub> shows very strong effects on G-addition and 3' splice site hydrolysis. In CU addition reactions NTP $\alpha$ S at U<sub>258</sub> and U<sub>259</sub> produced little effect; however, these effects could have been obscured by high levels of NTP $\alpha$ S substitution (Waring, 1989; Christian & Yarus, 1992). G<sub>264</sub> was not studied in the CU addition experiments. Positions which appear consistently important to activity are intriguing candidates for essential tertiary structure and/or catalytic function.

Certain NTP $\alpha$ S effects are specific for G-addition. Most notably, NTP $\alpha$ S substitution at A<sub>206</sub>, A<sub>207</sub>, and C<sub>208</sub> inhibits G-addition strongly but does not detectably inhibit CU-addition at the 3' splice site and only weakly inhibits ( $k/k' \ll 2$ -fold) 3' splice site hydrolysis. This is consistent with the finding from photo-cross-linking studies that suggests that position A<sub>207</sub> of loop L4 is positioned close to both the bound guanosine cofactor (Wang & Cech, 1992) and the splice junction (Wang et al., 1993). These positions on the ribozyme are likely to be involved specifically in the binding or activation of the guanosine or the exon (see below).

The finding that the strongest NTP $\alpha$ S effects correlate not only with positions of Mn<sup>2+</sup> rescue but also with the regions of close backbone apposition predicted in the Michel–Westhof three-dimensional model (1990) of the *Tetrahymena* intron suggests a role for the corresponding ions in stabilizing tertiary structure. In this model, the backbones at positions U<sub>305</sub> and A<sub>308</sub> approach each other by virtue of a sharp bend in the

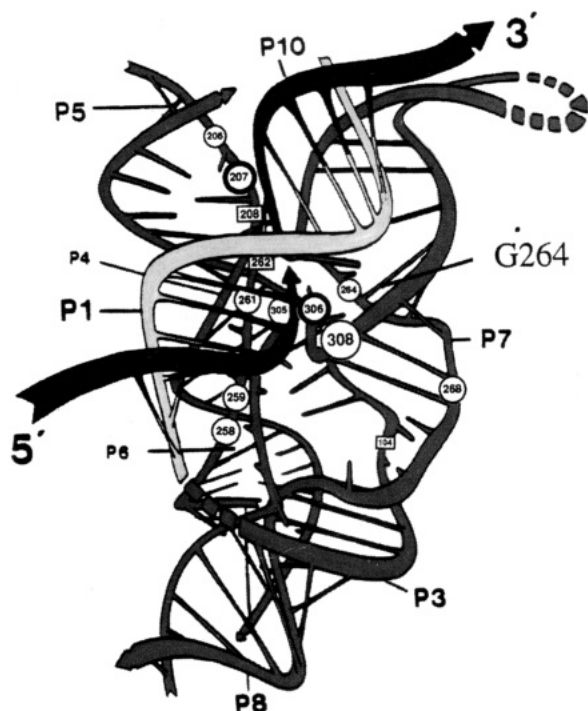


FIGURE 4: Positions of NTP $\alpha$ S effects on the three-dimensional model of the *Tetrahymena* core. The *Tetrahymena* core is represented as two helical domains: coaxially stacked helices P7, P3, and P8 (right) and a portion of helix 5, helix P4, and helix P6 (left back). Between these domains, 5' and 3' exon sequences are contained within helices P1 and P10, respectively, and are shown coaxially stacked in order to bring the 5' and 3' splice junctions together close to the guanosine binding domain (Michel et al., 1989; Yarus et al., 1991a,b) (adjacent to nucleotides 263–265). Squares denote NTP $\alpha$ S effects of 2-fold or greater on the rate of G-addition. Circles denote NTP $\alpha$ S effects that are also positions of implied metal ion coordination. Circles with darker outlines (positions 207 and 306) reflect candidates for metal ions involved in catalysis. Figure adapted from Michel and Westhof (1990) with permission.

chain between these two positions. Our results are consistent with the possibility of a single metal ion that stabilizes this sharp bend in the RNA backbone in a manner analogous to that observed in the sharp turn formed between the aminoacyl and D-stem in yeast tRNA<sup>Phe</sup> (Quigley et al., 1978). The model also predicts that the backbone at G<sub>264</sub> closely approaches the backbone at the base of helix P4 and the single-stranded region J3/4 where we observe smaller effects on hydrolysis. The metal ion we observe to be coordinated to position G<sub>264</sub> of the guanosine binding domain may stabilize an interaction between these backbone oxygens and join the guanosine binding domain to the rest of the ribozyme. Similarly, phosphate oxygens at positions U<sub>258</sub> and U<sub>259</sub> in helix P6 and the adjacent single-stranded region J6/7 are thought to closely approach the backbone of J8/7 near base A<sub>302</sub> where we also observe a smaller but significant effect ( $k'/k = 1.9$ ) on G-addition. Such an interaction could be stabilized by metal ions that appear to be coordinated to positions U<sub>258</sub> and U<sub>259</sub>.

A number of positions of apparent metal ion coordination also appear to be on the interface between the catalytic core and the RNA substrate. Strong NTP $\alpha$ S effects at U<sub>305</sub>, A<sub>306</sub>, and A<sub>308</sub> fall in positions thought to be adjacent to the backbone of the last two nucleotides of the 5' exon in helix P1, while the positions of NTP $\alpha$ S effects associated with A<sub>206</sub> and A<sub>207</sub> are close to the first nucleotides in the 3' exon of helix P10. Each of these positions appears to be involved in metal ion coordination. Thus, the simplest interpretation is that, as in tRNA<sup>Phe</sup>, Mg<sup>2+</sup> ion allows the assembly of negatively charged

domains into complex three-dimensional structures. Moreover, these results suggest that, in addition to base pairing and hydrogen bonding to sugar hydroxyls, ribozymes such as that from *Tetrahymena* may use metal ion coordination or a "metal bridge" in the recognition of nucleic acid substrates.

Changes in catalytic metal ion coordination can affect all RNA-catalyzed reactions because in the metal-depleted RNA the metal-catalyzed step becomes rate-limiting. Indeed, the positions at which we observe the strongest NTP $\alpha$ S effects (U<sub>259</sub>, U<sub>305</sub>, A<sub>306</sub>, and A<sub>308</sub>) are also those that appear to be universally important to activity in the *Tetrahymena* intron. The level of product formation approaches background when NTP $\alpha$ S is substituted at these positions. Therefore, we quote only a lower limit for the effect at these positions (Christian & Yarus, 1992). The actual level of NTP $\alpha$ S effects at the most sensitive positions may be much larger.

Biochemical evidence suggests that three of the positions that appear to be universally important to activity, U<sub>305</sub>, A<sub>306</sub>, and A<sub>308</sub>, are close to the splice junction since they are tethered at their 5' end by a tertiary interaction between the base at A<sub>302</sub> and the 2'-hydroxyl of U<sub>-3</sub> (Pyle et al., 1992) and at the 3' end by the guanosine binding domain contained in helix P7. Of these three positions, the Michel–Westhof three-dimensional model (1990) places phosphate oxygens at position A<sub>306</sub> closest to the 5' splice site. The metal ion associated with A<sub>306</sub> appears close enough to directly coordinate the 3' oxygen of the cleavage site and thus may act to stabilize the exon leaving group in G-addition. Interestingly, the substitution of the bridging oxygen of the leaving group with sulfur has a large effect on the rate of cleavage of the L-21 ribozyme (Piccirilli et al., 1993). Moreover, this effect is rescued with the addition of Mn<sup>2+</sup> ion. These experiments imply that metal ion coordination may act to stabilize the developing negative charge at the 3' ribose oxygen (or sulfur) as part of the transition state of the reaction. Thus, the *pro-R<sub>p</sub>* oxygen of A<sub>306</sub>, as part of a highly conserved group I geometry, may anchor this catalytically important metal ion to the active center of the ribozyme.

In a different experimental approach, the backbone adjacent to A<sub>306</sub> has been shown to be cleaved by Mn<sup>2+</sup>, Ca<sup>2+</sup> (T. S. McConnell, unpublished data), and Pb<sup>2+</sup> (Streicher et al., 1993) in solutions of *Tetrahymena* precursors and L-21 ribozyme, respectively. Although this does not identify the site of metal ion coordination or imply participation in any step in the splicing reaction, a specific cleavage does support a metal binding site near the splice junction. Interestingly, Fe<sup>2+</sup> (Wang & Cech, 1992) has been observed to induce cleavage of the backbone adjacent to position A<sub>207</sub> where we observe both Mn<sup>2+</sup> rescue and NTP $\alpha$ S effects that appear specific to the G-addition reaction. Moreover, mutations at A<sub>207</sub> strongly affect (ca. 18-fold) the chemical step of the G-dependent endonuclease reaction of the L-21 ribozyme (A. M. Pyle and F. L. Murphy, unpublished results). In addition to a metal ion that stabilizes the leaving group (3'O) in G-addition, it has been suggested (Piccirilli et al., 1993) that a second metal ion may activate the ribose of the guanosine nucleophile. These observations in conjunction with the cross-linking studies that place the A<sub>207</sub> region of loop L4 close to the bound guanosine cofactor (Wang & Cech, 1992) and splice junction (Wang et al., 1993) suggest a catalytic role for the metal ion we detect at position A<sub>207</sub>. In the current three-dimensional model, however, a metal ion coordinated to position A<sub>207</sub> is somewhat distant from the cleavage site and thus may interact indirectly through the coordination of water, or the conformation of the *Tetrahymena* ribozyme during



G-addition may be somewhat different than during the exon ligation step modeled by current three-dimensional structure.

Metal ions have also been implicated in the cleavage mechanisms of two other natural RNA catalysts. In RNase P, the M1 RNA-tRNA enzyme-substrate complex can form in the absence of divalent cation but is catalytically inactive (Smith et al., 1992). In the hammerhead ribozyme, NTP $\alpha$ S substitution at the cleavage site strongly inhibits the cleavage reaction in the presence of Mg<sup>2+</sup> ion but not in the presence of Mn<sup>2+</sup> ion, implying direct coordination of Mg<sup>2+</sup> ion to the *pro-R<sub>p</sub>* oxygen at the cleavage site as a requirement for catalysis (Dahm & Uhlenbeck, 1991). These results indicate that the *Tetrahymena* ribozyme, like other known RNA catalysts, functions as a metalloenzyme and support the notion that metal ions are a central feature of RNA active sites (Yarus, 1993).

## ACKNOWLEDGMENT

We thank Dr. Francois Michel and Dr. Eric Westhof for the coordinates of their three-dimensional model of the *Tetrahymena* group I core. We also thank Dr. Gregg Connell, Dr. Jonatha Gott, and Dr. Dennis Schultz for invaluable discussion and comments and Dr. Robin Gutell for his help in generating Figure 3.

## REFERENCES

- Brown, R. S., Dewan, J. C., & Klug, A. (1985) *Biochemistry* 24, 4785-4801.
- Celander, D. W., & Cech, T. R. (1991) *Science* 25, 401-407.
- Christian, E. L., & Yarus, M. (1992) *J. Mol. Biol.* 228, 743-758.
- Dahm, S. C., & Uhlenbeck, O. C. (1991) *Biochemistry* 30, 9464-9469.
- Dange, V., van Atta, R. B., & Hecht, S. M. (1990) *Science* 248, 585-588.
- Eckstein, F. (1985) *Annu. Rev. Biochem.* 54, 367-402.
- Frey, P. A., & Sammons, P. (1985) *Science* 228, 541-545.
- Gray, H. B. (1973) *Chemical Bonds*, pp 152-164, Benjamin/Cummings Publishing Co., London.
- Grosshans, C. A., & Cech, T. R. (1989) *Biochemistry* 28, 6888-6894.
- Guerrier-Takada, C., Haydock, K., Allen, L., & Altman, S. (1986) *Biochemistry* 25, 1509-1515.
- Holbrook, S. R., Sussman, J. L., Warrant, R. W., Church, G. M., & Kim, S. H. (1977) *Nucleic Acids Res.* 4, 2811-2820.
- Jack, A., Ladner, J. E., Rhodes, D., Brown, R. S., & Klug, A. (1977) *J. Mol. Biol.* 111, 315-328.
- Jaffe, E. K., & Cohn, M. (1978) *J. Biol. Chem.* 253, 4823-4825.
- Meyer, S. L. (1975) in *Data Analysis for Scientists and Engineers*, p 224, John Wiley & Sons Inc., New York.
- Michel, F., & Westhof, E. (1990) *J. Mol. Biol.* 216, 585-610.
- Michel, F., Hanna, M., Green, R., Bartel, D. P., & Szostak, J. W. (1989) *Nature* 342, 391-395.
- Pan, T., & Uhlenbeck, O. C. (1992) *Biochemistry* 31, 3887-3895.
- Pecoraro, V. L. (1984) *Biochemistry* 23, 5262-5271.
- Piccirilli, J. A., Vyle, J. S., Caruthers, M. H., & Cech, T. R. (1993) *Nature* 361, 85-88.
- Pyle, A. M., Murphy, F. L., & Cech, T. R. (1992) *Nature* 358, 123-128.
- Quigley, G. J., Teeter, M. M., & Rich, A. (1978) *Proc. Natl. Acad. Sci. U.S.A.* 75, 64-68.
- Saenger, W. (1984) in *Principles of Nucleic Acid Structure*, pp 201-219, Springer-Verlag Inc., New York.
- Schatz, D., Leberman, R., & Eckstein, F. (1991) *Proc. Natl. Acad. Sci. U.S.A.* 88, 6132-6136.
- Smith, D., Burgin, A. B., Haas, E. H., & Pace, N. R. (1992) *J. Biol. Chem.* 267, 2429-2436.
- Streicher, B., von Ashen, U., & Schroeder, R. (1993) *Nucleic Acids Res.* 21, 311-317.
- Wang, J. F., & Cech, T. R. (1992) *Science* 256, 526-529.
- Wang, J. F., Downs, W. D., & Cech, T. R. (1992) *Science* (in press).
- Waring, R. B. (1989) *Nucleic Acids Res.* 17, 10281-10293.
- Werner, C., Krebs, B., Kieth, G., & Dirheimer, G. (1976) *Biochim. Biophys. Acta* 432, 161-175.
- Yarus, M. (1993) *FASEB J.* 7, 31-39.
- Yarus, M., Illangesekare, M., & Christian, E. L. (1991a) *Nucleic Acids Res.* 19, 1297-1304.
- Yarus, M., Illangesekare, M., & Christian, E. L. (1991b) *J. Mol. Biol.* 222, 995-1012.