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Use of Both Direct and Indirect ^{13}C Tags for Probing Nitrogen Interactions in Hairpin Ribozyme Models by ^{15}N NMR[†]

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ABSTRACT

We have used the synthesis and ^{15}N NMR study of separate loop A and loop B domains of the hairpin ribozyme to demonstrate that multiple ^{15}N atoms can be incorporated into an RNA strand and be unambiguously distinguished through a combination of direct and indirect tagging by ^{13}C atoms. Absence of ^{15}N chemical shift changes shows that the G8N1 in loop A does not become deprotonated up to pH 8, and that the G21N7 of loop B does not bind to Mg^{2+} .

Key Words: Hairpin ribozyme; ^{15}N NMR; ^{13}C tag; Specific labeling.

INTRODUCTION

^{15}N NMR has proven to be a useful, non-perturbing tool for probing effects at nitrogen atoms in DNA and RNA. Changes in ^{15}N chemical shifts can report on several kinds of interactions, such as hydrogen bonding, protonation, metal binding and stacking, without introducing any modifications that could alter the structure.^[1–10]

[†]In honor and celebration of the 70th birthday of Professor Leroy B. Townsend.

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Although the ^{15}N nucleus has a spin of 1/2 and gives straightforward NMR spectra,^[11] its low natural abundance and low sensitivity require significant enrichment to be of practical use. Since uniform labeling usually leads to assignment difficulties, chemical labeling at specific sites in the nucleosides is desirable for this application. In recent years, we have reported high-yield methods to specifically incorporate ^{15}N into several sites at the same time, as well as ^{13}C to differentiate similar ^{15}N resonances.^[12–16] A ^{13}C incorporated at the purine C2 acts as a direct tag for adjacent nitrogens, because of the substantial couplings (6–23 Hz).^[12,16] In contrast, the very small C8–N7 coupling (<1 Hz) makes ^{13}C at the purine C8 more convenient as an indirect tag by taking advantage of the large C8–H8 coupling (213 Hz).^[15] To demonstrate the incorporation and study of six different ^{15}N atoms in two nucleosides of one RNA strand, using both direct and indirect tagging by ^{13}C , we report here our results for a model of the loop A domain of the hairpin ribozyme.

RESULTS AND DISCUSSION

The hairpin ribozyme is found in the satellite RNA of tobacco ringspot virus.^[17–19] This ribozyme encompasses a four-way helical junction, and it is the close interaction of non-Watson–Crick paired regions in two of the arms (A and B) that is primarily responsible for catalysis.^[20] Loop A contains the cleavage site, and loop B is the catalytic unit. Metal ions are required for activity, but help to form and maintain the correct tertiary structure rather than participate in the catalytic step.^[21,22] NMR structures of the separate loop A and B domains have been reported,^[23,24] as well as X-ray crystal structures of the full hairpin ribozyme.^[25,26] Comparison of these structures shows that significant conformational changes take place upon docking of the A and B domains.

We have synthesized two 14mer RNA strands that form the symmetrical loop A domain, with $[2\text{-}^{13}\text{C}\text{-}1,7,\text{NH}_2\text{-}^{15}\text{N}_3]\text{-guanosine}$ at G8 and $[8\text{-}^{13}\text{C}\text{-}1,7,\text{NH}_2\text{-}^{15}\text{N}_3]\text{-adenosine}$ at A9 (Figure 1). Resonances for the two amino groups can be distinguished, because that for A9 is a singlet, while that for G8 is split to a doublet ($J = 24\text{ Hz}$) by the $^{13}\text{C}2$ tag. The two N1 resonances can be distinguished by their markedly different chemical shifts (AN1 $\sim 223\text{ ppm}$, GN1 $\sim 145\text{ ppm}$). Although the $^{13}\text{C}8\text{-}^{15}\text{N}7$ coupling in A9 is too small to observe directly in 1D ^{15}N NMR spectra ($J < 1\text{ Hz}$), the ^{13}C still serves as an indirect tag. In a $^1\text{H}\text{-}^{15}\text{N}$ HSQC NMR spectrum of the labeled strand (Figure 2), the H8,N7 crosspeak of G8 is unsplit, while the H8,N7 crosspeak of A9 is split by 213 Hz along the ^1H dimension, due to the C8–H8 coupling.

The unlabeled strand of the loop A domain was titrated into the labeled strand in thirds, and ^{15}N spectra at each step clearly show the progression from single to double strand, since chemical shifts for A9N7, G8N7, and A9N1 differ in the two forms

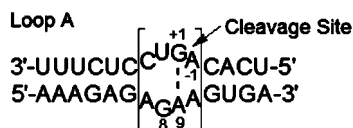


Figure 1. Loop A domain synthesized with $[2\text{-}^{13}\text{C}\text{-}1,7,\text{NH}_2\text{-}^{15}\text{N}_3]\text{-guanosine}$ at G8 and $[8\text{-}^{13}\text{C}\text{-}1,7,\text{NH}_2\text{-}^{15}\text{N}_3]\text{-adenosine}$ at A9.

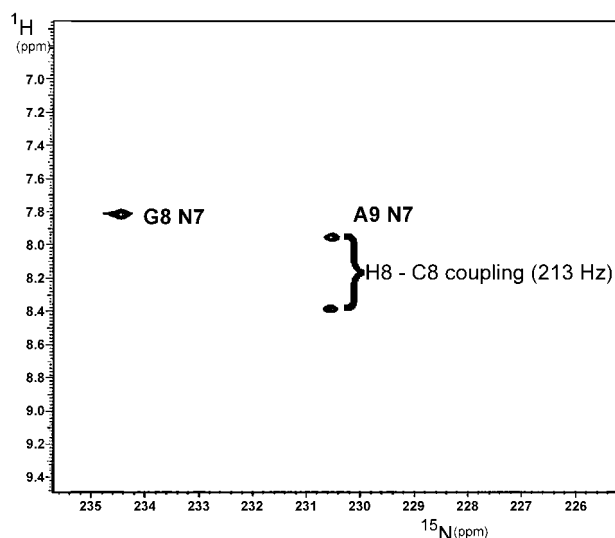


Figure 2. ^1H - ^{15}N HSQC NMR spectrum displaying the H8,N7 crosspeak of the loop A domain A9 that is split by 213 Hz along the ^1H dimension due to H8–C8 coupling, and that for G8 that is unsplit.

by 1–2 ppm (data not shown). This result indicates that the single strand and duplex are in slow exchange at 30.4 MHz. Figure 3 shows all six ^{15}N resonances for both forms.

G8 is in a non-Watson–Crick paired region of the loop A domain. Its N1H is close to the active site and is thought to participate in the cleavage step.^[26,27] Since guanosine N1 normally has a pKa of 9.4,^[28] the G8N1 would have to have a lowered pKa if it were to serve as an effective general acid/base catalyst at physiological conditions. Examples of such altered pKa's of nucleosides in very specific environments in RNA have been increasingly documented.^[29–33] If the G8N1 in fact gives up its proton to any significant extent, its ^{15}N chemical shift should move downfield accordingly.^[34] Although this process no doubt requires the docked complex of A and B, we wished to define the ^{15}N chemical shift behavior of the N1 of G8 in the isolated loop A domain. Figure 4 shows the ^{15}N NMR chemical shift of the G8N1 in the loop A duplex (closed squares) as a function of pH from 6 to 8, along with corresponding data for the G8N1 of the labeled loop A single strand (open squares) from pH 5.5 to 8. We did not go to a higher pH to avoid degradation. The superposition of the data shows that the duplex and the single strand have the same pH dependence in this range, indicating that the structure present in the isolated loop A domain does not lower the pKa of the G8N1.

In addition to the loop A domain, we also synthesized a model of the loop B domain, containing [8- ^{13}C -1,7,NH $_2$ - $^{15}\text{N}_3$]-guanosine at G21 (Figure 5), since it is a suspected metal binding site. Titration of the unlabeled strand into the labeled one again showed the progression from single strand to duplex (data not shown). In this case, the duplex signal is distinctly broader than that of the single strand, consistent with Feigon's observation that the isolated loop B domain is unusually dynamic and flexible.^[35] Addition of 4 and 8 equivalents of Mg^{2+} progressively increased the



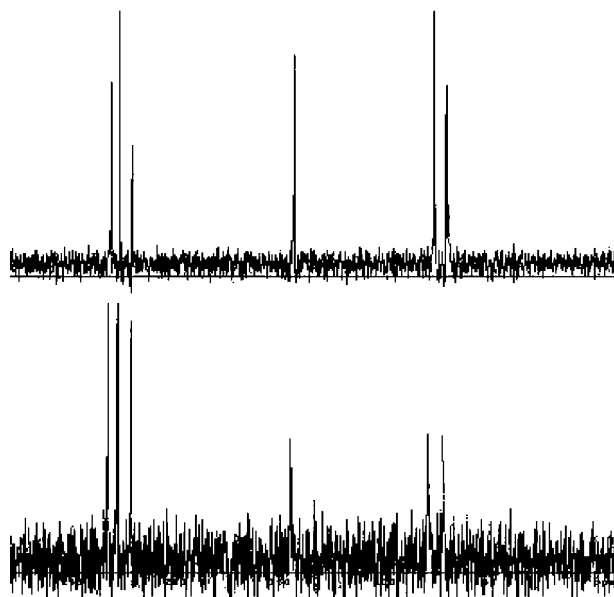


Figure 3. NMR spectra of the labeled loop A domain single strand (top) and duplex (bottom) at 30°C. (View this art in color at www.dekker.com.)

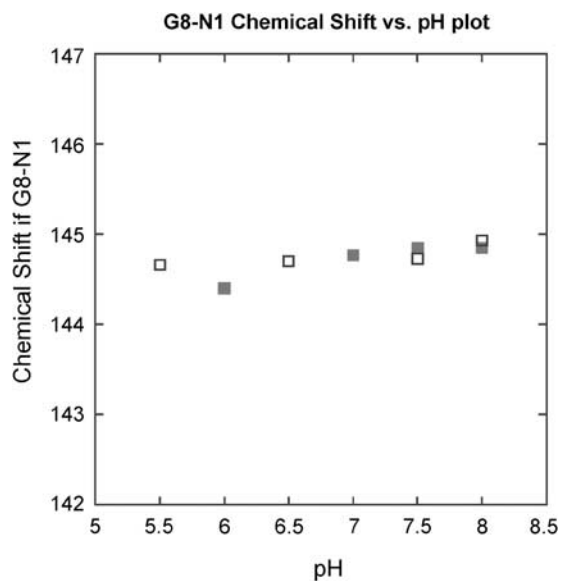


Figure 4. pH titration showing ^{15}N NMR chemical shifts for the G8N1 in the loop A domain duplex (closed squares) and in the loop A domain labeled single strand (open squares) at 30°C. (View this art in color at www.dekker.com.)



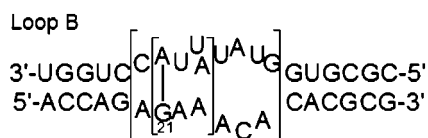


Figure 5. Loop B domain synthesized with $[8\text{-}^{13}\text{C}\text{-}1,7,\text{NH}_2\text{-}^{15}\text{N}_3]\text{-guanosine}$ at G21.

broadness of the signal (data not shown), but did not cause any upfield change, which would be expected for metal binding to the N7.^[36] This finding shows that Mg^{2+} has no significant binding to the G21N7, presumably because it is a hard metal and preferentially binds to oxygen.

CONCLUSION

The results reported here demonstrate that at least six ^{15}N atoms can be incorporated into an RNA strand and be unambiguously distinguished through the use of both direct and indirect tagging by ^{13}C atoms. The behavior of their chemical shifts can be used to probe the presence or absence of local interactions like deprotonation and metal binding, without introducing a perturbing change. In the work described here, G8N1 in the loop A domain did not display any signs of deprotonation up to pH 8, and G21N7 in the loop B domain did not show any binding to Mg^{2+} .

EXPERIMENTAL

The ^{13}C , ^{15}N labeled nucleosides were synthesized^[15] and protected^[37] as described previously, and their phosphoramidites were made by standard methods using 2-cyanoethyl tetraisopropylphosphorodiamidite^[38] and pyridinium trifluoroacetate.^[39] The oligonucleotides were synthesized on controlled pore glass supports using a Pharmacia OligoPilot II synthesizer at scales of 20–60 μmol using standard phosphoramidite chemistry with either 0.5 M tetrazole or 1.0 M dicyanoimidazole^[40] as an activator. The RNA was partially deprotected and removed from the support with aqueous methylamine at 65° for 10 minutes and then desilylated with $\text{Et}_3\text{N} \cdot \text{HF}/\text{NMP}/\text{Et}_3\text{N}$ at 65° for 2 hours.^[41] Excess fluoride was scavenged with trimethylsilyl isopropyl ether.^[42] The crude RNA was dissolved in 0.1 M TEAA and purified by reversed phase chromatography, first with the 5'-dimethoxytrityl group on, and again after detritylation. The pure RNA was desalted by reversed phase chromatography using 0.1 M NH_4HCO_3 , and then converted to the sodium form by cation exchange. The identities of the oligonucleotides were confirmed using ESI-MS.

NMR samples were 300 μL and contained 150 mM NaCl and 20 mM 4-(2-hydroxyethyl)-1 piperazineethanesulfonic acid (HEPES) in 90% $\text{H}_2\text{O}/10\%\text{D}_2\text{O}$. They were placed in Shigemitsu tubes after the pH was adjusted to 6.5–6.8, unless otherwise noted. The loop A sample was 6.2 mM total strand concentration and the loop B sample was 5.4 mM. Proton-decoupled 1D ^{15}N NMR spectra were acquired on a Varian



Oxford-300 NMR spectrometer at 30.4 MHz for about 14 hours and are reported relative to NH_3 using external 1 M $[\text{}^{15}\text{N}]$ -urea in DMSO at 25° at 77.0 ppm as a reference.^[43] Small volumes of MgCl_2 were titrated into the loop B sample as equivalents relative to the labeled strand. The ^1H - ^{15}N HSQC spectrum was acquired on a 600 MHz Varian Inova.

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