High-Resolution Nuclear Magnetic Resonance Determination of Transfer RNA Tertiary Base Pairs in Solution. 2. Species Containing a Large Variable Loop

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High-Resolution Nuclear Magnetic Resonance Determination of Transfer RNA Tertiary Base Pairs in Solution. 2. Species Containing a Large Variable Loop†

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ABSTRACT: The number of base pairs in the solution structure of several class III D3VN tRNA species from *E. coli* has been determined by analyzing the number of low-field (−15 to −11 ppm) proton resonances in their nuclear magnetic resonance spectra at 360 MHz. Contrary to previous reports indicating the absence of tertiary resonances, all the spectra exhibit the expected number of secondary base pair resonances plus approximately ten extra resonances derived from tertiary base pairs in the three-dimensional folding of these molecules. The possible origins of some of these tertiary resonances are discussed; none of the spectra exhibits the characteristic resonance of the 8-14 tertiary base pair seen in class I D4V5 tRNA spectra.

High-resolution NMR[1] spectroscopy has proven to be an extremely valuable tool in monitoring the solution base pairing of small nucleic acid molecules, especially tRNA. This derives from the fact that the ring NH hydrogen bond, if adequately long-lived (ca. 5 ms or longer), generates a resonance in the low-field region of the NMR spectrum (−11 to −15 ppm); furthermore there is only one ring NH hydrogen bond for each base pair. During the past 5 years, analysis of exchangeable proton resonances had been used to study nucleic acid structure in solution and the application of high-resolution NMR in the study of tRNA folding has been reviewed by Kearns and Shulman (1974) and by Kearns (1976).

The majority of transfer RNA molecules can be divided into two major groups, namely, those with small variable loops (typically 5 nucleotides) and those with large variable loops (typically 13 to 15 nucleotides or more). The former species typically contain four base pairs in their DHU stem and are designated class I tRNAs or D4V5 tRNAs (Kim et al., 1974). The latter species typically contain three base pairs in their DHU stem and contain internal base pairs in their large variable loops; they are designated class III tRNAs or D3VN tRNAs where N is usually 13 or 15 nucleotides and can be as large as 21 nucleotides (Kim et al., 1974). The ability of all tRNAs sequenced to date to be arranged in a two-dimensional cloverleaf representation facilitates the prediction of the expected number of secondary structure base pairs in any given tRNA. Hence an extremely valuable application of the NMR approach has been to ask if additional base pairs from tertiary folding exist in the tRNA structure in solution. D4V5 tRNAs, such as yeast $tRNA^{Phe}$, typically contain 20 secondary base pairs and the low-field spectrum of this tRNA has been interpreted to contain 19-20 resonances (Jones and Kearns, 1975; Wong et al., 1975b); i.e., tertiary resonances were claimed to be absent.

More recently Kearns and his co-workers have revised their method of integration and extended their studies to include *E. coli* $tRNA^{Asp}$ (20.2 resonances), *E. coli* $tRNA^{Trp}$ (21.6 resonances), *E. coli* $tRNA^{Glu}$ (21.5 resonances), *E. coli* $tRNA^{Val}_1$ (23 resonances), and *E. coli* $tRNA^{fMet}$ (23 resonances); i.e., the revised estimates suggest 1-3 tertiary resonances in class I tRNAs (Kearns, 1976; Bolton et al., 1976). Our own data on 14 class I tRNAs indicate that they all contain approximately seven tertiary base pair resonances in their NMR spectra (see Reid et al., 1977) and prompted the present study on class III tRNA species. There are only a few amino acids for which the corresponding tRNAs are always class III D3VN species regardless of the biological source. For instance, bacterial $tRNA^{Tyr}$ is a class III D3V13 species, whereas yeast $tRNA^{Tyr}$ contains only five nucleotides in its variable loop (Barrell and Clark, 1974). However, all serine-specific tRNAs and all leucine-specific tRNAs isolated to date from viral, bacterial, yeast, and mammalian sources are class III D3VN species (Barrell and Clark, 1974).

Relatively few studies have been carried out on the solution base pairing of class III tRNAs by NMR methods compared with studies on class I tRNAs. Perhaps the most studied class III tRNA is yeast $tRNA^{Leu}_3$ (UUG). This is a D3V13 species containing 22 secondary base pairs in the cloverleaf structure. NMR studies on this tRNA by Kearns and co-workers reported the presence of either 21.3 or 22 resonances in the low-field spectrum (Wong et al., 1973; Kearns et al., 1974a,b). A more recent analysis by this group reported an intensity of 21 ± 2 for the low-field spectrum of yeast $tRNA^{Leu}_3$ (UUG) and extended the study to another class III tRNA, namely, yeast $tRNA^{Leu}$ (CUA). This latter D3V13 species contains 21 secondary base pairs; its low-field NMR spectrum was reported to contain 20 resonances (Rordorf et al., 1976). The conclusion from these studies is that the low-field NMR spectrum contains no resonances from tertiary base pairs.

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[1] Abbreviations used are: UV, ultraviolet; tRNA, transfer ribonucleic acid; NMR, nuclear magnetic resonance; DHU, dihydrouridine; rT, ribothymidine; s^4U, 4-thiouridine; Ψ, pseudouridine; Tris, tris(hydroxymethyl)aminomethane; EDTA, ethylenediaminetetraacetic acid; BD, benzoylated diethylaminoethyl; DEAE, diethylaminoethyl; DSS, 2,2-dimethylsilapentane-5-sulfonate.

We have uncovered several errors in previous NMR analyses of tertiary base pairing in class I tRNAs (see Reid et al., 1977). Consequently we decided to extend our studies to include several class III tRNAs. We have purified to homogeneity four class III leucine-accepting tRNAs from *E. coli* and studied their low-field NMR spectra at 360 MHz. Contrary to previous claims that the spectra contain no tertiary resonances, we find that the low-field spectra contain approximately ten resonances from tertiary base pairs.

Materials and Methods

Isolation of tRNA. There are four, and perhaps a fifth, species of *E. coli* leucine tRNA which can be resolved on RPC5 columns (Natale and Eilat, 1976; Kelmers and Heatherly, 1971) and which can be equally well-resolved by BD-cellulose chromatography using the conditions of Gillam et al. (1967). However, there is some confusion in the literature concerning the ambiguous numbering of these isoaccepting leucine tRNAs.

$tRNA^{Leu}_1$. Unfractionated *E. coli* B tRNA was chromatographed on BD-cellulose according to Gillam et al. (1967) using a gradient from 0.4 to 1.3 M NaCl. Two leucine tRNA species were not eluted in the NaCl gradient and remained adsorbed to the column; they were later eluted with 10% ethanol. The first species in the NaCl gradient eluted at 0.85 M NaCl and is quantitatively the major leucine tRNA. It was purified to homogeneity by DEAE-Sephadex chromatography (Nishimura, 1971) followed by Sepharose 4B chromatography (Holmes et al., 1975). The final pure material accepted 1600 pmol of leucine per A_{260} unit; RNase T1 fingerprinting revealed its sequence to be that of *E. coli* $tRNA^{Leu}_1$ (Dube et al., 1970; Allaudeen et al., 1972).

$tRNA^{Leu}_2$. A later leucine peak, eluting in the gradient at 1.08 M NaCl, was further purified to homogeneity by DEAE-Sephadex chromatography and Sepharose 4B chromatography. The final pure material accepted 1580 pmol of leucine per A_{260} unit. The elution position of this tRNA during Sepharose 4B chromatography under the conditions of Holmes et al. (1975) is just before the major $tRNA^{Leu}_1$ species. Chromatography of this species on RPC5 according to Kelmers and Heatherly (1971) reveals that it is the third leucine isoaccepting tRNA eluted from the column. This has led Kelmers and Heatherly (1971) and Natale and Eilat (1976) to designate this species *E. coli* $tRNA^{Leu}_3$. Fingerprints of this pure tRNA reveal that it is identical with the species designated *E. coli* $tRNA^{Leu}_2$ by Blank and Soll (1971) based on its being the second leucine species eluted from BD-cellulose. Hence we have shown that the RPC5 $tRNA^{Leu}_3$ is the BD-cellulose $tRNA^{Leu}_2$. Since this sequence is already listed in the catalog of tRNA sequences according to the Blank and Soll nomenclature (Barrell and Clark, 1974), we prefer to designate it $tRNA^{Leu}_2$.

$tRNA^{Leu}_4$ and $tRNA^{Leu}_5$. *E. coli* $tRNA^{Leu}_4$ and $tRNA^{Leu}_5$ were eluted from the BD-cellulose column with 1.3 M NaCl containing 10% ethanol. This material was dialyzed and fractionated on DEAE-Sephadex according to Nishimura (1971). This produced an early eluting peak of $tRNA^{Leu}_5$ followed by a peak of $tRNA^{Leu}_4$ in the middle of the gradient which in turn was followed by later-eluting peaks of $tRNA^{Tyr}_1$ and $tRNA^{Tyr}_2$ which were resolved from each other. The $tRNA^{Leu}_5$ was purified to homogeneity on Sepharose 4B columns from which it elutes extremely early. The $tRNA^{Leu}_4$ was also purified to homogeneity on Sepharose 4B columns from which it elutes extremely late in the gradient.

Thus *E. coli* $tRNA^{Leu}_1$ is the major leucine tRNA; it is the first leucine species eluted during both BD-cellulose chromatography and RPC5 chromatography. *E. coli* $tRNA^{Leu}_2$ is the second most predominant leucine tRNA; it is the third leucine species eluted in RPC5 chromatography and Sepharose 4B chromatography and has been called $tRNA^{Leu}_3$ by Kelmers and Heatherly (1971) and by Natale and Eilat (1976). *E. coli* $tRNA^{Leu}_4$ and $tRNA^{Leu}_5$ are minor leucine species and both require ethanol to be eluted from BD-cellulose. *E. coli* $tRNA^{Leu}_4$ is the last leucine species eluted from Sepharose 4B columns and the fourth species eluting from RPC5 columns just before $tRNA^{Leu}_5$. *E. coli* $tRNA^{Leu}_5$ is the first leucine species eluting from Sepharose 4B columns and the last species eluting from RPC5 columns.

As mentioned earlier, the BD-cellulose ethanol fraction also contained $tRNA^{Tyr}_1$ and $tRNA^{Tyr}_2$ which resolved from each other on DEAE-Sephadex chromatography. The later-eluting $tRNA^{Tyr}_2$ was further purified to homogeneity by Sepharose 4B chromatography and RPC5 chromatography. The final material accepted 1530 pmol of tyrosine per A_{260} unit.

Lastly, we often observed a variable peak of leucine tRNA eluting from BD-cellulose between $tRNA^{Leu}_1$ and $tRNA^{Leu}_2$. Further purification revealed that most of this material was $tRNA^{Leu}_1$ covalently nicked in the variable loop. However, it may also contain a fifth minor leucine tRNA, i.e., $tRNA^{Leu}_3$ (it would be designated $tRNA^{Leu}_2$ in the Kelmers RPC5 nomenclature). We have not studied this material further. The nicked $tRNA^{Leu}_1$ is apparently identical with the material produced upon T2 phage infection (Kano-Sueoka and Sueoka, 1968). We note that Natale and Eilat (1976) observed only four leucine tRNA species upon RPC5 fractionation of uninfected *E. coli* C-3000.

NMR Spectra. The purified tRNA species were dialyzed against distilled water containing 0.1 mM sodium thiosulfate at pH 7.0 and lyophilized. Aliquots of 5 mg were dissolved in 10 mM sodium cacodylate–100 mM NaCl–15 mM $MgCl_2$ (pH 7.0) to give a final volume of 0.18 mL which was transferred to a 5 mm × 8 mm NMR microtube (Wilmad Glass Co., Buena, N.J.). Spectra were obtained at 360 MHz using either correlation spectroscopy (2400 Hz per 2 s; signal averaged for 20–30 min) or continuous wave spectroscopy (2400 Hz per 12 s; signal averaged for 4–7 h). Chemical shifts are reported in ppm from DSS (2,2-dimethylsilapentane-5-sulfonate). They were experimentally determined as chemical shifts from the water solvent to which the known chemical shift of water from DSS at the appropriate temperature was added.

Integration and Simulation of Spectra. The intensity of each peak was determined by measuring its area in cm^2 on the original full scale spectrum. These values were corroborated by computer simulation of the spectra using a series of Lorentzian lines having the observed line width of single resolved resonances. These Lorentzian peaks were convoluted to generate an approximation of the spectrum and the line positions adjusted until the simulated spectrum matched the experimental spectrum. The resulting computer listing then revealed the number of resonances in each peak and the chemical shifts of the component resonances.

Results

The cloverleaf sequences of *E. coli* $tRNA^{Leu}_1$ (Dube et al., 1970), $tRNA^{Leu}_2$ (Blank and Soll, 1971), $tRNA^{Tyr}_1$ and $tRNA^{Tyr}_2$ (Goodman et al., 1968) are shown in Figure 1. They are all class III D3VN tRNAs where N is either 15 or 13 and contain a total of 87 or 85 nucleotides. *E. coli* $tRNA^{Leu}_2$ and $tRNA^{Tyr}_2$ contain 23 normal Watson–Crick base pairs in their

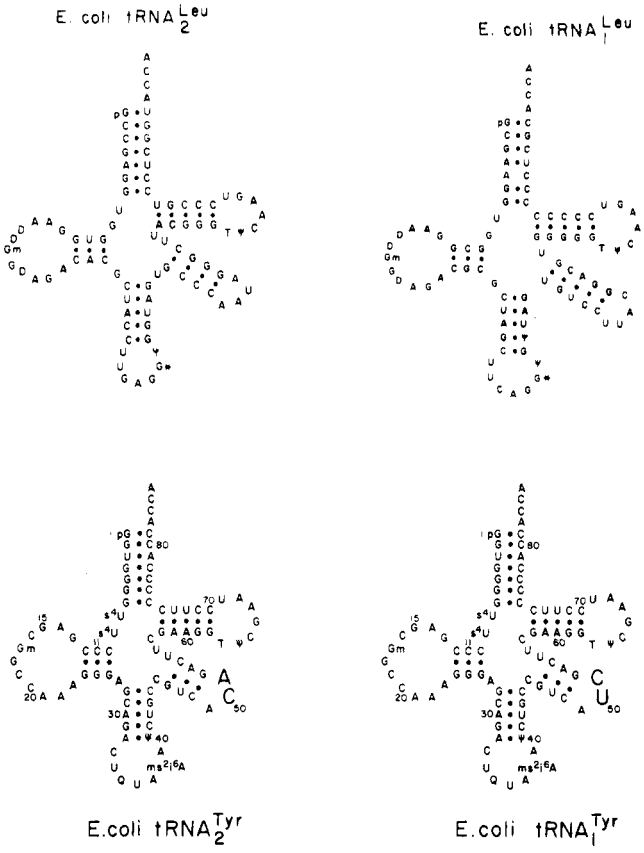

FIGURE 1: The cloverleaf sequences of representative class III D3VN tRNA species from *E. coli*. The sequences are taken from the literature references cited in Materials and Methods.

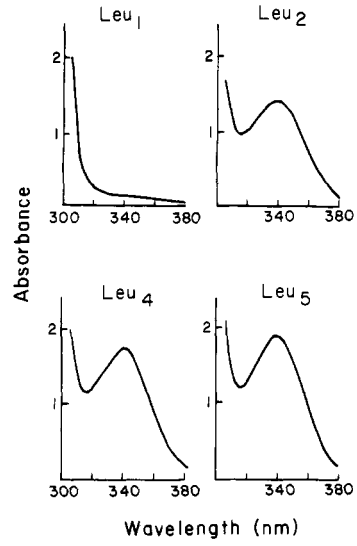

FIGURE 2: The UV spectra of the isoaccepting leucine tRNA species from *E. coli* in the 300–380-nm region. The samples, in 10 mM Tris-Cl–10 mM $MgCl_2$ (pH 7.0), were adjusted to an absorbance of 100 at 260 nm so that the extinction at each wavelength directly indicates the percent of the 260-nm absorption.

secondary structure and *E. coli* $tRNA^{Leu}_1$ contains 22 secondary base pairs. In addition they all contain nonstandard interactions such as GU, AC, GΨ, and AΨ "pairing". *E. coli* $tRNA^{Leu}_4$ and $tRNA^{Leu}_5$ have not yet been sequenced; however, we have shown that they are both class III D3VN species by several methods. Both species have a larger chain length than the 76-nucleotide $tRNA^{Val}_1$ when chromatographed on Sephadex G-200 at high temperature under the size-calibration conditions reported previously (Reid et al., 1972). Gel electrophoresis in 7 M urea at pH 7.2 easily resolved $tRNA^{Leu}_1$ (87 nucleotides) from $tRNA^{Val}_1$ (76 nucleotides) or any other class I tRNA. Similarly $tRNA^{Leu}_4$ and $tRNA^{Leu}_5$ were easily resolved from $tRNA^{Val}_1$ on the basis of size in urea gel electrophoresis; yet neither could be resolved from $tRNA^{Leu}_1$ (Azhderian and Reid, unpublished observations). Hence we estimate the chain length of $tRNA^{Leu}_4$ and $tRNA^{Leu}_5$ to be 87 ± 2 nucleotides. Furthermore we emphasize that all leucine tRNA species isolated to date, regardless of their biological source, are class III D3VN species containing a large variable loop.

The minor nucleoside 4-thiouridine has an ultraviolet extinction maximum in the 335–340-nm region and its presence in bacterial tRNA was demonstrated several years ago (Lipsett, 1965). The majority of *E. coli* tRNA species sequenced to date contain a single 4-thiouridine residue which is always located at position 8 in the sequence (Barrell and Clark, 1974). Our studies on several class I tRNAs containing a single s^4U8 residue per 76 nucleotides indicate that the absorbance at 340 nm varies between 1.9 and 2.1% of the 260-nm absorbance, depending on the tRNA species.

Figure 2 shows the UV spectra of the isoaccepting leucine tRNAs from *E. coli* in the 300 to 380 nm range. The samples were adjusted to an absorbance of 100 at 260 nm so that the observed absorbance in the longer wavelength UV region directly reflects the percentage of the 260-nm extinction. The presence of 4-thiouridine was not detected during the sequencing of *E. coli* $tRNA^{Leu}_1$ (Dube et al., 1970), and we observe no 340-nm peak for this tRNA. Although Blank and Soll (1971) did not detect 4-thiouridine in $tRNA^{Leu}_2$, they point out the need to confirm this with unlabeled tRNA due to the difficulty of identifying this residue with only very small amounts of labeled tRNA. As shown in Figure 2, we observe the characteristic s^4U absorption peak at 340 nm in $tRNA^{Leu}_2$, $tRNA^{Leu}_4$, and $tRNA^{Leu}_5$; our fingerprint data and partial fragmentation of these tRNAs are consistent with this residue being in position 8 as expected. Quantitatively the 340-nm absorbance amounts to only 1.5 to 1.8% of the 260-nm extinction and this presumably reflects the 87-nucleotide chain length of these class III tRNAs. We conclude that *E. coli* $tRNA^{Leu}_2$, $tRNA^{Leu}_4$, and $tRNA^{Leu}_5$ contain a s^4U8 residue, whereas $tRNA^{Leu}_1$ does not. The UV spectrum of our $tRNA^{Tyr}_2$ sample contained a discrete 340-nm peak with an intensity of 3.9% of the 260-nm extinction; this reflects the presence of s^4U at position 9 as well as position 8 in this tRNA (Goodman et al., 1968).

Figure 3 shows the low-field NMR correlation spectrum of *E. coli* $tRNA^{Leu}_4$ at 360 MHz. Most of the intensity is located between −13.6 and −12.2 ppm in three large, poorly resolved complex peaks. If we assume that the resolved peaks at −14.2, −13.9, −11.7, and 11.4 ppm contain a single proton, then the total intensity between −15 and −11 ppm reflects the presence of approximately 30 base pairs.

The 360-MHz spectrum of *E. coli* $tRNA^{Leu}_5$ is shown in Figure 4. The spectrum shows somewhat better resolution in the −14 to −12 ppm region and prompted us to attempt to integrate the complex peaks. Integration with respect to the single resonances at −14.6, −14.2, −11.9, −11.8, and −11.4 ppm gave the values indicated on the spectrum. This led to a total intensity estimate of approximately 30 protons in the −15 to −11 ppm region; the difficulty of integrating incompletely resolved peaks causes an uncertainty of at least 10% and we

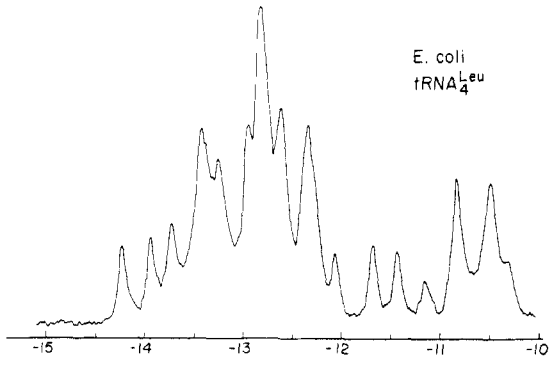

FIGURE 3: Correlation 360-MHz NMR spectrum of *E. coli* $tRNA^{Leu}_4$ at 45 °C. The sample (ca. 1 mM tRNA) was dissolved in 10 mM sodium cacodylate–100 mM NaCl–15 mM $MgCl_2$ (pH 7.0). The spectrum was signal-averaged for 1 h under correlation sweep conditions.

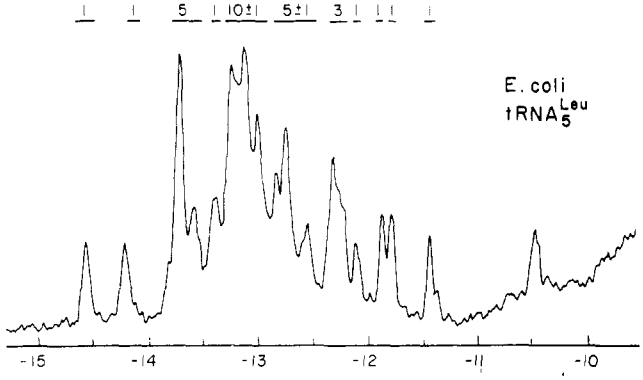

FIGURE 4: The 360-MHz NMR spectrum of *E. coli* $tRNA^{Leu}_5$ at 45 °C in 10 mM sodium cacodylate–100 mM NaCl–15 mM $MgCl_2$. The continuous wave spectrum was signal-averaged for 3 h. The integrated area of each peak is indicated on the spectrum.

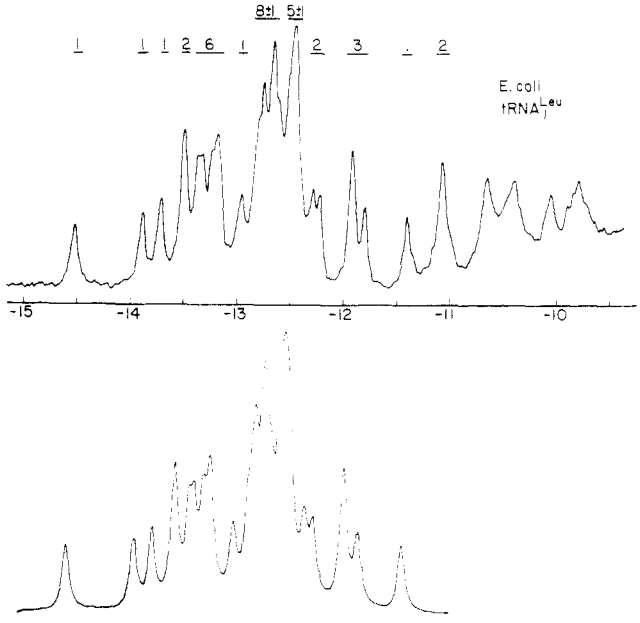

FIGURE 5: The 360-MHz low-field NMR spectrum of *E. coli* $tRNA^{Leu}_1$ at 35 °C. The sample (1 mM) was dissolved in 10 mM sodium cacodylate–100 mM NaCl–15 mM $MgCl_2$ (pH 7.0). The upper, experimental spectrum contains the integrated intensities indicated; the lower, simulated spectrum contains 30 Lorentzian lines of 28 Hz line width, excluding the two protons at −11.1 ppm.

estimate that the spectrum contains 30 ± 3 low-field resonances.

The low-field NMR spectrum of *E. coli* $tRNA^{Leu}_1$ is reasonably well-resolved and is shown in Figure 5. There are resolved single proton peaks at −14.5, −13.9, −13.7, −11.8, and −11.4 ppm. Based on these intensities, the peaks at −13.5, −12.3, and −11.9 ppm each contain 2 protons; the spectrum integrates to a total intensity of 33 ± 2 resonances between −15 and −11 ppm. The improved resolution in this class III tRNA spectrum encouraged us to simulate the spectrum with a series of convoluted Lorentzian lines having the experimentally observed 28 Hz line width. The lower trace in Figure 5 is the computer-simulated $tRNA^{Leu}_1$ spectrum; it required 30 lines, not including the two protons at −11.1 ppm, and thus corroborates the independent estimate of 33 ± 2 low-field ring NH hydrogen bonds by direct integration. The computer simulation result of 32 low-field protons indicated that there were in fact 13 protons in the −12.8 to −12.4 ppm region but also suggested that the −13.5 to −13.1 ppm region contained 7 protons rather than 8 protons.

Figure 6 shows the 360-MHz NMR spectrum of *E. coli* $tRNA^{Leu}_2$. The resolution is quite good in that the seven complex peaks between −14 and −12 ppm are reasonably separated from each other. The spectrum was integrated as shown and led to a value of 33 ± 1 protons in the −15 to −11.3 ppm region. The computer simulation in the lower trace contains 32 lines of 30-Hz line width and a 20-Hz line of unit intensity at −11.4 ppm.

The last class III tRNA to be analyzed in this series was *E. coli* $tRNA^{Tyr}_2$ and its 360-MHz low-field spectrum is shown in Figure 7. While not as well-resolved as the spectra of $tRNA^{Leu}_1$ and $tRNA^{Leu}_2$, the complex peaks are nevertheless reasonably evenly distributed throughout the −14 to −12 ppm region. The intensity value for the various complex peaks are indicated on the spectrum; during the signal averaging of this spectrum, we experienced serious 3.3-KHz water interference at −13.9 ppm and, despite efforts to correct for it, the intensity of this peak is somewhat uncertain. In spite of these uncertainties, the $tRNA^{Tyr}_2$ spectrum, like the other class III tRNA NMR spectra, apparently contains 33 ± 3 low-field protons of which approximately 10 must be derived from tertiary structure. Rordorf and Kearns (1976) have reported 25–26 low-field resonances (2–3 tertiary) in the low-field spectrum of *E. coli* $tRNA^{Tyr}$.

Discussion

Since each base pair can generate only one ring NH hydrogen bond resonance in the low-field NMR spectrum, the most important question to be answered from these studies is whether or not extra base pairs from tertiary folding are detectable in solution. The class III D3VN tRNA species we have studied contain 22 or 23 base pairs; the number of stable base pairs detected in solution from the corresponding NMR spectra are listed in Table I. It is apparent that class III tRNAs show extensive tertiary interactions involving approximately 10 extra base pairs in their three-dimensional folding. This result does not agree with the class III leucine tRNA NMR studies of Kearns and co-workers (Wong et al., 1973; Kearns et al., 1974a,b; Rordorf et al., 1976). In these studies they claim that the low-field (11–15 ppm) region of the yeast $tRNA^{Leu}_3$ (UUG) spectrum contains 21 or 22 resonances and the spectrum of $tRNA^{Leu}$ (CUA) contains only 20 resonances. In no cases was there even one extra resonance that could be attributed to tertiary base pairing. We are now in a position to explain the errors which led to this incorrect conclusion. The

TABLE I: The Number of Secondary and Tertiary Base Pairs Detectable in the Low-Field NMR Spectra of Class III tRNA Species.

tRNA Species	Conditions	No. of Low-Field Base-Pair Resonances	Secondary Base Pairs	No. of Tertiary Base Pairs
E. coli $tRNA^{Leu}_1$	35 °C, 15 mM $MgCl_2$	33 ± 2	22	11 ± 2
E. coli $tRNA^{Leu}_2$	35 °C, 15 mM $MgCl_2$	33 ● 1	23	10 ± 1
E. coli $tRNA^{Tyr}_2$	35 °C, 15 mM $MgCl_2$	33 ± 3	23	10 ± 3
E. coli $tRNA^{Leu}_4$	45 °C, 15 mM $MgCl_2$	Uncertain	(23 ± 1 ?)	
E. coli $tRNA^{Leu}_5$	35 °C, 15 mM $MgCl_2$	30 ± 3	(23 ± 1 ?)	7 to 11

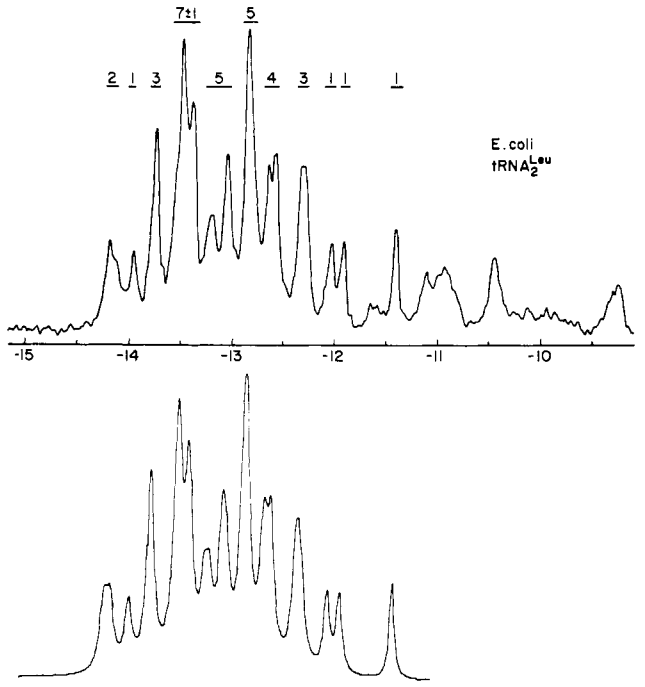

FIGURE 6: The 360-MHz low-field NMR spectrum of *E. coli* $tRNA^{Leu}_2$ at 35 °C. The solvent is 10 mM sodium cacodylate–100 mM NaCl–15 mM $MgCl_2$ and the CW spectrum was signal-averaged for 10 h. The experimental spectrum (upper) contains the relative peak areas indicated; the computer-simulated spectrum (lower) contains 32 Lorentzian lines of 30 Hz line width and 1 Lorentzian line of 20 Hz line width at −11.4 ppm.

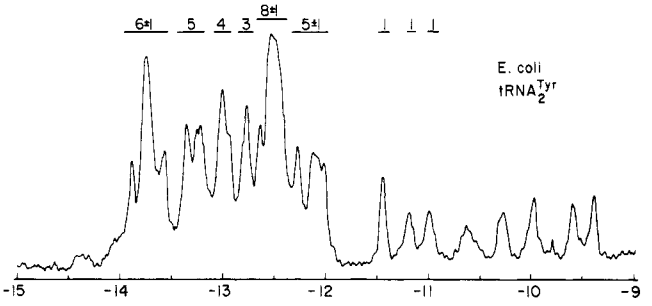

FIGURE 7: The 360-MHz NMR spectrum of *E. coli* $tRNA^{Tyr}_2$ at 35 °C in a solvent of 10 mM sodium cacodylate–100 mM NaCl–15 mM $MgCl_2$. The estimated intensities of the various peaks are shown on the spectrum.

first error is that "the integrated intensity in the appropriate spectral region of the $tRNA^{Leu}_3$ sample was compared with the intensity of a standard sample of yeast $tRNA^{Phe}$ which exhibits 19 resonances in the 11–15-ppm region" (Kearns et al., 1974b). We have recently shown that yeast $tRNA^{Phe}$ exhibits 26 ± 1 resonances in the 11–15-ppm region (see Reid et al., 1977). The second error in the case of the native $tRNA^{Leu}_3$ spectrum was "the peak at 14.3 ppm was assumed to correspond to two protons and the rest of the spectrum was integrated on this basis" (Kearns et al., 1974b). It is not possible to simulate the shape of their peak at −14.3 ppm with two Lorentzian lines; the line shape of this peak can only be duplicated by three resonances. Hence the integration methods used lead to values of 66 to 75% of the correct values. Correction of these errors by the appropriate factor converts their estimate of approximately 22 base pairs to values approaching our own estimates for class III tRNAs which we find to contain even more tertiary base pairing in solution than class I tRNAs.

The 8–14 Tertiary Base Pair. The crystal structure of yeast $tRNA^{Phe}$ reveals a reversed Hoogsteen base pair between U8 and A14 (Kim et al., 1974). Most *E. coli* class I tRNAs contain s^4U instead of U at position 8 (Barrell and Clark, 1974) and also exhibit a single resonance at the extreme low-field end of their −15 to −11 ppm spectrum at approximately −14.8 ppm. The observation that this extreme low-field resonance moves upfield by ca. 0.6 ppm upon conversion of s^4U8 to U8 has led us, and others, to assign the −14.8 ppm resonance to the s^4U8-A14 base pair (Reid et al., 1975; Wong et al., 1975a). The class I *E. coli* tRNAs containing s^4U8 which we have analyzed include $tRNA^{Val}_1$, $tRNA^{Val}_{2A}$, $tRNA^{Val}_{2B}$, $tRNA^{His}$, $tRNA^{Arg}_1$, $tRNA^{Lys}$, $tRNA^{Thr}_1$, $tRNA^{Gly}_1$, $tRNA^{fMet}$, $tRNA^{mMet}$, and $tRNA^{Ala}$; we have not found a single exception to the rule that class I tRNAs containing a s^4U8-A14 tertiary base pair contain a low-field resonance at −14.8 ± 0.1 ppm. However, this correlation is totally absent in class III tRNAs. *E. coli* $tRNA^{Leu}_1$ contains no s^4U but contains a resonance at −14.55 ppm; this same resonance is present in $tRNA^{Leu}_5$ which does contain s^4U8. *E. coli* $tRNA^{Leu}_2$ contains s^4U8 (and also A14) and $tRNA^{Leu}_4$ also contains s^4U8 (and probably A14; Azhderian and Reid, unpublished preliminary sequence data); neither contains a resonance lower than −14.2 ppm. There are no resonances lower than −13.9 ppm in the low-field spectra of *E. coli* $tRNA^{Tyr}_1$ and $tRNA^{Tyr}_2$, yet both s^4U8 (and s^4U9) as well as A14. Thus class III tRNAs with s^4U8 and A14 in their sequence do not exhibit the −14.8-ppm resonance characteristic of the s^4U8-A14 tertiary base pair seen in class I tRNA spectra. From this we conclude that class III tRNAs do not contain the 8–14 interaction and may well fold differently in this region of the molecule. The reason we do not observe the 8–14 interaction may be due to the absence of a secondary base pair involving G13 in the DHU stem in class III tRNAs. A further possibility is that the 8–14 interaction may exist in solution but with too short a lifetime to be detected by magnetic resonance methods. However, we feel this to be unlikely based on the long lifetimes of the other tertiary interactions. Unequivocal answers to these questions must await crystallographic structure determination of a D3VN tRNA.

Other Tertiary Interactions. The NMR data we have presented indicate that class III tRNAs utilize more tertiary base

pairs in their three-dimensional folding than do class I tRNAs. When their sequences are compared with yeast $tRNA^{Phe}$, we note the common sequences TΨCNA in the rT loop and two adjacent G residues at position 18 in the DHU loop. Hence the potential is certainly present to form the "T54-A58" base pair (65-69 in $tRNA^{Leu}$ and 63-67 in $tRNA^{Tyr}$) as well as the "G18-Ψ55" and "G19-C56" interactions. There is obviously no class III interaction corresponding to G46-G22 in yeast $tRNA^{Phe}$; however, the complementarity between Pu15 and the nucleotide preceding the internal terminus of the rT helix discussed by Klug et al. (1974) and Kim et al. (1974) is maintained and may form a tertiary base pair analogous to the reversed Watson-Crick G15-C48 interaction in yeast $tRNA^{Phe}$. The identity of the remaining tertiary interactions in class III tRNAs remains unknown. Preliminary comparative studies on class III tRNA spectra have led us to tentatively suggest hydrogen-bonding interactions involving two of the four nucleotides in the loop at the end of the variable stem.

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