
Yeast phenylalanine transfer RNA: atomic coordinates and torsion angles

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ABSTRACT

The atomic coordinates of yeast phenylalanine transfer RNA (tRNA) as well as the torsion angles of the polynucleotide chain are presented as derived from an x-ray diffraction analysis of orthorhombic crystals. A comparison is made between the coordinates obtained from analysis of monoclinic crystals of the same material. It is concluded that the molecule has substantially the same form in the orthorhombic and the monoclinic lattices, except for differences found between residues at the 3' end of the polynucleotide chain. A number of observations are made concerning hydrogen bonding interactions which may account for many of the residues conserved in all tRNA sequences.

INTRODUCTION

Approximately three years ago, the folding of the polynucleotide chain of yeast phenylalanine tRNA was described from a 4Å x-ray diffraction analysis of orthorhombic crystals (1). It was shown that the molecule was bent into an L-shape with the acceptor and T ψ C stems of the familiar tRNA cloverleaf forming one limb, while the D stem and the anticodon stem form the other limb. In this conformation, the 3' acceptor terminus is at one end of the L-shaped molecule 75Å from the anticodon at the other end. Somewhat over a year ago, the tertiary interactions in this molecule were described in an analysis at 3Å resolution of the orthorhombic crystals (2). At the same time, a similar 3Å resolution analysis of the monoclinic crystal form was reported in which most of the polynucleotide chain was traced with the exception of the interactions between the T ψ C and D loops at the corner of the L-shaped molecule (3).

X-ray diffraction data from orthorhombic crystals have been obtained to 2.5 Å resolution (4). The 2.7 Å data have been analyzed by two independent refinement methods to obtain preliminary atomic coordinates. The results of these analyses are presented here and in another paper (5). These two independent refinements have produced similar sets of atomic coordinates. Recently, atomic coordinates from the monoclinic crystal have been published (6). The coordinates from these two crystal forms are compared here and it is shown that the structures are almost identical in the orthorhombic and monoclinic lattices with the exception of the conformation near the 3' end of the polynucleotide chain.

RESULTS

The atomic coordinates of yeast phenylalanine tRNA are presented in Table 1. The general conformation of the molecule including the secondary and tertiary interactions has been described earlier (1, 2, 7). Rough coordinates were measured in an optical comparitor and these coordinates were refined using a method similar to that described by Huber *et al.* (8), coupled with extensive idealization. At this stage in the refinement, the R factor is 0.33 at 3 Å and 0.35 at 2.7 Å. The positions of most of the residues in the polynucleotide chain are well defined, with the exception of residues 16, 17, 47 and 76 where the electron density is consistently weak and diffuse. Thus, it is possible that these may change their conformation slightly upon further refinement. We do not anticipate substantial changes in the atomic positions of the other residues. Most of the ribose residues in the molecule are in

Table 1. Atomic Coordinates of Yeast Phenylalanine tRNA

The Cartesian x, y, z coordinates, with distances in angstroms, correspond to the a, b and c axes of the orthorhombic unit cell (1). The origin of the unit cell is taken as the origin of the coordinate system. These coordinates have been deposited in the Protein Data Bank at Brookhaven National Laboratories, Upton, Long Island, New York (11). They can also be obtained upon request from the authors. The oxygen atoms attached to the phosphorus atom are labeled O1P and O2P, such that when the phosphate group is viewed from the O5' position, the atoms O3', O1P and O2P are organized in a clockwise arrangement. Methyl groups are designated as M, followed by the numbering of the atoms to which the methyl groups are attached.

the standard 3'-endo conformation; however, several are found which adopt the 2'-endo conformation: 7, 9, 18, 19, 48, 58 and 60. All of the purines and pyrimidines appear to be in the anti-conformation with the exception of residue A44. A44 is presented in the syn-conformation in Table 1 although it is possible to place the residue in the anti-conformation using the same electron density. Either conformation could form two hydrogen bonds to m_2^2 G26. Further refinement should clarify this ambiguity.

The torsion angles in the polynucleotide chains are presented in Table 2, together with the angle χ which describes the conformation of the glycosyl linkage. The major torsional variations are in the two phosphoester linkages (β, γ) as had been suggested previously (9).

Table 2. Torsion Angles in the Polynucleotide Chain

LINK	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
ALPHA		204	218	195	209	224	198	162	265	213	271	210	188	155	232	210	250	218	199
BETA		302	271	290	289	269	275	54	232	345	244	307	324	343	303	193	176	289	206
GAMMA	352	266	334	320	310	322	6	210	333	163	305	269	342	209	292	156	44	194	21
DELTA	175	189	151	171	153	151	184	186	235	114	142	184	194	137	158	126	207	233	171
EPSILON	50	50	55	51	55	46	52	54	41	42	41	46	46	39	48	57	50	70	14
CHI	9	-10	21	9	5	2	55	12	117	-28	-10	21	12	-5	12	35	95	68	110
LINK	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38
ALPHA	156	209	146	209	215	197	169	183	193	225	197	200	243	218	203	234	208	174	208
BETA	57	308	309	284	288	321	345	335	305	277	306	329	298	292	327	279	308	316	314
GAMMA	177	55	216	307	296	309	273	261	301	295	304	238	321	311	181	294	296	302	287
DELTA	217	188	139	172	167	192	177	202	171	146	183	127	175	166	138	157	181	174	159
EPSILON	56	50	54	49	42	45	51	55	47	56	49	55	50	47	52	51	49	49	62
CHI	-17	45	7	21	18	8	17	-6	-10	13	30	5	38	30	-1	5	18	13	0
LINK	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57
ALPHA	211	162	179	199	198	199	204	234	168	122	175	203	191	178	176	209	233	235	137
BETA	322	333	327	297	297	287	338	233	266	110	137	302	313	319	330	295	292	232	17
GAMMA	295	254	291	298	294	329	288	45	157	334	350	281	294	278	238	317	287	137	253
DELTA	185	196	200	160	161	184	174	146	179	222	217	187	182	186	167	173	157	241	191
EPSILON	45	54	51	52	49	48	50	41	49	49	58	54	50	52	66	49	45	43	79
CHI	4	6	17	18	14	-163	31	82	30	45	-5	15	31	12	11	24	12	-11	45
LINK	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76
ALPHA	193	83	176	136	235	229	183	198	199	193	234	189	215	198	194	201	195	203	224
BETA	337	196	335	44	235	287	300	304	292	308	279	318	268	295	312	315	313	335	142
GAMMA	324	269	277	130	330	264	293	299	322	283	296	294	309	301	258	307	284	286	250
DELTA	237	253	218	180	119	187	170	177	172	159	161	173	159	169	172	184	175	180	151
EPSILON	42	84	21	59	51	51	43	51	44	45	52	51	53	56	52	48	49	52	46
CHI	111	-16	91	-28	-7	9	15	17	22	0	11	25	2	18	-9	11	20	13	10

The system defining the torsion angles of the internucleotide linkage is described elsewhere (12). α refers to the torsion angle defined by C4', C3', O3', P; β is defined by C3', O3', P, O5'; γ is defined by O3', P, O5', C5'; δ is defined by P, O5', C5', C4'; ϵ is defined by O5', C5', C4', C3'. The angle χ describes the torsion angle about the glycosyl linkage. The internucleotide linkage has the same number as the nucleotide on the O5' side of the phosphorus atom.

Recent publication of the atomic coordinates for yeast phenylalanine tRNA in the monoclinic crystal (6) has made it possible to compare the conformation in these two crystal forms. In the initial description of the conformation in the monoclinic crystal, Robertus *et al.* (3) were unable to define the vital interactions between the D loop and the T ψ C loop at the corner of the molecule. Inspection of the atomic coordinates in the monoclinic cell shows that they have confirmed the assignments which we made of the tertiary interactions in the orthorhombic unit cell somewhat over a year ago (2). Their coordinates indicate the interaction between ψ 55 and G18 as well as the stacking interactions of the other bases in the complex intertwining of these two loops (2, 7). In addition, they appear to have reinterpreted the conformation of the molecule in the segment lying between the acceptor stem and the D stem. In their initial description, m₂²G26 was described as partially intercalated between the bases A44 and G45 (3). In their revised interpretation (6), they have adopted a geometry very similar to that which we described earlier, including appropriate modifications in the stacking interactions in this part of the molecule (2, 7). Thus the similarities in the conformation of the molecule in these two different crystal forms is greater than was initially apparent.

A comparison of the conformation of yeast phenylalanine tRNA in the two different crystal forms is shown in Figure 1. A projection is shown in which lines connect the group coordinates in the molecule as described in the figure legend. It can be seen that the conformation of the two molecules is quite similar with the exception of the two terminal residues at the end of the acceptor stem. Leaving out these two residues, the mean deviation in the positions of the atomic coordinates is 1.1Å while the mean difference in the positions of the group coordinates is 0.99Å. The residues for which there is a significant difference in conformation include D17, U47 and the side chain of Y37.

Using an independent refinement analysis on the orthorhombic data, another set of coordinates has been obtained (5). The group coordinates of the two different refinement analyses of the orthorhombic crystal form have a mean deviation of 0.96Å. This comparison makes

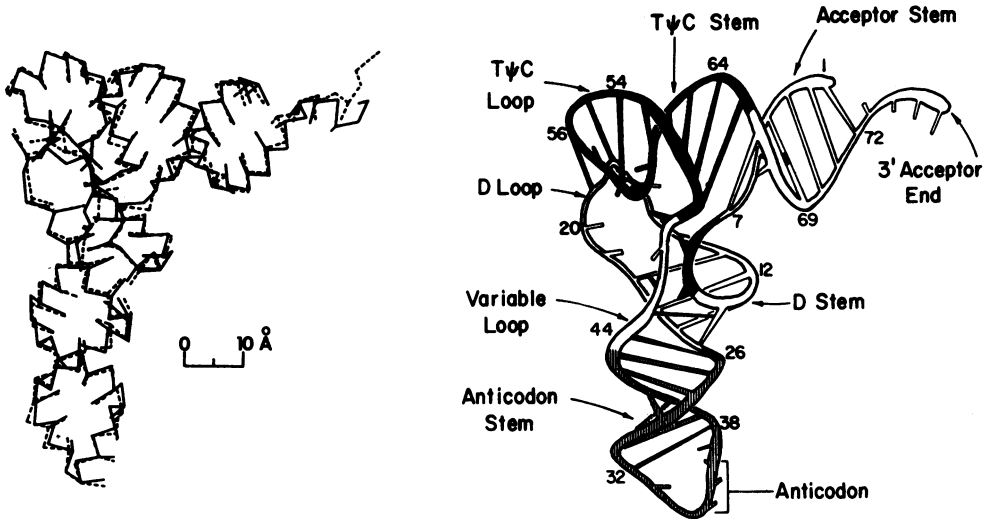


Figure 1. Comparison of the conformation of yeast phenylalanine tRNA in two crystal forms. The two molecules from the orthorhombic and monoclinic unit cells have been fitted by a least squares procedure (10). Three group coordinates are plotted: the position of the phosphorus atom, the centroid of the five atoms in the furanose ring of ribose, and the centroid of the six atoms which make up the six-membered ring in either pyrimidines or purines. The solid line connecting the group coordinates represents the conformation of the molecule in the orthorhombic unit cell, while the dashed line shows its conformation in the monoclinic unit cell. In the schematic diagram at the right, secondary and tertiary hydrogen bonds between bases are shown with different shading (2). The numbers refer to the residues in the polynucleotide chain.

it very clear that the conformations of the molecule in the monoclinic and the orthorhombic unit cells are essentially indistinguishable at this resolution except for the nucleotides at the 3' end of the molecule.

Several features of the hydrogen bonding interactions of yeast phenylalanine tRNA have been described recently (4). However, some additional observations can be made. It is interesting, for example, that both the orthorhombic and monoclinic analyses appear to show a GU base pair held together by two hydrogen bonds. Position 57 is always a purine (7). In the structure, there is a hydrogen bond between ribose 55 O2' and N7 of G57, a bond which can be preserved even if position 57 is adenine. In the present structure, G57 also has two other potential hydrogen bonds between the amino group N2 and O2' of

ribose 18 and O1' of ribose 19. These may further stabilize the structure.

Position 55 is always ψ while position 33 is always uracil in tRNAs involved in polypeptide chain elongation (7). There may be structural reasons for these constancies. Both of these residues occur in a position where the polynucleotide chain turns a corner. As described previously (4), ψ 55 has P37 on top of the base while the N3 of ψ 55 forms a hydrogen bond to the phosphate group of P58. In a similar way, U33 is near the bend in the anticodon loop and it has P35 on top of the base U33, while N3 of U33 forms a hydrogen bond with phosphate P36. Thus the bases of both ψ 55 and U33 stabilize the corner in analogous ways. The geometry suggests a possible additional hydrogen bond from N1 of ψ 55 to phosphate 54, although the distance is too long at the present stage of refinement.

It is of interest that the anticodon loop is likely to be further stabilized by a hydrogen bond between N6 of A38 and O2 of C32. Since position 32 is always occupied by a pyrimidine containing O2 and position 38 usually has an appropriately positioned proton donor, it is possible that this interaction is of a general nature. The present coordinates show a hydrogen bonding distance between N4 of C61 and a phosphate oxygen of C60. If this distance remains after further refinement, it may provide an explanation for the constant GC pair found at the base of the T ψ C stem. Finally, there is limited space around the constant pyrimidine site C60 and this may prevent insertion of a purine at this position in those tRNAs involved in the elongation of polypeptide chains.

With these observations, we can now give structural reasons for almost all of the base conservation in tRNA sequences.

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