

AMINOACYL-tRNA SPECIFICITY OF A 40S RIBOSOMAL SUBUNIT BINDING FACTOR
FROM RABBIT RETICULOCYTES

J. Miguel Cimadevilla and Boyd Hardesty

Clayton Foundation Biochemical Institute
Department of Chemistry, The University of Texas
Austin, Texas 78712

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A factor, isolated from rabbit reticulocytes, catalytically promotes the codon directed, GTP independent binding of aminoacyl-tRNA to 40S ribosomal subunits. High specificity is observed for binding of Met-tRNA_f in the presence of ApUpG or ApUpG(U)_n, but much of this apparent specificity is lost when poly(A,G,U) is used as the template. The factor promotes poly(A,G,U) directed binding of at least Met-tRNA_m and Val-tRNA in addition of Met-tRNA_f to 40S ribosomal subunits. However, Met-tRNA_f is almost exclusively bound when both Met-tRNA species are present in a ratio similar to that observed in reticulocytes.

We have described an isolation procedure for a factor present in the rabbit reticulocyte postribosomal supernatant and ribosomal wash that promotes the codon directed, GTP independent binding of aminoacyl-tRNA (1) and deacylated tRNA (2) to 40S ribosomal subunits. The factor was shown to be a heat sensitive protein that is inactivated by N-ethylmaleimide. It has a molecular weight of approximately 50,000 and is composed of two nonidentical subunits of about 30,000 and 20,000. Formation of a factor mediated 40S·poly(U)·Phe-tRNA initiation complex lowers the Mg⁺⁺ concentration optimum for subsequent polyphenylalanine synthesis from about 8 mM to 4 mM (1).

A functionally similar factor has been isolated from the brine shrimp, Artemia salina, by Zasloff and Ochoa (3). This factor, named EIF-1, is also a sulphydryl reagent sensitive protein, but its molecular weight was estimated to be 145,000. It appeared to contain two identical subunits of approximately 74,000. The A. salina EIF-1 has been shown to promote the ApUpG directed binding of both fMet-tRNA_f and Met-tRNA_f to 40S ribosomal subunits (4). It was shown to be interchangeable with preparations of IF-M₁ in lowering the Mg⁺⁺ concentration optimum for polyphenylalanine

synthesis in conjunction with IF-M₂ (5). Rabbit reticulocyte IF-M₁ has a molecular weight of 65,000 (6).

MATERIALS AND METHODS

Poly(U), poly(A,G,U), ApUpG and UDP were obtained from Miles Laboratories, Inc., Elkhart, Ind.; ³⁵S methionine (2 Ci/mmol) and [³H] methionine (9 Ci/mmol) were obtained from Amersham/Searle, Arlington Heights, Ill.; [¹⁴C] amino acids and BD-cellulose were obtained from Schwarz/Mann, Orangeburg, N.Y.; and Micrococcus lysodeikticus polynucleotide phosphorylase (12 U/mg) was obtained from Worthington Biochemical Corp., Freehold, N.J.

Preparation of unfractionated tRNA from rabbit liver, ribosomes and soluble enzymes used with the reticulocyte cell-free system have been described before (7,8). Reticulocyte ribosomal subunits were prepared by the procedure of Falvey and Staehelin (9) with minor modifications (10). ApUpG(U)_n was prepared from ApUpG and UDP in the presence of polynucleotide phosphorylase from Micrococcus lysodeikticus (11). Aminoacyl-tRNAs were formed from deacylated rabbit liver tRNA (12). Met-tRNA_f was separated from Met-tRNA_m by chromatography on BD-cellulose (13). N-acetylMet-tRNA_f was formed by the treatment of Met-tRNA_f with acetic anhydride (14).

A detailed description of the isolation procedure of the rabbit reticulocyte tRNA binding factor from the postribosomal supernatant and ribosomal wash fractions has been presented (1).

Standard Binding Assay System

The incubation mixture of the standard Met-tRNA_f binding assay system contained the following in a final volume of 0.10 ml: 50 mM Tris·HCl (pH 7.5), 125 mM KCl, 5 mM MgCl₂, 10 mM β-mercaptoethanol, 1.0 A₂₆₀ units of 40S ribosomal subunits, 0.1 A₂₆₀ units of ApUpG, 20 pmoles [³⁵S] Met-tRNA_f, and 0.3 μg of rabbit reticulocyte tRNA binding factor. After incubation for 20 min. at 0°, Met-tRNA_f bound to 40S ribosomal subunits was determined as material retained on nitrocellulose filters (15). The

reaction mixture was diluted by addition of 5 ml of a cold solution containing 20 mM Tris-HCl (pH 7.5), 100 mM KCl, 5 mM MgCl₂ and filtered immediately. Each filter was washed 3 times with the same cold solution, then dried at 120° for 5 min. and counted by liquid scintillation.

RESULTS AND DISCUSSION

As shown in Table I, the rabbit reticulocyte tRNA binding factor efficiently promotes binding of Met-tRNA_f and N-acetylMet-tRNA_f to 40S ribosomal subunits in the presence of either ApUpG or ApUpG(U)_n. Also, these tRNAs are bound enzymatically to ApUpG-ribosomal subunit complexes

TABLE I

ApUpG and ApUpG(U)_n Directed Met-tRNA Binding to 40S Ribosomal Subunits

tRNA	mRNA	Mg ⁺⁺ Concentration mM	Factor Addition	Binding pmoles
Met-tRNA _f	ApUpG	5	-	0.94
		5	+	10.84
		40	-	18.29
	ApUpG(U) _n	5	-	0.46
		5	+	4.92
Met-tRNA _m	ApUpG	5	-	0.30
		5	+	0.88
		40	-	1.13
	ApUpG(U) _n	5	-	0.18
		5	+	0.44
N-AcMet-tRNA _f *	ApUpG	5	-	0.87
		5	+	11.05
		40	-	17.89
	ApUpG(U) _n	5	-	0.52
		5	+	5.62

*N-acetylMet-tRNA_f.

The standard assay procedure was modified by substitution of the indicated type of tRNA and 0.8 A₂₆₀ units of ApUpG(U)_n where indicated.

TABLE II
Aminoacyl-tRNA Binding to 40S Ribosomal Subunits
in the Presence of poly(A,G,U)

tRNA	Binding Factor μ g	Total Binding pmoles
Met-tRNA _f	-	0.09
	+	2.77
Met-tRNA _m	-	0.08
	+	1.76
Val-tRNA	-	0.45
	+	1.07
Phe-tRNA	-	0.37
	+	0.57
Lys-tRNA	-	0.35
	+	0.41
Ser-tRNA	-	0.35
	+	0.37

The standard assay procedure was modified by substitution of the indicated type of tRNA and of 10 μ g of poly(A,G,U). Where indicated, 0.3 μ g of tRNA binding factor was added.

in reaction mixtures containing 40 mM Mg^{++} . Very little Met-tRNA_m is bound under either of these sets of conditions.

In contrast, Met-tRNA_m was observed to bind to 40S ribosomal subunits at 40 mM Mg^{++} if poly(A,G,U) was used as the template (16). Thus, poly(A,G,U) was used to test the activity of the binding factor with other tRNAs. The results shown in Table II indicate that the binding factor can promote

binding of at least Met-tRNA_m and Val-tRNA in addition to Met-tRNA_f. Also, Phe-tRNA is bound very efficiently in the presence of poly(U) (1). On this basis we conclude that the binding factor is not specific for tRNA^{Met}. However, poly(A,G,U) should contain codons for Phe-tRNA, Lys-tRNA and Ser-tRNA. Factor-dependent binding of these species is very low. The significance of this low level of binding is not clear. It may be important that the three aminoacyl-tRNAs efficiently bound with poly(A,G,U), Met-tRNA_f, Met-tRNA_m and Val-tRNA, are coded by the triplets AUG and/or GUG.

Even though the binding factor can promote binding of several species of tRNA with poly(A,G,U), the data of Table II indicate that binding of Met-tRNA_f is relatively efficient compared with binding of Met-tRNA_m or Val-tRNA. The difference in binding of Met-tRNA_f and Met-tRNA_m was investigated further by thermal decay studies of the Met-tRNA binding complexes and by competition experiments with the two Met-tRNA species. Figure 1 shows the thermal decay curves for the Met-tRNA_f and Met-tRNA_m

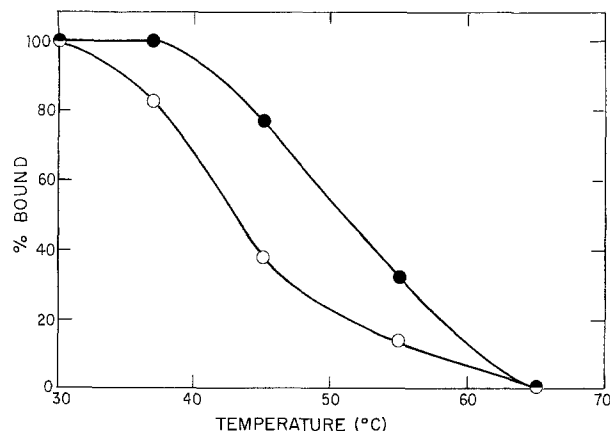
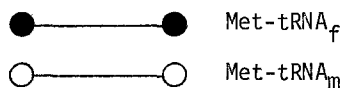


Figure 1. Thermal stability of factor promoted Met-tRNA·40S complexes formed in the presence of poly(A,G,U). Factor dependent binding of Met-tRNA_f and Met-tRNA_m to 40S ribosomal subunits was carried out as described in the legend to Table II. The preformed complexes were incubated an additional 5 min. at the indicated temperatures; then the bound Met-tRNA was determined as described under Methods. The percent bound is calculated from the amount of Met-tRNA bound before and after the second incubation.



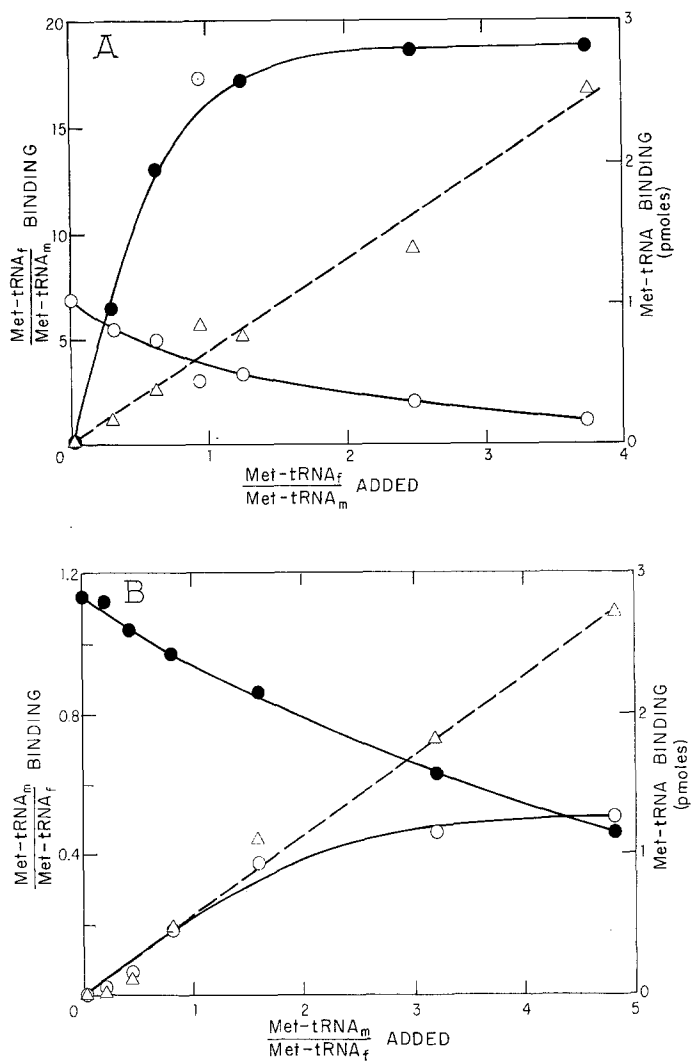
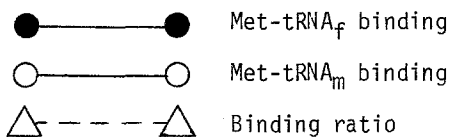


Figure 2. Competition of Met-tRNA_f and Met-tRNA_m for binding in the presence of poly(A,G,U).

A. Factor dependent Met-tRNA binding was determined as described in the legend to Table II. Each incubation mixture contained 8 pmoles of [³H] Met-tRNA_m and [³⁵S] Met-tRNA_f to give the indicated ratio.

B. Each reaction mixture contained 8 pmoles of [³H] Met-tRNA_f and [³⁵S] Met-tRNA_m to give the indicated ratio.



40S ribosomal subunit complexes. In these experiments Met-tRNA was bound to 40S ribosomal subunits in the presence of poly(A,G,U) and the tRNA

binding factor. Then the reaction mixture was incubated for an additional 5 min. at the indicated temperatures. The Met-tRNA_f complex appears to be reasonably stable. Its T_m value is 51°. The Met-tRNA_m complex has a T_m value of only 43°.

Figure 2A shows the relationship between the ratio of Met-tRNA_f to Met-tRNA_m added to the binding reaction and the ratio of Met-tRNA_f to Met-tRNA_m bound to the 40S ribosomal subunits. In this experiment the amount of [³H] Met-tRNA_m was held constant while increasing amounts of [³⁵S] Met-tRNA_f were added to the incubation mixture. Approximately four times more Met-tRNA_f than Met-tRNA_m is bound when the two Met-tRNA species are present in the incubation mixture at a ratio of one to one. A similar relationship is expected if the concentration of [³H] Met-tRNA_f is held constant and increasing amounts of [³⁵S] Met-tRNA_m are added to the reaction mixture. This anticipated result is observed, as shown in Figure 2B. In this case, the ratio of Met-tRNA_m to Met-tRNA_f bound to ribosomes is approximately 0.25 when the ratio of the two Met-tRNA species present in the reaction mixture is one.

Smith and McNamara (17) have reported that in rabbit reticulocytes tRNA_f^{Met} and tRNA_m^{Met} account for 85.9% and 14.1% respectively, of the total tRNA^{Met} present in these cells. Similar results have been reported by Hardesty *et al.* (18). At this ratio of Met-tRNA_f to Met-tRNA_m, *in vitro*, the factor promotes binding almost exclusively of Met-tRNA_f. This may reflect the specificity for Met-tRNA_f during peptide initiation *in vivo*.

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