# Mitochondrial Polypeptide Elongation Factor EF-Tu of Saccharomyces cerevisiae Functional and Structural Homologies to Escherichia coli EF-Tu

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The polypeptide elongation factor EF-Tu was isolated from a mitochondrial  $100000 \times g$  supernatant of the yeast Saccharomyces cerevisiae and purified over 880-fold by DEAE-Sephadex chromatography and gel filtration.

The factor efficiently replaces bacterial EF-Tu in a phenylalanine polymerizing cell-free system of *Escherichia coli*, it binds GDP and it protects phenylalanyl-tRNA against hydrolysis of the ester bond in the presence of 10 mM GTP. The polymerizing activity of the mitochondrial factor is inhibited to 90 % by 50  $\mu$ M *N*-ethylmaleimide and to 50 % by 2.5  $\mu$ M kirromycin.

The purified factor contains two major polypeptides of apparent molecular weights 48000 and 34000. Antibodies raised against the 48000- $M_r$  protein react with EF-Tu<sub>*E.coli*</sub>, as revealed by immune blotting and by the inhibition of phenylalanine polymerization. No reaction was observed between anti-(34000- $M_r$ ) and 48000- $M_r$  protein or EF-Tu<sub>*E.coli*</sub>. The 48000- $M_r$  protein has the same isoelectric point (pI = 6.2) and a content of cysteine and basic amino acids similar to the bacterial EF-Tu.

It is concluded that the  $48000-M_r$  protein is the analogue to EF-Tu<sub>E.coli</sub>, and that yeast mitochondrial EF-Tu is functionally and structurally more related to bacterial EF-Tu than cytosolic EF-1 of the same cell.

A complex mitochondrion-specific genetic apparatus is required to express a few mitochondrial genes coding for hydrophobic proteins of the inner mitochondrial membrane [1]. The RNA components of this genetic system (rRNAs and tRNAs) are coded by mitochondrial genes [2], whereas all enzymes involved in the replication, transcription and processing of mitochondrial nucleic acids (with the exception of introncoded splicing maturases), all ribosomal proteins (one exception), ribosomal initiation and elongation factors and aminoacyl-tRNA synthetases are coded by nuclear genes, synthesized on cytosolic ribosomes and transported into the mitochondrion [3, 4]. An unsolved question is the relation between functionally homologous heterotopic isoproteins: a pair of nuclear-cytosolic and organellar isoproteins could either be coded by two separate nuclear genes, or a single gene product could function in both compartments, perhaps in two different modifications of the same precursor.

A prominent member of the class of heterotopic isoproteins is the polypeptide elongation factor EF-Tu responsible for binding aminoacyl-tRNA and transferring it to the ribosomal A site [5].

The best-studied EF-Tu species is that of *Escherichia coli*, where it represents one of the most abundant proteins [6]: the primary structure of the protein [7] and the nucleotide sequences of the two genes (*tufA* and *tufB*), coding for two EF-Tu variants [8, 9], have been determined. The cytosolic EF-Tu of eukaryotes (EF-1 or EF-Tu<sub>cyt</sub>) also belongs to the group of abundant proteins [10], and EF-1 preparations of various degrees of purity have been obtained from several animal organisms [11-13], yeast [14] and *Euglena gracilis* [15]. The latter organism has been shown to contain a chloroplast EF-Tu encoded by a chloroplast gene [16].

Much less is known about the mitochondrial isoprotein EF-Tu<sub>mt</sub>. Earlier studies have demonstrated that mitochondrial elongation factors of *Neurospora crassa* [17] and yeast [18] can be separated into two complementary fractions corresponding to bacterial EF-Tu (or EF-Tu · EF-Ts) and EF-G, and that fungal mitochondrial elongation factors are interchangeable with bacterial factors on either bacterial or mitochondrial ribosomes [18, 19]. Unfractionated elongation factors as well as the EF-G fractions of *N. crassa* mitochondria are inactive on cytosolic ribosomes [19], whereas yeast mitochondrial EF-T (but not EF-G) is partially exchangeable with the corresponding yeast cytosolic factors on cytosolic ribosomes [18].

Here we report the purification and characterization of yeast mitochondrial EF-Tu.

### MATERIALS AND METHODS

#### Chemicals

[<sup>14</sup>C]Phenylalanine (specific activity 10 Ci/mol) and [<sup>3</sup>H]GDP (specific activity 10 Ci/mmol) were purchased from Amersham/Buchler (Braunschweig, FRG). Phosphoenolpyruvate, GTP, ATP, poly(U), pyruvate kinase and tRNA<sup>Phe</sup> were obtained from Boehringer (Mannheim, FRG). DEAE-Sephadex CL-6B, protein-A-Sepharose CL-4B, and standard proteins for isoelectric focussing were from Pharmacia (Uppsala, Sweden). AcA 44 was from LKB (Broma, Sweden). Molecular weight standard proteins for sodium dodecylsulfate/polyacrylamide gel electrophoresis were obtained from

Dedicated to Friedrich Cramer at the occasion of his sixtieth birthday.

Bio-Rad Laboratories (München, FRG). Fluoresceinisothiocyanate-labeled goat anti-rabbit antibodies were obtained from Nordic Immunology (London, Great Britain). Complete and incomplete Freund's Adjuvant was from Behring (Marburg, FRG). Nitrocellulose filter discs were from Schleicher & Schüll (Dassel, FRG). Nitrocellulose filter sheets were from Sartorius (Göttingen, FRG). Acrylamide, bisacrylamide, and dithiothreitol were from Biomol (Ilvesheim, FRG). All other reagents were of analytical grade and purchased from Merck (Darmstadt, FRG). Escherichia coli C6 cells (M 1157, 1/2 log) were also from Merck. Saccharomyces cerevisiae was obtained from ABC All-Back (Hamm, FRG).

# Isolation of Mitochondria and Mitochondrial $100000 \times g$ Supernatant Protein

3 kg frozen yeast cells (*S. cerevisiae*, commercial baker's yeast) were suspended in 6000 ml buffer A (2 mM ethylenediaminetetraacetic acid (EDTA), 50 mM Tris/HCl pH 7.5, 10  $\mu$ M GDP, 1 mM dithiothreitol, 20  $\mu$ M phenylmethylsulfonyl fluoride, 0.22 M sucrose, 5% glycerol) and disrupted in a Dyno mill (glass beads: 0.5 mm, flow rate 5 l/h) [20]. All further steps were at 4°C. After removing cell debris by two centrifugations (GS 3 rotor, 8000 rev./min, 10 min) mitochondria were pelleted by centrifugation at 13000 rev./min, 45 min, and washed twice with an equal volume of buffer A. The yield was about 80 g mitochondria (wet weight)/3 kg yeast.

Mitochondria were disrupted by grinding with two volumes alumina (Alcoa), and a  $100000 \times g$  supernatant was prepared by centrifugation at  $20000 \times g$  for 20 min, followed by centrifugation at  $100000 \times g$  for 2 h.

# Purification of Polypeptide Elongation Factors

EF-Tu was isolated from E. coli and from yeast mitochondrial  $100000 \times g$  supernatant protein by the two-step method (DEAE-Sephadex Cl-6B chromatography and AcA 44 gel filtration) described by Leberman et al. [21], with the following modifications: E. coli cells were lysed by lysozyme in buffer B (50 mM Tris/HCl pH 7.5,-40 µM GDP, 0.5 mM dithiothreitol, 20 µM phenylmethylsulfonyl chloride, 5 mM EDTA, 5 % glycerol) and treated with DNase I (5  $\mu$ g/ml) in the presence of 30 mM MgSO<sub>4</sub>. A 100000  $\times$  g supernatant of E. coli or yeast mitochondria was applied to a DEAE-Sephadex CL-6B column  $(4 \times 20 \text{ cm})$  equilibrated with buffer C (1 mM dithiothreitol, 10 mM MgSO<sub>4</sub>, 10 % glycerol, all other components as in buffer B without EDTA). The active fractions (assayed by phenylalanine polymerization) were precipitated by 70%(NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, dialyzed against buffer C containing 50 mM KCl, resuspended in a small volume of this buffer and subjected to AcA 44 gel filtration ( $3 \times 150$ -cm column). Active fractions of mitochondrial origin were concentrated by DEAE-Sephadex CL-6B chromatography  $(1 \times 5 \text{ cm})$ , and the bacterial and mitochondrial EF-Tu fractions were precipitated by 70% (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, dialyzed against buffer C containing 50 mM KCl and 50 % glycerol and stored at -60 °C.

# Isolation of EF-G and Ribosomes from E. coli

EF-G was isolated as described [21] and assayed by complementation of EF-Tu in the phenylalanine polymerizing system. 70-S ribosomes were isolated, washed three times with 1 M NH<sub>4</sub>Cl, 10 mM Tris/HCl pH 7.5, 50 mM KCl, 10 mM MgCl<sub>2</sub>, resuspended in the same buffer without NH<sub>4</sub>Cl and stored in 50-µl aliquots at -60 °C.

#### EF-Tu Assays

Poly(U)-Dependent Polyphenylalanine Synthesis. The reaction mixture (100 µl) contained 60 mM Tris/HCl pH 7.6, 70 mM KCl, 10 mM MgCl<sub>2</sub>, 1 mM dithiothreitol, 1 mM GTP, 1 mM ATP, 1 mM phosphoenolpyruvate, 0.2 unit pyruvate kinase, 50 µg poly(U), 10 nM [<sup>14</sup>C]phenylalanine, 4  $A_{260}$  units E. coli tRNA<sup>Phe</sup>-C-C-A, 0.73 µg E. coli phenylalanyl-tRNA synthetase and 36 µg partially purified EF-G. The concentrations of EF-Tu are given in the legends to the figures. The reaction was started by the addition of ribosomes and incubated at 37 °C. 20-µl aliquots were withdrawn at indicated time intervals and spotted onto Whatmann 3MM filter discs. The formation of polyphenylalanine was determined by washing the filters for 5 min in 10% trichloroacetic acid at 90°C, followed by two washings in 10 % trichloroacetic acid (5 min at room temperature), one wash in ethanol and one wash in ether. The residual radioactivity on the filters was measured in a Tricarb liquid-scintillation counter.

 $[{}^{3}H]GDP$  Binding. The reaction mixture (20 µl) containing 50 mM Tris/HCl pH 7.5, 10 mM MgSO<sub>4</sub>, 250 mM NH<sub>4</sub>Cl, 10 mM dithiothreitol, 10 µl  $[{}^{3}H]GDP$  (50 µM, 100 counts min<sup>-1</sup> pmol<sup>-1</sup>) and 70 µl of EF-Tu was incubated for 10 min at 37 °C. The reaction was stopped by the addition of 1 ml ice-cold buffer and the mixture was filtered through the nitrocellulose filter discs (0.45 µm). Filters were washed with 5 ml buffer and counted in a Tricarb liquid-scintillation counter.

Formation of a Ternary Complex EF-Tu  $\cdot$  GTP  $\cdot$  PhetRNA<sup>Phe</sup> and Spontaneous Hydrolysis of the Ester Bond. 100 µg EF-Tu (corresponding to a concentration of 13 µM) was incubated with 1 mM GTP, 60 mM Tris/HCl pH 7.6, 70 mM KCl, 10 mM MgCl<sub>2</sub>, 1 mM dithiothreitol, 1 mM phosphoenolpyruvate and 0.2 unit pyruvate kinase for 10 min at 37 °C in a total volume of 150 µl, in order to form an EF-Tu  $\cdot$  GTP complex [22]. [<sup>14</sup>C]Phe-tRNA<sup>Phe</sup> (*E. coli*) was added to a final concentration of 3 µM, and the rate of deacylation at 37 °C was measured by determination of the remaining amount of PhetRNA<sup>Phe</sup> in the reaction mixture. 15-µl aliquots were removed at indicated periods and applied to Whatman 3MM filters. Filters were treated with 10% trichloroacetic acid, and the acidinsoluble radioactivity was determined.

# Gel Electrophoresis of Protein

Sodium dodecylsulfate gel electrophoresis was performed in 0.1 M Tris/HCl pH 8.3, 0.1 M glycine, 0.1 % sodium dodecylsulfate, with 10 % acrylamide (cross-linking factor 2.7); running conditions: 40 min at 70 V. Isoelectric focussing was performed according to the LKB manual 1804-101, using a pH gradient between 3.5 and 9.5

#### Amino Acid Composition

Denatured  $48000-M_r$  protein was isolated by preparative sodium dodecylsulfate gel electrophoresis, precipitated by six volumes of acetone to remove electrophoresis buffer and suspended in 20% performic acid. Samples were hydrolyzed with 6 M HCl for 24 h and analyzed with a Durrum amino acid analyzer.

#### Preparation of Antiserum and Antibodies (IgG)

About 500 µg denatured or native antigen together with Complete Freund's Adjuvant was injected intracutaneously into both sides of the backbone of a rabbit (Chinchilla rabbit:

# Table 1. Purification of the mitochondrial EF-Tu from yeast

Total protein represents the yield from 500 g wet weight mitochondria from yeast. The total activity is given by the  $[^{14}C]$  polyphenylalanine polymerized under standard conditions after 30 min

Purification step	Total protein mg	$10^{-6} \times \text{Total activity}$	Specific activity	Yield	Purification -fold
		counts min <sup>-1</sup>	counts min <sup>-1</sup> mg <sup>-1</sup>	%	
$100000 \times g$ supernatant	40 300	4.6	0.115	100	1
chromatography	567	5.4	9.52	100	82.8
Eluate of AcA 44 gel filtration	70.9	5.2	72.84	96.7	633.4
Dialysate	47.6	4.8	102.2	90.2	888.8

Ch bb, female, 2.5-3.0 kg from Thomae, Biberach, FRG). About 14 days after the first injection blood was taken from the artery of the ear. After determination of the titer of antibodies a second injection with 200 µg antigen and Incomplete Freund's Adjuvant was performed. After 4 days about 30 ml blood was taken from the artery of the ear. For coagulation the blood was left 1-2 h at room temperature and overnight at 4°C. After centrifugation the antiserum could be decanted.

Immunoglobulines (IgG) were prepared on a protein-A-Sepharose CL-4B column. The procedure was followed as described in the Pharmacia manual (Affinity Chromatography – Principles and Methods).

# Immunological Detection of Blotted Proteins on Nitrocellulose Filters

The electrophoretic transfer of proteins from sodium dodecylsulfate/polyacrylamide gels to nitrocellulose sheets was carried out as described by Towbin et al. [23].

The blotted and stained nitrocellulose filters were incubated in 3% bovine serum albumin in saline (0.9% NaCl, 10 mM Tris/HCl pH 7.4) for 1 h at 37°C, and afterwards rinsed twice in buffer D (0.2% sodium dodecylsulfate, 0.5% Triton-X-100, 0.5% bovine serum albumin, 0.01% NaN<sub>3</sub> in saline). Antibodies were diluted in buffer D (1 µg purified IgG/ml). The blots were shaken in the antibody solution for 5-10 h at room temperature, washed with buffer D for 30 min (five changes) and incubated again for 5-10 h at room temperature with fluoresceinisothiocyanate-labeled goat anti-rabbit antibodies (diluted 1/100 in buffer D). The blot was washed in buffer D for 30 min with five changes, air-dried and screened under ultraviolet light.

#### **RESULTS AND DISCUSSION**

Mitochondria were isolated from mechanically disrupted yeast cells, washed with EDTA-containing buffer to remove cytosolic ribosomes and homogenized by grinding with alumina (Alcoa). Alternative methods of extracting mitochondria (sonication or French press treatment) were found to be much less efficient, since the final yield of EF-Tu was only about 1/4 of that of alumina-treated mitochondria.

A mitochondrial high-speed supernatant  $(100000 \times g)$  was further purified by a two-step procedure developed for isolating *Escherichia coli* EF-Tu [21].

The mitochondrial protein was applied to DEAE-Sephadex CL-6B column and eluted by a linear KCl gradient (0-0.4 M). The fractions active in a poly(U)-programmed phenylalanine-



Fig. 1. Assay of EF- $Tu_{E, coli}$  and EF- $Tu_{mt}$  in a poly(U)-dependent cell-free system of E. coli complemented with EF- $G_{E, coli}$ . The conditions are described in Materials and Methods. Reaction mixtures (100 µl) contained: no EF-Tu ( $\Box$ — $\Box$ ), 4 µg EF- $Tu_{mt}$  (O—O), 8 µg EF- $Tu_{mt}$  ( $\Delta$ — $\Delta$ ), 16 µg EF- $Tu_{mt}$  ( $\times$ — $\infty$ ) and 25.2 µg EF- $TU_{E, coli}$  ( $\blacksquare$ — $\blacksquare$ ). The amount of mitochondrial factor refers to the 48000- $M_r$  protein (about 50 % of total protein, as estimated from gel data of Fig. 6). 20-µl aliquots were removed at indicated times and processed as described under Materials and Methods

polymerizing cell-free system of *E. coli* elute well behind the bulk of mitochondrial matrix proteins at a similar KCl concentration as  $\text{EF-Tu}_{E. coli}$ . The peak fractions (about 80-fold enriched) were pooled and further purified by AcA 44 gel filtration. Most of the phenylalanine polymerizing activity elutes at about the same volumes as the bacterial EF-Tu, and the final preparation was enriched over 880-fold, as summarized in Table 1.

Fig. 1 demonstrates that the mitochondrial factor efficiently replaces the bacterial EF-Tu in an *E. coli* ribosomal system. The specific activities of bacterial and mitochondrial factors varied between 22 pmol and 80 pmol phenylalanine polymerized in 30 min at  $37 \,^{\circ}C/\mu g$  factor on  $1 \, A_{260}$  unit of 70-S ribosomes, depending on the quality of the ribosomal preparations. However, the specific activity of the heterologous

mitochondrial factor was always slightly higher than that of the homologous bacterial factor, if tested under identical conditions.

Fig. 2 shows the stimulation of the polymerizing activity of mitochondrial factor and *E. coli* EF-Tu by adding *E. coli* EF-G. Both factors are stimulated to about the same extent, and since the *E. coli* EF-Tu is free of EF-G, the polymerizing activity in the absence of added EF-G has to be explained by ribosomebound EF-G. Furthermore, the 70-S ribosomes used in these experiments contain enough bound EF-Ts to regenerate the EF-Tu  $\cdot$  GTP complex during protein synthesis. However, it is not clear whether the mitochondrial factor is regenerated by the *E. coli* EF-Ts or by a mitochondrial EF-Ts co-purifying with EF-Tu.

The polymerizing activity of *E. coli* EF-Tu is extremely sensitive to *N*-ethylmaleimide (90% inhibition by 50  $\mu$ M *N*ethylmaleimide [24]. Fig. 3 demonstrates that the mitochondrial factor is as sensitive as the bacterial one, suggesting the presence of at least one essential cysteine residue in the GTP or aminoacyl-tRNA binding site.

Another characteristic property of prokaryotic EF-Tu is the sensitivity against the antibiotic kirromycin, which appears to prevent the release of EF-Tu from the ribosome [25]. According to the data of Fig. 4 the mitochondrial factor is about ten times less sensitive (50 % inhibition by 6  $\mu$ M) than the bacterial factor (50 % inhibition by 0.6  $\mu$ M kirromycin). Finally two other functional tests were used to compare mitochondrial and bacterial EF-Tu [5]: the binding of GDP and the protection of aminoacyl-tRNA against hydrolysis in the presence of GTP. Both factors bind comparable amounts of [<sup>3</sup>H]GDP (13.2  $\mu$ M and 8.8  $\mu$ M GDP/ $\mu$ g protein of bacterial and mitochondrial factor respectively), and both factors form a ternary complex with GTP and aminoacyl-tRNA, as revealed by the GTP-dependent protection of [<sup>14</sup>C]Phe-tRNA<sup>Phe</sup> against the spontaneous hydrolysis of the ester bond at pH 7.6 (Fig. 5). The mitochondrial factor requires about 20 times more GTP than the bacterial one for a comparable protection of the aminoacyl ester linkage.

The bacterial and mitochondrial EF-Tu preparations, obtained by the same two-step procedure [21], were analyzed by polyacrylamide gel electrophoresis in the presence of sodium dodecylsulfate. As seen in Fig. 6, the *E. coli* factor contains a single protein species of apparent molecular weight 45000, whereas the mitochondrial preparation contains two major components of  $M_r = 48000$  and  $M_r = 34000$ , as well as a minor band of  $M_r = 38000$ .

In order to test structural and functional relationships between EF-Tu<sub>E. coli</sub> and the two mitochondrial proteins, we have prepared antibodies (IgG) against the native bacterial factor and the denatured  $48000-M_r$  and  $34000-M_r$ .

Fig. 7 demonstrates that the polymerizing activity of EF-Tu<sub>*E*, coli</sub> and EF-T<sub>mt</sub> is inhibited up to 70% by the heterologous



Fig. 2. Dependence of EF-Tu activity on addition of  $EF-G_{E, coli}$ . The polymerization activity of  $EF-Tu_{mi}$  (black columns) or  $EF-Tu_{E, coli}$  (white columns) was measured in the absence or presence of  $EF-G_{E, coli}$  (36 µg, partially purified). The assay conditions were the same as in Fig. 1.  $EF-G_{E, coli}$  had no activity in the absence of EF-Tu

Fig. 3. Inhibition of EF-Tu from E. coli and yeast mitochondria by Nethylmaleimide. 10 µg EF-Tu<sub>E. coli</sub> (A) or 10 µg of yeast EF-Tu<sub>mt</sub> (B) were pre-incubated for 5 min at room temperature in the absence ( $\times ----\times$ ) or presence of 50 µM N-ethylmaleimide (O---O) and assayed as in Fig. 1, except that dithiothreitol was absent from all buffers



Fig. 4. *Kirromcycin sensitivity of EF-Tu from* E. coli *and yeast mitochondria*. The polymerization activity of 5.6  $\mu$ g EF-Tu<sub>*E. coli*</sub>(A) and 7  $\mu$ g EF-Tu<sub>*m*t</sub>(B) was measured in the absence ( $\bullet$   $\bullet$ ) and presence of 0.63  $\mu$ M ( $\times$  ---  $\times$ ), 6.3  $\mu$ M ( $\bullet$  ---  $\bullet$ ) and 126  $\mu$ M kirromycin ( $\blacktriangle$   $\bullet$ ) as described in the legend to Fig. 1



antibodies [anti-(48000- $M_r$ ) and anti-(EF-Tu<sub>E,coli</sub>) respectively], whereas anti- $(34000-M_r)$  does not affect the activity of both factors. The observation that the bacterial EF-Tu activity is more sensitive to the heterologous than to the homologous antibody may be explained by the possibility that more antigenic sites were exposed in the denatured  $48000-M_r$  polypeptide than in the native EF-Tu<sub>E. coli</sub> protein during immunization of rabbits. Similar results were obtained by immune blotting, as seen in Fig. 8: EF-Tu<sub>E.coli</sub> and 48000-M<sub>r</sub> protein strongly interact with anti-( $48000-M_r$ ), but not with anti- $(34000-M_r)$ . The second mitochondrial polypeptide interacting with anti(48000- $M_r$ ) (lane b of Fig. 9) is believed to be a proteolytic fragment of 48000-M, protein co-migrating with  $34000-M_r$  protein, because a second band is almost invisible in other blotting experiments, using different mitochondrial preparations.

The data of Fig. 7 and 8 clearly demonstrate that EF-Tu<sub>*E.coli*</sub> and 48000- $M_r$  protein share antigenic sites, whereas the 34000- $M_r$  component is immunologically unrelated to both EF-Tu factors. The latter protein possibly represents the analogue to EF-Ts<sub>*E.coli*</sub>, which has the same size [26] and also forms a complex with EF-Tu at low GTP concentrations [27]. Since the isolation procedure used for both the bacterial and mitochondrial factor results in a dissociation of the bacterial EF-Tu · EF-Ts complex, the mitochondrial complex would be more stable than the bacterial one. Further functional tests are required to elucidate the role of the 34000- $M_r$  protein.



Fig. 5. Protection of Phe-tRNA<sub>Phe</sub> against deacylation by the formation of a ternary complex with EF-Tu and GTP. The rate of E. coli [<sup>14</sup>C]Phe-tRNA<sup>Phe</sup> deacylation was measured in the absence of EF-Tu ( $\Box$ — $\Box$ ) and in the presence of 100 µg EF-Tu<sub>E. coli</sub> and 1 mM GTP or 10 mM GTP (×—×), 100 µg EF-Tu<sub>mt</sub> and 1 mM GTP ( $\odot$ — $\odot$ ) and 100 µg EF-Tu<sub>mt</sub> and 1 mM GTP ( $\odot$ — $\odot$ ). Assay conditions are described in Materials and Methods

Another structural similarity between bacterial and mitochondrial EF-Tu is revealed by isoelectric focussing: both factors band at a pH of 6.2, whereas the functionally analogous cytosolic EF-1 of yeast is reported to have an isoelectric point of 8.5-8.75 [14].

In Table 2 the amino acid composition of the mitochondrial EF-Tu (48000- $M_r$  protein) is compared to that of EF-Tu<sub>*E.coli*</sub>[7] and yeast cytosolic EF-1 [14], and it is not unexpected that the mitochondrial factor differs both from its cytosolic counterpart and from the bacterial factor. It should be noted, however, that cysteine residues are found in the *N*-ethylmaleimide-sensitive factors of bacteria and mitochondria, but are absent from the *N*-ethylmaleimide insensitive cytosolic factor [14]. Furthermore the mitochondrial and bacterial factors have a lower content of basic amino acids (56–57 residues) than the cytosolic factor (77 residues). This may be correlated with the differential pI values observed, although the number of acidic residues is not known for the two heterotopic yeast factors.

In summary, we conclude from the following observations that the yeast mitochondrial EF-Tu is functionally and structurally more related to the bacterial EF-Tu than to the yeast cytosolic EF-1.

1. The bacterial and mitochondrial factors are interchangeable on bacterial and mitochondrial ribosomes [17-19], and both factors can replace cytosolic EF-1 on cytosolic ribosomes, whereas EF-1 does not function on bacterial and mitochondrial ribosomes [18].



Fig. 6. Sodium dodecylsulfate/polyacrylamide gel electrophoresis of EF-Tu from E. coli and yeast mitochondria. Lane 1: EF-Tu<sub>E,coli</sub>, lane 2: re-isolated 48000- $M_r$  protein, lane 3: molecular weight standard proteins (Bio-Rad), lane 4: re-isolated 34000- $M_r$  protein, lane 5: EF-Tu<sub>mt</sub> and lane 6: mixture of EF-Tu<sub>mt</sub> and standard proteins. The samples of lanes 1, 2 and 4 contain the protease inhibitor aprotonin (Sigma)



Fig. 7. Inhibition of EF-Tu activity by antibodies (IgG and antiserum) against EF-Tu from E. coli and yeast mitochondria. The phenylalanine-polymerization activity of 7 µg EF-Tu<sub>E. coli</sub> (A) and 1 µg EF-Tu<sub>mt</sub> (B) was determined in the absence of antibodies (×—-×) or in the presence of anti-EF-Tu<sub>E. coli</sub> IgG (O—O), anti-(48000- $M_r$ ) IgG (□—O), anti-(34000- $M_t$ ) IgG (▲—--▲) and antiserum against EF-Tu<sub>E. coli</sub> or EF-Tu<sub>mt</sub> (■—■). EF-Tu was pre-incubated with 3µl IgG (10µg/µl) or 3µl antiserum for 10 min at 4°C in the polymerization assay mixture (see legend to Fig. 1). Before adding ribosomes



Fig. 8. Immune blotting assay of EF-Tu. Lanes a, c and e contain EF-Tu<sub>E.coli</sub> lanes b, d and f contain EF-Tu<sub>mt</sub>. Lanes a and b were incubated with anti-(48000- $M_{\star}$ ) IgG, lanes c and d with anti-(34000- $M_{\star}$ ) IgG and lanes e and f with anti-EF-Tu<sub>E.coli</sub> IgG. For details see Materials and Methods.

Table 2. Amino acid composition of EF-Tu from E. coli and yeast (cytosol and mitochondrial)

Asp and Asn, Glu and Gln were taken as Asx and Glx. EF-T values are given as average residues/mol (8 determinations). EF-Tu values are calculated from gene sequence data [8]. EF-1 data are taken from [14]

Amino acid	Yeast mito- chondrial EF-T	<i>E. coli</i> EF-Tu	Yeast cytosolic EF-1
Asx	54.2	32	41
Thr	28.7	30	29
Ser	30.8	10	19
Glx	60.4	45	47
Pro	16.7	20	26
Gly	33.1	41	45
Ala	28.6	27	35
Cys	1.5	3	trace
Val	26.8	37	47
Met	10.6	10	n.d.
Ile	29.7	29	31
Leu	36.2	28	28
Tyr	14.1	10	7
Phe	19.8	14	17
Trp	n.d.	1	n.d.
His	7.8	11	12
Lys	23.9	23	46
Arg	23.8	23	19

2. The bacterial and mitochondrial factors are sensitive to kirromycin, although the mitochondrial factor requires an about ten times higher kirromycin concentration for 50% inhibition (6  $\mu$ M) than the bacterial factor (0.6  $\mu$ M). The effect of kirromycin on yeast cystosolic EF-1 has not been reported to our knowledge. However, the cytosolic EF-1 of *Euglena gracilis* is unaffected by the drug of concentrations up to 10  $\mu$ M [15].

3. The bacterial and mitochondrial factors show immunological cross-reactivity in the functional test (polymerization activity) and in the immune blotting assay (Fig. 7 and 8), whereas antibodies against yeast EF-1 do not react with mitochondrial EF-Tu of the same organism [18].

4. The bacterial and mitochondrial factors contain cysteine residues, and the strong inhibition by N-ethylmaleimide indicates the presence of at least one cysteine in the nucleotidebinding and/or tRNA-binding site [5]. In contrast, the cytosolic EF-1 is insensitive to N-ethylmaleimide and does not contain cysteine in the active site [14]. 5. The bacterial and mitochondrial factors are acidic proteins (pI = 6.2), the cytosolic factor is a basic protein (pI = 8.5-8.75) [14].

We further conclude that the two heterotopic EF-Tu factors of yeast are different proteins encoded by two different genes. Since mitochondrial elongation factors cannot be coded by mitochondrial genes [28, 29] both EF-Tu genes must reside in the nucleus. They could have originated by duplication of an ancestral nuclear gene, but the prokaryotic properties of the mitochondrial factor would rather point to an independent endosymbiotic origin and a subsequent transfer of a mitochondrial EF-Tu gene to the nuclear genome.

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## REFERENCES

- 1. Tzagoloff, A. (1982) Mitochondria, Plenum Press, New York.
- Slonimski, P., Borst, P. & Attardi, G., eds (1982) Mitochondrial Genes, Cold Spring Harbor Monograph, Cold Spring Harbor, New York.
- 3. Küntzel, H. (1971) Curr. Top. Microbiol. Immunol. 54, 94-118.
- 4. Schatz, G. & Mason, T. L. (1974) Annu. Rev. Biochem. 43, 51-87.
- Miller, D. L. & Weissbach, H. (1977) in *Nucleic Acid-Protein Recognition* (Vogel, H. J., ed.) pp. 409-440, Academic Press, New York.
- 6. Furano, A. V. (1975) Proc. Natl Acad. Sci. USA, 72, 4780-4784.
- Jones, M. D., Petersen, T. E., Nielsen, K. M., Magnusson, S., Sottrup-Jensen, L., Gausing, K. & Clark, B. F. C. (1980) *Eur. J. Biochem. 108*, 507-526.
- Yokota, T., Sugisaki, H., Takanami, M. & Kaziro, Y. (1980) Gene, 12, 25-31.
- 9. An, G. & Friesen, J. D. (1980) Gene, 12, 33-39.
- 10. Slobin, L. I. (1980) Eur. J. Biochem. 110, 555-563.
- 11. Slobin, L. I. & Möller, W. (1976) Eur. J. Biochem. 69, 351-366.
- Kemper, W. M., Merrick, W. C., Redfield, B., Liu, C. K. & Weissbach, H. (1976) Arch. Biochem. Biophys. 174, 603-612.
- Iwasaki, K., Nagata, S., Mizumoto, K. & Kaziro, Y. (1974) J. Biol. Chem. 249, 5008-5010.
- Dasmahapatra, B., Skogerson, L. & Chakraburtty, K. (1981) J. Biol. Chem. 256, 10005-10011.
- 15. Beck, C. M. & Spremulli, L. L. (1982) Arch. Biochem. Biophys. 215, 414-424.
- 16. Spremulli, L. (1982) Arch. Biochem. Biophys. 214, 734-741.
- 17. Grandi, M. & Küntzel, H. (1970) FEBS Lett. 10, 25-28.
- 18. Richter, D. & Lipmann, F. (1970) Biochemistry, 9, 5065-5070.
- 19. Küntzel, H. (1969) FEBS Lett. 4, 140-142.
- Deters, D., Müller, U. & Homberger, H. (1976) Anal. Biochem. 70, 263-267.
- Leberman, R., Antonsson, B., Giovanelli, R., Guariguata, R., Schuhmann, R. & Wittinghofer, A. (1980) Anal. Biochem. 104, 29-36.
- 22. Wagner, T. & Sprinzl, M. (1980) Eur. J. Biochem. 108, 213-221.
- Towbin, H., Staehelin, T. & Gordon, J. (1979) Proc. Natl Acad. Sci. USA, 76, 4350-.4354.
- Miller, D. L., Hachmann, J. & Weissbach, H. (1971) Arch. Biochem. Biophys. 144, 115-121.
- Wolf, H., Chinali, G. & Parmeggiani, A. (1974) Proc. Natl Acad. Sci. USA, 71, 4910-4914.
- Arai, K., Kawakita, M., Kaziro, Y., Kondo, T. & Ui, N. (1973) J. Biochem. (Tokyo) 73, 1095-1105.
- Weissbach, H., Miller, D. L. & Hachmann, J. (1970) Arch. Biochem. Biophys. 137, 262-269.
- 28. Richter, D. (1971) Biochemistry, 10, 4422-4425.
- 29. Parisi, B. & Cella, R. (1971) FEBS Lett. 14, 209-213.

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