A minimalist mitochondrial threonyl-tRNA synthetase exhibits tRNA-isoacceptor specificity during proofreading

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ABSTRACT

Yeast mitochondria contain a minimalist threonyl-tRNA synthetase (Thrs) composed only of the catalytic core and tRNA binding domain but lacking the entire editing domain. Besides the usual tRNA<sup>Thr</sup>², some budding yeasts, such as <i>Saccharomyces cerevisiae</i>, also contain a non-canonical tRNA<sup>Thr</sup>¹ with an enlarged 8-nucleotide anticodon loop, reprograming the usual leucine CUN codons to threonine. This raises interesting questions about the aminoacylation fidelity of such Thrs and the possible contribution of the two tRNA<sup>Thrs</sup> during editing. Here, we found that, despite the absence of the editing domain, <i>S. cerevisiae</i> mitochondrial Thrs (ScmtThrs) harbors a tRNA-dependent pre-transfer editing activity. Remarkably, only the usual tRNA<sup>Thr</sup>² stimulated pre-transfer editing, thus, establishing the first example of a synthetase exhibiting tRNA-isoacceptor specificity during pre-transfer editing. We also showed that the failure of tRNA<sup>Thr</sup>¹ to stimulate tRNA-dependent pre-transfer editing was due to the lack of an editing domain. Using assays of the complementation of a ScmtThrs gene knockout strain, we showed that the catalytic core and tRNA binding domain of ScmtThrs co-evolved to recognize the unusual tRNA<sup>Thr</sup>¹. In combination, the results provide insights into the tRNA-dependent editing process and suggest that tRNA-dependent pre-transfer editing takes place in the aminoacylation catalytic core.

INTRODUCTION

Accurate transfer of genetic information is of critical significance for cellular function and maintenance. Several steps, including DNA replication, mRNA transcription and protein synthesis, contribute to high accuracy with different levels of fidelity (1). Protein synthesis is initiated by an ancient group of enzymes, the aminoacyl-tRNA synthetases (aaRSs) containing 20 members in the majority of living species (2–4). These enzymes catalyze the ligation of a specific amino acid to their specific tRNA-isoacceptors. This reaction, aminoacylation, is performed by most aaRSs in two successive steps. The first step involves adenosine triphosphate (ATP)-dependent amino acid activation in which an intermediate aminoacyl-(adenosine monophosphate (AMP)) is generated with the release of pyrophosphate. This is followed by the transfer of the activated amino acid moiety from the aminoacyl-AMP to the tRNA (2). Protein synthesis, which is the last step in the expression of the genetic code, has a very high level of global fidelity, with a mis-incorporation of only one in every 10 000 codons under normal growth conditions (1). This high level of fidelity is challenging for some aaRSs, which have to discriminate between different amino acids and metabolites that can be structurally and chemically very similar. This critical paradox has been solved by the evolution of the proofreading (editing) function of some error-prone tRNA synthetases (5,6). Editing is critical for translational quality control and its impairment or abolition leads to ambiguities in the genetic code and serious cellular dysfunction (7,8). The ‘double sieve mechanism’ has been proposed to control editing function, in which only mis-activated non-cognate amino acids are removed, while access of the cognate residue to the editing active site is blocked by steric exclusion (9). Editing activity is based on the hydroly-

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sis of mis-activated aminoacyl-AMPs (pre-transfer editing) and/or the hydrolysis of mis-charged aminoacyl-tRNAs (post-transfer editing) (5). Pre-transfer editing can be further divided into tRNA-independent and tRNA-dependent types according to whether the aminoacyl-AMP hydrolysis is stimulated by tRNA. Post-transfer editing usually takes place in a separated editing domain, such as the CP1 domain in class Ia aaRSs and the N2 domain of class II threonyl-tRNA synthetase (ThrRS) (5,6). Furthermore, tRNA-independent pre-transfer editing is believed to occur in the aminoacylation domain, as illustrated by the hydrolysis of aminoacyl-AMP by glutaminyl-tRNA synthetase (GlnRS), seryl-tRNA synthetase (SerRS), prolyl-tRNA synthetase (ProRS) and CP1-deprived leucyl-tRNA synthetase (LeuRS) (for a review see (5,6)). In contrast, the location of the tRNA-dependent pre-transfer editing site is still under debate and several controversial reports suggest that it is located in the editing domain (10–16) or in the aminoacylation domain (17–19). In addition, most natural aaRSs exhibiting tRNA-dependent pre-transfer editing capacity also possess an editing domain to catalyze post-transfer editing, thus, further complicating the assignment of the active site of tRNA-dependent pre-transfer editing.

The mitochondrion has its own translational system, producing several protein components of respiratory complexes. AaRSs for mitochondrial translation are usually encoded by the nuclear genome and then transported into the mitochondrion; however, most tRNAs are encoded by the mitochondrial genome (20). For instance, human mitochondria express 22 tRNA-isoacceptors corresponding to 20 amino acids with two tRNAs decoding serine [tRNA^Ser(AGY) and tRNA^Ser(UCN)] or leucine [tRNA^Leu(CUN) and tRNA^Leu(UUR)] ([http://mamit.trna. u-strasbourg.fr/Summary.asp](http://mamit.trna.u-strasbourg.fr/Summary.asp)). The mitochondrial genome of *Saccharomyces cerevisiae* encodes 24 tRNA-isoacceptors that decode all codons, including two tRNAs^Arg^, tRNAs^Ser^, tRNAs^Thr^ and tRNAs^Met^ (21). However, *S. cerevisiae* mitochondria express only tRNA^Leu(UUR)^ without tRNA^Leu(CUN)^ (21). The mechanism underlying the translational quality control of the mitochondrial system is an interesting issue since it directly regulates the precise flow of the mitochondrial genetic code. Human mitochondrial leucyl-tRNA synthetase (hmtLeuRS) has been reported to be defective in post-transfer editing because of a degenerate CP1 domain; however, it has a more rigorous amino acid activation site to exclude non-cognate amino acids (22). Similarly, in contrast to its bacterial and eukaryotic cytoplasmic counterparts, yeast mitochondrial phenylalanyl-tRNA synthetase (PheRS) harbors no editing domain but selects Phe over Tyr more efficiently (23).

Components of the translational machinery of some budding yeasts, such as *S. cerevisiae*, display unique characteristics. First, the canonical leucine (Leu) codon CUN (N: A, G, C, T) is reassigned to threonine (Thr) in the *S. cerevisiae* mitochondrion (24), although the evolutionary benefit of this reassignment is unclear. This reassignment is mediated by a structurally unique *S. cerevisiae* mitochondrial tRNA^Thr^1 (tRNA^Thr^1) with an enlarged anticodon loop containing the ^34^UAG^36^ anticodon. The loop enlargement is due to the insertion of U between U33 and the ^34^UGU^36^ anticodon, which is designated as U33a here (Figure 1A) (25). The ^34^UAG^36^ anticodon is harbored by mitochondrial tRNA^Leu(CUN)^ in other organisms, such as humans and even the yeasts *Schizosaccharomyces pombe*, *Candida albicans*, tRNA^Leu(CUN)^ has been consistently lost in the *S. cerevisiae* mitochondrion during the evolution of the 24 mitochondrial tRNA genes (Figure 1A) (26). However, phylogenetic and biochemical data show that, in fact, tRNA^Thr^1 is not derived from the lost tRNA^Leu(CUN)^ but from tRNA^His^ with a ^34^GUG^36^ anticodon (27). In addition, a canonical *S. cerevisiae* mitochondrial tRNA^Thr^2 (tRNA^Thr^2) with the ^34^UGU^36^ anticodon decodes normal ACN Thr codons in the *S. cerevisiae* mitochondrion (Figure 1A) (25). Second, the enzyme catalyzing the aminocoylation of tRNA^Thr^1 and tRNA^Thr^2, *S. cerevisiae* mitochondrial ThrRS (ScmtThrRS), encoded by the *MST1* gene, is devoid of an editing domain, and consists only of the aminoacylation catalytic core connected to the C-terminal tRNA binding domain (CTD) (Figure 1B) (28,29). This phenomenon also occurs in the mitochondria of other yeasts, such as *S. pombe* and *C. albicans*, although the CUN codons still encode Leu. This phenomenon suggests that loss of the editing domain occurred at a very early stage in the evolution of yeast, while CUN reassignment was a more recent event. In contrast, bacterial, eukaryotic cytoplasmic and other mitochondrial ThrRSs contain a N2 editing domain that hydrolyzes mischarged Ser-tRNA^Thr^ (19,30). ScmtThrRS has been reported to mis-activate Ser and to use tRNA-independent pre-transfer editing to remove Ser-AMP (31). In addition, only ScmtThrRS, but not *S. pombe* or *C. albicans* mitochondrial ThrRS (SptmtThrRS or CmtThrRS), recognizes tRNA^Thr^1, suggesting the evolution of tRNA^Thr^1 recognition elements in ScmtThrRS, which have yet to be identified (27). Furthermore, whether other ThrRSs, such as bacterial and eukaryotic cytoplasmic, and mitochondrial ThrRSs can recognize the unique tRNA^Thr^1 is also unclear. Above all, investigation of the aminocoylation and editing mediated by ScmtThrRS/tRNA^Thr^ is an interesting model with the two partners developing significant peculiarities during evolution. In the present study, we showed that ScmtThrRS exhibits a tRNA-dependent pre-transfer editing activity that is specific for the tRNA^Thr^2 isoacceptor, whereas tRNA^Thr^1 was unable to stimulate such activity. We further confirmed the editing capability of tRNA^Thr^1, but demonstrated a requirement for the presence of an editing domain. We also identified the editing determinants of tRNA^Thr^2 and the editing antideterminants of tRNA^Thr^1. Finally, we constructed a yeast *MST1* gene knockout strain and, using a plasmid shuffle assay and different chimeric constructs, we showed that the catalytic core and tRNA binding domain of ScmtThrRS co-evolved to recognize the unusual tRNA^Thr^1. In combination, the results of the present study provide insights into the tRNA-dependent editing process and also suggest that tRNA-dependent pre-transfer editing takes place in the aminocoylation catalytic core.
Figure 1. Representations of tRNAs and *S. cerevisiae* ThrRSs investigated in this study. (A) Cloverleaf structures of *S. cerevisiae* mitochondrial tRNA<sub>Thr</sub>1, tRNA<sub>Thr</sub>2, tRNA<sub>Leu</sub>(<i>UUR</i>)<sub>Sc</sub>, tRNA<sub>Leu</sub>(<i>CUN</i>)<sub>Sp</sub> and *S. pombe* mitochondrial tRNA<sub>Leu</sub>(<i>CUN</i>)<sub>Sp</sub>, which has been lost in *S. cerevisiae* mitochondria during evolution. (B) Linear representation of the domain arrangement of ScytThrRS and ScmtThrRS. Aminoacylation domain and CTD of ScytThrRS or ScmtThrRS are colored in black or gray, respectively.

**Materials and Methods**

**Materials**

L-Thr, L-Ser, dithiothreitol, ATP, CTP, GTP, UTP, 5′-GMP, tetrasodium pyrophosphate, inorganic pyrophosphate, Tris-HCl, MgCl<sub>2</sub>, NaCl and activated charcoal were purchased from Sigma (St. Louis, MO, USA). [14C]Thr was obtained from Biotrend Chemicals (Destin, FL, USA); [14C]Ser and [α-32P]ATP were obtained from Perkin Elmer Inc. (Waltham, MA, USA). The DNA fragment rapid purification kits and plasmid extraction kits were purchased from YPH (China). KOD-plus mutagenesis kits were obtained from TOYOBO (Japan). T4 DNA ligase and restriction endonucleases were obtained from Thermo Scientific (Pittsburgh, PA, USA). Phusion high-fidelity DNA polymerase was purchased from New England Biolabs (Ipswich, MA, USA). Ni<sup>2+</sup>-NTA Superflow was purchased from Qiagen Inc. (Germany). Polyethyleneimine cellulose plates were purchased from Merck (Germany). Pyrophosphatase (PPase) was obtained from Roche Applied Science (China). The dNTP mixture was obtained from TaKaRa (Japan). Oligonucleotide primers were synthesized by Invitrogen (China). *Escherichia coli* BL21 (DE3) cells were purchased from Stratagene (Santa Clara, CA, USA). A diploid yeast strain (BY4743-MST1<sup>+</sup>/MST1<sup>-</sup>) was obtained from Thermo Scientific. Recombinant plasmid pET28a-ScytThrRS was constructed in our laboratory (19). *C. albicans* genome was a gift from Prof. Jiang-Ye Chen in our Institute. p425TEF was kept in our laboratory (19).

**Cloning and mutagenesis**

The *MST1* gene encoding the ScmtThrRS precursor was amplified from the *S. cerevisiae* genome and cloned into pET28a(+) between the NdeI and XhoI restriction sites. The gene fragment encoding the mature ScmtThrRS without its mitochondrial targeting sequence (MTS) (Met<sup>1</sup>-Ser<sup>11</sup>) (27) was then subcloned into pET28a(+) using the NdeI and XhoI sites to generate pET28a(+) ScmtThrRS, from which the mature ScmtThrRS was expressed. Construction of the gene encoding the chimeric *S. cerevisiae* cytoplasmic-mitochondrial ThrRS (CmThrRS) was performed in two steps. First, the gene encoding the N-terminal fragment of ScytThrRS (Met<sup>1</sup>-Gln<sup>337</sup>, including the N-extension, N1 and N2 domains), was amplified by polymerase chain reaction (PCR) using pET28a- ScytThrRS as a template and cleaved by NdeI and SmaI enzymes. Second, the DNA fragment encoding the aminoacylation and C-terminal domains of ScmtThrRS (Phe<sup>49</sup>-Lys<sup>462</sup>) was similarly obtained by PCR using pET28a-ScmtThrRS as a template and digested by SmaI and XhoI. The two fragments were then co-ligated into pET28a pre-cleaved by NdeI and XhoI to obtain pET28a-CmThrRS. For construction of the chimeric CmThrRS2 gene, a DNA fragment encoding Met<sup>1</sup>-His<sup>618</sup> of ScytThrRS (including the N-extension, N1, N2 and aminoacylation domains) was amplified by PCR using pET28a- ScytThrRS as a template and cleaved by NdeI and SmaI; a second DNA fragment encoding the C-terminal domains of ScmtThrRS (Gly<sup>339</sup>-Lys<sup>462</sup>) was obtained by PCR using pET28a-ScmtThrRS as a template and digested by SmaI and XhoI. The two fragments were then co-ligated into pET28a (pre-cleaved by NdeI and XhoI) to generate pET28a-CmThrRS2. For subcloning into p425TEF (32),
the two genes encoding CmThrRS and CmThrRS2 were PCR amplified, digested and inserted into the gap between the PstI and XhoI of p425TEF to obtain p425TEF-CmThrRS and p425TEF-CmThrRS2.

Genes encoding the ScmtThrRS precursor or mature ScmThrRS were inserted into the yeast expression vector p425TEF at the PstI and XhoI sites, respectively, to produce the p425TEF-ScmThrRS precursor (with the MTS) or p425TEF-ScmThrRS (without the MTS). Genes encoding EcThrRS or ScyctThrRS were amplified from the E. coli genome or pET28a(+) and inserted into the site of HindIII and SalI or PstI and XhoI sites, respectively, in p425TEF. The gene encoding mature CamtThrRS (Ser124-Lys455) (27) was amplified from the C. albicans genome, digested by PstI and XhoI and inserted into the complementary sites of p425TEF. Construction of p425TEF-hcThrRS (human cytoplasmic ThrRS) has been described in a previous report (19). The fragment encoding the MTS of ScmThrRS (Met1-Ser31) was inserted just upstream of the open reading frame (ORF) of EcThrRS, ScyctThrRS, hcThrRS, mature mitochondrial ThrRS (HmtThrRS, LeuS3-Phe718, unpublished results), mature CamtThrRS, CmThrRS and CmThrRS2 to facilitate guided mitochondrial import of these exogenously expressed proteins. All constructs were confirmed by DNA sequencing. DNA swapping and mutation were carried out according to the procedures provided with KOD mutagenesis kits.

Protein gene expression and purification

E. coli BL21 (DE3) was transformed with various constructs. A single colony of each of the transformants was chosen and cultured in 500 ml of 2× YT medium at 37°C. When the cells reached mid-log phase (A600 = 0.6), expression of the recombinant proteins was induced by the addition of 0.2 mM isopropyl-1-thio-β-D-galactopyranoside for 8 h at 22°C. Protein purification was performed according to a previously described method (33).

tRNA gene cloning and transcription

tRNAThr1 and tRNAThr2 genes were inserted between the PstI and EcoRI sites of pTrc99b downstream of an S′ inserted T7 promoter. All tRNA sequences were confirmed by DNA sequencing. Detailed in vitro T7 run-off transcription of tRNAThr1 and tRNAThr2 was performed as described previously (34). The accepting capacity of tRNAThr1 and tRNAThr2 was 1156 and 1327 pmol/A260, respectively. All tRNA mutants were constructed based on the protocol provided with KOD mutagenesis kits and transcribed as tRNAThr1 and tRNAThr2.

Enzymatic assays

ATP-PPi exchange measurement was carried out at 30°C in a reaction mixture containing 60 mM Tris-HCl (pH 8.5), 10 mM MgCl2, 5 mM DTT, 0.1 mg/ml BSA, 2.5 mM ATP, 2 mM tetradsodium [32P]pyrophosphate, 1 mM Thr or 300 mM non-cognate Ser and 200 nM ScmThrRS or CmThrRS. Aliquots of 15 μl were taken and quenched to 200 μl with a solution containing 2% activated charcoal, 3.5% HClO4 and 50 mM tetradsodium pyrophosphate at various time intervals. The solution was filtered through a Whatman GF/C filter, followed by washing with 20 ml of 10 mM tetradsodium pyrophosphate solution and 10 ml of 100% ethanol. The filters were dried and [32P]ATP was measured using a scintillation counter (Beckman Coulter).

Assays of aminoacylation activity of ScmThrRS or various ThrRSs were performed at 30°C in a reaction mixture containing 60 mM Tris-HCl (pH 8.5), 10 mM MgCl2, 5 mM DTT, 0.1 mg/ml BSA, 2.5 mM ATP, 250 μM [32C]Ser, 10 μM tRNAThr1 or tRNAThr2 and 2 μM ScmThrRS. [32C]Ser-tRNAThr2 was prepared with ScyctThrRS-H151A/H155A (19). Post-transfer editing activity of ThrRSs was indicated by the hydrolytic rate of [32C]Ser-tRNAThr and was measured at 30°C in a reaction mixture containing 60 mM Tris-HCl (pH 7.5), 10 mM MgCl2, 5 mM DTT, 0.1 mg/ml BSA, 2 μM [32C]Ser-tRNAThr2 and 200 nM ScmThrRS or CmThrRS or ScmThrRS-H151A/H155A. Aliquots were taken and quenched on Whatman filter pads pre-soaked with 5% trichloroacetic acid (TCA) at various time intervals. The filters were washed three times for 15 min each in cold 5% TCA and then three times for 10 min each in 100% ethanol. Filters were dried and the radioactivity content of the precipitates was quantified using a scintillation counter (Beckman Coulter).

AMP formation assay

The AMP formation assay (thin-layer chromatography (TLC)) was carried out at 30°C in a reaction mixture containing 60 mM Tris-HCl (pH 8.5), 10 mM MgCl2, 5 mM DTT, 0.1 mg/ml BSA, 10 U/ml pyrophosphatase (PPiase), 40 mM Ser (or 4 mM Thr), 3 mM [α-32P]ATP and 2 μM ScmThrRS or CmThrRS in the presence or absence of tRNAThr1 or tRNAThr2 or its mutants. Samples (1.5 μl) were quenched in 6 μl of 200 mM NaAc (pH 5.0). The quenched aliquots (1.5 μl of each sample) were spotted onto polyethyleneimine cellulose plates pre-washed with water. Separation of Ser-[α-32P]AMP, [α-32P]AMP and [α-32P]ATP was performed in 0.1 M NH4Ac and 5% acetic acid. The plates were visualized by phosphorimaging and the data were analyzed using Multi Gauge Version 3.0 software (FUJIFILM). Quantification of [α-32P]AMP was achieved by densitometry in comparison with [α-32P]ATP samples of known concentrations. The rates were obtained using only the initial time points, where the plot of [α-32P]AMP versus time was linear. The data were then fit to the following equation: \( y = b + k_{obs} t \), where \( b \) and \( k \) represent the burst amplitude and the steady-state rate, respectively. The observed reaction rate constants (\( k_{obs} \)) were obtained by dividing the steady-state rate of the reaction by the total enzyme concentration.
ScΔMST1 complementation assay

For complementation assays, all genes of interest were recombined into the yeast expression vector, p425TEF as described previously. Plasmids were introduced into ScΔMST1 using the lithium acetate (LiAc) procedure (35). Transformants were selected on SD/Ura−/Leu− plates and a single clone was cultured in liquid SD/Leu− medium. The culture was then diluted to a concentration equivalent to 1 OD600 and a 10-fold dilution of the yeast was plated onto yeast-extract peptone glycerol (YPG) or YPG/5-FOA (5-floroorotic acid) to induce the loss of the rescue plasmid (pRS426-MST1). Complementation was observed by comparing the growth rates of ScΔMST1 expressing ScmtThrRS or various ThrRSs on YPG and YPG/5-FOA plates. The DNA fragment encoding a His6-tag was added downstream of the gene encoding CmThrRS or CmThrRS2 for facilitating a comparison of the levels of the two proteins expressed from ScΔMST1.

RESULTS

U33a and G36 of tRNAThr1 are critical nucleotides for aminoacylation by ScmtThrRS

We initially investigated whether E. coli ThrRS (EcThrRS) and S. cerevisiae cytoplasmic ThrRS (Sc cyt ThrRS) were able to recognize the unusual tRNAThr1 and whether ScmtThrRS could aminoacylate other canonical forms of tRNAThr, such as S. cerevisiae cytoplasmic tRNAThr(AGU) (Sc tRNAThr). Our data showed that all ThrRSs readily recognized canonical tRNAThrSs, including Sc tRNAThr and tRNAThr2, however, only ScmtThrRS was able to charge tRNAThr1 (Figure 2). Therefore, ScmtThrRS must use different tRNAThr1-specific recognition elements and patterns (which are absent in EcThrRS and Sc cyt ThrRS) to aminoacylate tRNAThr1.

The most striking feature of the unusual tRNAThr1 is the enlarged anticodon loop. We deleted U33a or inserted an additional G36a in the anticodon loop to either reduce or further enlarge the size of the loop, thus, obtaining ΔU33a or ΔG36a (Figure 3A). Consistent with data from others (29), the size reduction decreased the rate of Thr acceptance to ~70%, suggesting that the 8-nucleotide size of the anticodon loop plays a role in regulating tRNA charging. In contrast, aminoacylation of ΔG36a showed that size enlargement from eight to nine nucleotides slightly increased aminoacylation of the tRNA (Figure 3B).

Next, we examined if a U residue at position 33a was critical for a functional enlarged 8-nucleotide anticodon loop. We changed U33a to A, C or G to obtain U33aA, U33aC, U33aG mutants (Figure 3A). Aminoacylation assays showed that, compared to wild-type tRNAThr1, the U33aC mutation slightly decreased accepting activity, whereas both the U33aA and U33aG mutations decreased the activity considerably (Figure 3B). These data showed that a pyrimidine (U or C) at position 33 was more suitable than a purine nucleotide (A or G). A pyrimidine nucleotide might directly interact with ScmtThrRS or alternatively, contribute to anticodon loop plasticity during its interaction with the synthetase.

Figure 2. Cross-species aminoacylation of different tRNAThrSs by EcThrRS, Sc cyt ThrRS S and ScmtThrRS. Aminoacylation time-course of Sc tRNAThr (A), tRNAThr1 (B) and tRNAThr2 (C) by EcThrRS (■), Sc cyt ThrRS ( ● ) and ScmtThrRS (▲).
Finally, we mutated each of U34, A35 or G36 of tRNA\textsuperscript{Thr\textsubscript{1}} to the three other nucleotides to obtain U34A, U34C, U34G, A35U, A35C, A35G, G36A, G36C and G36U, respectively (Figure 3A). Charging assays showed that mutations at position 34 or 35 had little effect on aminoacylation (data not shown). In contrast, at position 36, the two mutants G36A and G36C showed a significant reduction in aminoacylation, indicating that G36 is an important determinant of ScmtThrRS charging. The third nucleotide, G36U, displayed intact aminoacylation properties (Figure 3B). We further calculated aminoacylation kinetics of ScmtThrRS for all the mutants derived from U33a and G36. The data showed that only U33aC and G36U displayed nearly full aminoacylation activity (99.8% and 76%, respectively); however, activity of other mutants decreased to only about 10% of that of wild-type tRNA\textsuperscript{Thr\textsubscript{1}} (Table 1). Our data were consistent with results of Ling et al., who deleted the U33a or simultaneously mutated A35 and G36 to G and U (obtaining A35G/G36U mutant) and revealed that the inserted U33a played a crucial role in aminoacylation (29).

**ScmtThrRS has isoacceptor-specific tRNA-dependent pre-transfer editing activity**

Recently, it was shown that ScmtThrRS catalyzes the mis-activation of non-cognate Ser and uses pre-transfer editing to hydrolyze Ser-AMP (31). However, despite the presence of pre-transfer editing activity against Ser, ScmtThrRS still formed Ser-tRNA\textsuperscript{Thr} \textit{in vitro} (31) indicating that the editing activity was not sufficient to prevent Ser mis-charging. Here, we performed mis-charging assays with non-cognate Ser and confirmed that both tRNA\textsuperscript{Thr\textsubscript{1}} and tRNA\textsuperscript{Thr\textsubscript{2}} were mis-charged by Ser with a higher rate for tRNA\textsuperscript{Thr\textsubscript{1}} (with \(k_{\text{obs}}\) of \([0.36 \pm 0.05] \times 10^{-3}\ \text{s}^{-1}\)) compared to tRNA\textsuperscript{Thr\textsubscript{2}} (with \(k_{\text{obs}}\) of \([0.11 \pm 0.02] \times 10^{-3}\ \text{s}^{-1}\)) (Figure 4A) \(k_{\text{obs}}\) value was calculated with the same equation with AMP formation as described in the Materials and Methods). Such a preference for tRNA\textsuperscript{Thr\textsubscript{1}} has already been reported (31) showing that ScmtThrRS is an error-prone tRNA synthetase, at least \textit{in vitro}. Here, we evaluated the tRNA\textsuperscript{Thr\textsubscript{1}} dependent pre-transfer editing activity of ScmtThrRS since, theoretically, tRNA\textsuperscript{Thr\textsubscript{1}} isoacceptors might also bind the enzyme before the hydrolysis or release of Ser-AMP. Therefore, we performed editing assays in the presence of the non-cognate amino acid Ser using TLC-based AMP formation from \([\alpha-\text{32P}]\text{ATP}\). Compared to the traditional \([\alpha-\text{32P}]\text{ATP}\) consumption assay, the AMP formation assay allows the simultaneous, direct separation and measurement of [\alpha-\text{32P}]AMP and aminoacyl-[\alpha-\text{32P}]AMP (17). We performed AMP formation assays with ScmtThrRS in the presence of either tRNA\textsuperscript{Thr\textsubscript{1}} or tRNA\textsuperscript{Thr\textsubscript{2}}. The results showed that tRNA\textsuperscript{Thr\textsubscript{1}} stimulated the tRNA-dependent pre-transfer editing activity of ScmtThrRS only slightly, with \(k_{\text{obs}}\) of \((11.78 \pm 1.54) \times 10^{-3}\ \text{s}^{-1}\) (with tRNA\textsuperscript{Thr\textsubscript{1}}) as compared to a \(k_{\text{obs}}\) of \((7.78 \pm 1.12) \times 10^{-3}\ \text{s}^{-1}\) without tRNA\textsuperscript{Thr\textsubscript{1}} (Table 2). These data suggest that ScmtThrRS has little tRNA\textsuperscript{Thr\textsubscript{1}}-dependent pre-transfer editing activity (Figure 5A and B). In contrast, tRNA\textsuperscript{Thr\textsubscript{2}} stimulated greater tRNA-dependent editing by ScmtThrRS of tRNA\textsuperscript{Thr\textsubscript{1}} with a \(k_{\text{obs}}\) of \((30.39 \pm 2.63) \times 10^{-3}\ \text{s}^{-1}\) (Figure 5C and D) (Table 2). Compared to the rate of formation of Ser-tRNAs\textsuperscript{Thr} \([0.36 \pm 0.05]\) and \((0.11 \pm 0.02) \times 10^{-3}\ \text{s}^{-1}\) for tRNA\textsuperscript{Thr\textsubscript{1}} and tRNA\textsuperscript{Thr\textsubscript{2}}, respectively, the AMP formation rates are much higher indicating that ATP was exhausted during the editing assay. We further performed Thr-included AMP formation assays in the absence or presence of either tRNA\textsuperscript{Thr\textsubscript{1}} or tRNA\textsuperscript{Thr\textsubscript{2}}. Data showed that, without any tRNA, the \(k_{\text{obs}}\) of AMP formation with Thr \([2.65 \pm 0.32] \times 10^{-3}\ \text{s}^{-1}\) was significantly lower than with that with Ser \([7.78 \pm 1.12] \times 10^{-3}\ \text{s}^{-1}\). Similarly, the \(k_{\text{obs}}\) value of AMP formation with Thr in the presence of either tRNA\textsuperscript{Thr\textsubscript{1}} \([3.25 \pm 0.30] \times 10^{-3}\ \text{s}^{-1}\) or with tRNA\textsuperscript{Thr\textsubscript{2}} \([5.24 \pm 0.86] \times 10^{-3}\ \text{s}^{-1}\) was obviously lower than that with Ser \([11.78 \pm 1.54] \times 10^{-3}\ \text{s}^{-1}\) or tRNA\textsuperscript{Thr\textsubscript{2}} \([30.39 \pm 2.63] \times 10^{-3}\ \text{s}^{-1}\) (Table 2). Therefore, these data indicated that Ser-induced AMP formation was the result of an editing reaction.

**Role of anticodon of tRNA\textsuperscript{Thr\textsubscript{2}} in tRNA-dependent pre-transfer editing by ScmtThrRS**

In a previous study, we showed that the conserved G35 and U36 are key determinants of editing by SccytThrRS, whereas the discriminator base A73 is of little importance in editing (19). To check whether this editing recognition mode was conserved in mitochondrial tRNA\textsuperscript{Thr\textsubscript{2}}, we mutated G35, U36 and A73 to C, obtaining G35C, U36C and A73C, respectively. The aminoacylation of all the mutants was severely impaired (data not shown), consistent with their function as recognition elements in the EcThrRS and
Figure 4. Mis-charging of mitochondrial tRNA\textsuperscript{Thr} by ScmThrRS and CmThrRS. Mis-charging time-course of ScmttRNA\textsuperscript{Thr1} (■) and ScmttRNA\textsuperscript{Thr2} (▲) with non-cognate Ser catalyzed by ScmThrRS (A) and CmThrRS (B). Mis-charging reaction in the absence of tRNA (●) was performed as a control for either enzyme.

Figure 5. Isoacceptor-specific editing by ScmThrRS. (A) Representative TLC plate of the editing assay performed in the presence of Ser and ScmThrRS in the absence or presence of tRNA\textsuperscript{Thr1}. [\textsuperscript{32}P]AMP and Ser-[\textsuperscript{32}P]AMP are indicated. (B) Graphic representation of AMP formation without (●) or with (○) tRNA\textsuperscript{Thr1} as shown in (A). (C) Representative AMP formation assay with Ser catalyzed by ScmThrRS in the absence or presence of tRNA\textsuperscript{Thr2}. (D) Graphic representation of AMP formation without (●) or with (○) tRNA\textsuperscript{Thr2} as shown in (C). Known amounts of [\alpha-\textsuperscript{32}P]ATP were serially diluted and spotted onto the TLC plate in (A) and (C) after separation for quantification.
The results are the average of three independent repeats with standard deviations indicated. The $k_{\text{cat}}/K_m$ values are relative to tRNA$^{Thr_1}$.

<table>
<thead>
<tr>
<th>tRNA</th>
<th>$k_{\text{cat}}$ (min$^{-1}$)</th>
<th>$K_m$ (µM)</th>
<th>$k_{\text{cat}}/K_m$ (min$^{-1}$ µM$^{-1}$)</th>
<th>Relative (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>tRNA$^{Thr_1}$</td>
<td>2.03 ± 0.32</td>
<td>0.45 ± 0.05</td>
<td>4.51</td>
<td>100</td>
</tr>
<tr>
<td>ΔU33a</td>
<td>0.71 ± 0.10</td>
<td>2.07 ± 0.25</td>
<td>0.34</td>
<td>7.5</td>
</tr>
<tr>
<td>U33aA</td>
<td>1.98 ± 0.17</td>
<td>1.91 ± 0.24</td>
<td>0.43</td>
<td>9.5</td>
</tr>
<tr>
<td>U33aC</td>
<td>1.89 ± 0.14</td>
<td>0.44 ± 0.04</td>
<td>4.50</td>
<td>99.8</td>
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<tr>
<td>U33aG</td>
<td>1.73 ± 0.16</td>
<td>2.20 ± 0.31</td>
<td>0.40</td>
<td>8.9</td>
</tr>
<tr>
<td>G36A</td>
<td>0.69 ± 0.13</td>
<td>1.56 ± 0.19</td>
<td>0.44</td>
<td>9.8</td>
</tr>
<tr>
<td>G36C</td>
<td>2.06 ± 0.25</td>
<td>0.60 ± 0.07</td>
<td>3.43</td>
<td>76.1</td>
</tr>
</tbody>
</table>

The results are the average of three independent repeats with standard deviations indicated.

<table>
<thead>
<tr>
<th>tRNA</th>
<th>$k_{\text{obs}}$ ($\times 10^{-3}$) (s$^{-1}$)$^a$</th>
<th>Relative $k_{\text{obs}}$ (%)$^a$</th>
</tr>
</thead>
<tbody>
<tr>
<td>tRNA$^{Thr_2}$</td>
<td>30.39 ± 2.63</td>
<td>100</td>
</tr>
<tr>
<td>G35C</td>
<td>11.30 ± 1.76</td>
<td>37</td>
</tr>
<tr>
<td>U336C</td>
<td>4.85 ± 0.64</td>
<td>16</td>
</tr>
<tr>
<td>A73C</td>
<td>29.85 ± 3.07</td>
<td>97</td>
</tr>
</tbody>
</table>

$^a$The $k_{\text{obs}}$ values are relative to that of tRNA$^{Thr_2}$.
$^b$The results are the average of three independent repeats with standard deviations indicated.

ScyctRS systems (19). We then used these mutants to measure tRNA-dependent AMP formation by ScmThrRS in the presence of non-cognate Ser. We found that the A73C mutant displayed nearly full efficiency [$k_{\text{obs}} = (29.85 ± 3.07) \times 10^{-3} s^{-1}$] compared to wild-type tRNA$^{Thr_2}$ [$k_{\text{obs}} = (30.39 ± 2.63) \times 10^{-3} s^{-1}$]. In sharp contrast, the $k_{\text{obs}}$ values of G35C [(11.30 ± 1.76) $\times 10^{-3} s^{-1}$] and U336C [(4.85 ± 0.64) $\times 10^{-3} s^{-1}$] fell to a level close to that of tRNA-independent pre-transfer editing [(7.78 ± 1.12) $\times 10^{-3} s^{-1}$], suggesting that the tRNA mutant were not able to stimulate pre-transfer editing (Table 3). In summary, aminoacylation-impaired A73C stimulated a similar level of editing compared with wild-type tRNA$^{Thr_2}$; thus, A73 is only critical for the synthetic activity, while G35 and U336 play a role in both the aminoclaylation and editing activities.

tRNA$^{Thr_1}$ stimulates pre-transfer editing in the presence of an editing domain

We previously showed that the N2 editing domain of ScyctRS contributes to both the aminoclaylation and editing activities (19). Therefore, as tRNA$^{Thr_1}$ was unable to stimulate tRNA-dependent pre-transfer editing, we checked if the absence of the editing domain in ScmThrRS could explain this incapacity. To address this question, we first added the complete N-terminal domain of the cytosolic ScyctRS, including the N1 and N2 editing domains (Met$^{N1}$-Gln$^{337}$), to ScmThrRS. This chimeric enzyme, designated CmThrRS (cytoplasmic-mitochondrial ThrRS), showed some remarkable catalytic features. First, CmThrRS exhibited intact aminoclaylation activity for both tRNA$^{Thr_1}$ and tRNA$^{Thr_2}$ substrates (Figure 6A), despite a decrease in the Thr activation rate to 30% of the wild-type level (Figure 6B). Second, we observed that the added editing domain in CmThrRS induced recovery of the post-transfer editing activity as shown by deacylation of Ser-tRNA$^{Thr}$ (Figure 6C), thus, CmThrRS accumulated neither Ser-tRNA$^{Thr_1}$ nor Ser-tRNA$^{Thr_2}$ (Figure 4B). Third, AMP formation was measured in the absence or presence of tRNA$^{Thr_1}$ in order to clarify whether tRNA$^{Thr_1}$ was able to stimulate pre-transfer editing by CmThrRS. In the presence of non-cognate Ser, AMP formation was induced significantly in the presence of tRNA$^{Thr_1}$ with a $k_{\text{obs}}$ of (14.30 ± 2.31) $\times 10^{-3} s^{-1}$, which was almost 4-fold higher than $k_{\text{obs}}$ in the absence of tRNA$^{Thr_1}$ (3.59 ± 0.74) $\times 10^{-3} s^{-1}$ (Figure 6D and E). Similarly, tRNA$^{Thr_2}$ stimulated AMP formation by CmThrRS with an even higher $k_{\text{obs}}$ of (20.86 ± 2.10) $\times 10^{-3} s^{-1}$ (Table 4); however, this value was still lower than that of the original ScmThrRS [(30.39 ± 2.63) $\times 10^{-3} s^{-1}$, Table 3] (here, the AMP formation of CmThrRS with tRNA$^{Thr_1}$ or tRNA$^{Thr_2}$ included both pre-transfer editing and post-transfer editing since CmThrRS harbors an active editing domain). These data revealed that tRNA$^{Thr_1}$ has the intrinsic capacity to stimulate editing, but requires the presence of an additional editing domain in ScmThrRS. We have demonstrated that His$^{51}$ and His$^{55}$ in the editing domain of ScyctRS are responsible for the post-transfer editing reaction but not for pre-transfer editing (19). To verify that the increased AMP formation rate was due to pre-transfer and not post-transfer activity, we mutated residues His$^{51}$ and His$^{55}$ of the CmThrRS derived from ScyctRS to Ala residues to produce a mutant CmThrRS-H151A/H155A. As expected, the double mutant was deficient in post-transfer editing activity and could not deacylate preformed Ser-tRNA$^{Thr}$ (Figure 6C) but it could still catalyze tRNA$^{Thr_1}$- or tRNA$^{Thr_2}$-dependent pre-transfer editing with $k_{\text{obs}}$ values of (12.75 ± 2.21) $\times 10^{-3} s^{-1}$ or (14.20 ± 2.67) $\times 10^{-3} s^{-1}$, respectively (Table 4) (here, the AMP formation of CmThrRS-H151A/H155A with tRNAs included only pre-transfer editing). In combination, these data suggested that tRNA$^{Thr_1}$ has the intrinsic capacity to stimulate pre-transfer editing, but requires the presence of a classical editing domain to express this activity.
Figure 6. Fusion of the editing domain to ScmtThrRS restored its tRNA\textsuperscript{Thr}1-dependent pre-transfer editing capacity. (A) Aminoacylation of tRNA\textsuperscript{Thr}1 or tRNA\textsuperscript{Thr}2 by either ScmtThrRS (● for tRNA\textsuperscript{Thr}1 and □ for tRNA\textsuperscript{Thr}2) or CmThrRS (▲ for tRNA\textsuperscript{Thr}1 and ▼ for tRNA\textsuperscript{Thr}2). (B) ATP-PPi exchange assay showing Thr activation catalyzed by ScmtThrRS (●) and CmThrRS (▲). (C) Deacylation of Ser-tRNA\textsuperscript{Thr}2 by ScmtThrRS (■), CmThrRS (▲) and CmThrRS-H151A/H155A (▼). Spontaneous hydrolysis of mis-charged tRNA (control) was also carried out in the absence of enzyme (●). (D) Representative TLC plates showing AMP formation catalyzed by CmThrRS in the absence or presence of tRNA\textsuperscript{Thr}1. (E) Graphic representation of AMP formation without (●) or with (▲) tRNA\textsuperscript{Thr}1 detected in (C). A series of known amounts of [\textsuperscript{32P}]ATP were loaded for quantification.

Table 4. Observed rate constants of AMP formation by CmThrRS or CmThrRS-H151A/H155A with non-cognate Ser in the presence of the two tRNA\textsuperscript{Thr} isoacceptors

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>tRNA</th>
<th>$k_{\text{obs}} \times 10^{-3}$ (s\textsuperscript{-1})$^a$</th>
</tr>
</thead>
<tbody>
<tr>
<td>CmThrRS</td>
<td>No tRNA</td>
<td>3.59 ± 0.74</td>
</tr>
<tr>
<td></td>
<td>tRNA\textsuperscript{Thr}1</td>
<td>14.30 ± 2.31</td>
</tr>
<tr>
<td></td>
<td>tRNA\textsuperscript{Thr}2</td>
<td>20.86 ± 2.10</td>
</tr>
<tr>
<td>CmThrRS-H151A/H155A</td>
<td>tRNA\textsuperscript{Thr}1</td>
<td>12.75 ± 2.21</td>
</tr>
<tr>
<td></td>
<td>tRNA\textsuperscript{Thr}2</td>
<td>14.20 ± 2.67</td>
</tr>
</tbody>
</table>

$^a$The results are the average of three independent repeats with standard deviations indicated.

Role of the tRNA\textsuperscript{Thr}1 anticodon in editing by CmThrRS

We previously showed that the anticodon nucleotides of ScsThrRS or tRNA\textsuperscript{Thr}2 are critical for the pre-transfer editing activity of ScsThrRS or ScmtThrRS (Table 3) (19). Here we showed that, despite its extended size in anticodon loop, the tRNA\textsuperscript{Thr}1 stimulated the tRNA-dependent editing activity of CmThrRS in the presence of non-cognate Ser. Therefore, to explore the plasticity of the anticodon loop, especially of the U33aU AG\textsuperscript{36} tetranucleotide of tRNA\textsuperscript{Thr}1 during pre-transfer editing stimulation, we carried out AMP formation assays using the chimeric enzyme CmThrRS in the presence of our constructed ΔU33a, VG36a, U33aA, U33aC, U33aG, U34A, U34C, U34G, A35U, A35C, A35G, G36A, G36C or G36U forms of tRNA\textsuperscript{Thr}1. Results from the editing stimulation assays could be classified into three major categories. Nine of the 14 mutants (ΔU33a, A35C and G36A) exhibited decreased (by ~50%) editing stimulation with $k_{\text{obs}}$ values of (7.92 ± 0.94) × 10\textsuperscript{-3} s\textsuperscript{-1}, (7.96 ± 0.87) × 10\textsuperscript{-3} s\textsuperscript{-1} and (8.35 ± 1.32) × 10\textsuperscript{-3} s\textsuperscript{-1}, respectively. Finally, a third category, comprising two mutants (U33aA and G36U) exhibited $k_{\text{obs}}$ values of (4.51 ± 0.56) × 10\textsuperscript{-3} s\textsuperscript{-1} and (3.56 ± 0.48) × 10\textsuperscript{-3} s\textsuperscript{-1}, respectively, comparable with that in absence of tRNA (3.59 ± 0.74) × 10\textsuperscript{-3} s\textsuperscript{-1}, which demonstrated the failure of these two mutants to induce significant tRNA-dependent editing (Table 5). These data indicated that the
The capacity to acylate tRNA Thr1, indicating that we constructed a yeast minimal media minus uracil (SD Ura−). Therefore, guided single-point mutagenesis in the C-terminal domain structure-guided single-point mutagenesis in the C-terminal domain of ScmThrRS provided some insights but did not reveal critical residues specific only for tRNA Thr1 (Figure 3C and Table 1), failed to stimulate any editing, further suggesting that Ser-induced AMP formation was the result of editing but not aminoacylation activity.

The MST1 gene knockout strain, ScΔMST1, reveals that aminoacylation and tRNA binding domains co-evolved to acquire tRNA Thr1 recognition capability

Both the primary and tertiary structures of ScmThrRS and other ThrRSs (such as EcThrRS) are highly similar (Supplementary Figure S1); however, only ScmThrRS has the capacity to acylate tRNA Thr1, indicating that tRNA Thr1-specific recognition elements are highly conserved and difficult to identify. Indeed, extensive in vitro structure-guided single-point mutagenesis in the C-terminal domain of ScmThrRS provided some insights but did not reveal critical residues specific only for tRNA Thr1 (29). Therefore, we constructed a yeast MST1 gene knockout strain to establish a genetic complementation assay to investigate the in vivo complementation capacity of other ThrRSs and to provide insights into tRNA Thr1 recognition.

We purchased a diploid yeast strain (BY4743-MST1+/−) from Thermo Scientific, exhibiting one wild-type copy of MST1, while the other copy was replaced by a kanamycin gene (36). Strain BY4743-MST1+/− was transformed with the rescue plasmid [pRS426-MST1, (pRS426: MST1−, Ura−)] and transformants were cultured on Dropout minimal media minus uracil (SD/Ura−). Ura− colonies were selected and sporulation was induced. Tetrad were dissected and separated on YPG plates. YPG respiratory and SD/Ura− media supported growth of the haploid MST1-knockout (ScΔMST1); however, the strain did not survive on YPG plates supplemented with 5-FOA, the toxic product of which, 5-flourouracil, excluded the rescue plasmid (Supplementary Figure S2A). This result showed that MST1 is an essential gene for respiratory metabolism. We also confirmed MST1 knockout using a PCR-based method (Supplementary Figure S2B and C).

We then tested several ThrRSs originating from different organisms in the ScΔMST1 strain (Figure 7A). The genes of these proteins were recombined into the yeast expression vector p425TEF. The entire ORF of the MST1 precursor was first cloned as well as the protein deprived of its MTS. These constructs, together with the p425TEF empty vector were introduced into ScΔMST1 and transformants were grown on YPG and YPG/5-FOA plates. The 5-FOA supplemented respiratory-medium supported growth of clones harboring the gene for the ScmThrRS precursor only, confirming that the MTS is a critical element for targeting exogenously expressed mature ScmThrRS into the mitochondrion (Figure 7B).

Subsequently, we tested several other natural ThrRSs, including cytosolic Sc cyt ThrRS, EcThrRS, mature ScmThrRS (Ser29-Lys455), hScThrRS and mature hmThrRS (Leu20-Phe18) (Figure 7A). Genes encoding these ThrRSs were ligated downstream of the sequence encoding the MTS. Shuffle assays on 5-FOA-medium showed that all these natural ThrRSs were unable to rescue respiratory deficiency (Figure 7B). This raises the question of whether the origin of these deficiencies was the lack of tRNA Thr1 aminoacylation or of mitochondrial import. From our present aminoacylation studies (Figure 2) and reports by others (27), we know that EcThrRS, Sc cyt ThrRS and CmThrRS readily charge tRNA Thr2 but not tRNA Thr1 in vitro. Here, the shuffle assay confirmed that aminoacylation did not occur in vivo either. On the other hand, to further test the mitochondrial import capacity of the MTS with an exogenous ThrRS, we added the MTS upstream of the chimeric CmThrRS that was able to aminoacylate tRNA Thr1 to form MTS-CmThrRS (Figure 6A). The knockout strain was growth-capable under respiratory conditions, showing that MTS-CmThrRS complemented the yeast strain (Figure 7B). These data confirmed that the MTS efficiently directed import of the exogenous ThrRS sequence and strongly implied that the natural enzymes were inefficient in aminoacylating tRNA Thr1 in vivo.

Since only the MTS-CmThrRS and ScmThrRS precursor, both harboring the aminoacylation and C-terminal domains of mitochondrial origin, were able to complement the yeast strain, we speculated that the presence of the mitochondrial C-terminal domain was responsible for in vivo aminoacylation of tRNA Thr1. To address this question, we replaced the C-terminal domain of Sc cyt ThrRS with its counterpart derived from ScmThrRS to generate CmThrRS2 (Figure 7A). Therefore, CmThrRS2 and CmThrRS differed only in the aminoacylation domains, which were of cytoplasmic and mitochondrial origin, respectively (Figure 7A). After fusion with the MTS, MTS-CmThrRS2 was found to be unable to support mitochondrial protein synthesis in vivo despite comparable levels of CmThrRS and CmThrRS2 protein in ScΔMST1 (Supplementary Figure S3). In vitro aminoacylation data also confirmed that CmThrRS2 charged tRNA Thr2 but

Table 5. Observed rate constants of AMP formation by CmThrRS with non-cognate Ser in the presence of tRNA Thr1 or mutated derivatives

<table>
<thead>
<tr>
<th>tRNA</th>
<th>( k_{\text{obs}} \times 10^{-3} ) (s(^{-1}))(^a)</th>
<th>Relative ( k_{\text{obs}} ) (%)(^b)</th>
</tr>
</thead>
<tbody>
<tr>
<td>No tRNA</td>
<td>3.59 ± 0.74</td>
<td>25</td>
</tr>
<tr>
<td>tRNA Thr1</td>
<td>14.30 ± 2.31</td>
<td>100</td>
</tr>
<tr>
<td>ΔU33a</td>
<td>7.92 ± 0.94</td>
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</tr>
<tr>
<td>VG6a</td>
<td>15.91 ± 2.79</td>
<td>111</td>
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<tr>
<td>U33aC</td>
<td>4.51 ± 0.56</td>
<td>32</td>
</tr>
<tr>
<td>U33aG</td>
<td>14.47 ± 1.89</td>
<td>101</td>
</tr>
<tr>
<td>U34A</td>
<td>11.98 ± 2.01</td>
<td>84</td>
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<tr>
<td>U34E</td>
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<tr>
<td>A35C</td>
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<td>A35G</td>
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<td>G36C</td>
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</tr>
<tr>
<td>G36U</td>
<td>3.56 ± 0.48</td>
<td>25</td>
</tr>
</tbody>
</table>

\(^a\)The \( k_{\text{obs}} \) values are relative to that of tRNA Thr1.

\(^b\)The results are the average of three independent repeats with standard deviations indicated.

Values of U33aA and G36U mutants, which are significantly reduced, are shown in bold.

---

**References**

Figure 7. Complementation assay of the yeast knockout strain ScΔMST1 by different ThrRS genes and chimeric constructs. (A) Scheme showing domain composition of the various ThrRSs tested. N-terminal domains (including N-extension, N1 and N2 editing domains) are colored white; aminoacylation and CTDs of ScmtThrRS or of other ThrRSs are colored gray or black, respectively. The MTS of ScmtThrRS precursor is indicated by a diamond. (B) Shuffle assay performed under respiratory conditions without (YPG) or with 5-FOA (YPG/5-FOA) to induce loss of the rescue plasmid. The p425TEF empty vector was introduced as a negative control. Sequence encoding the functional MTS of ScmtThrRS precursor was added before the ORF of all ThrRSs (including natural cytoplasmic or mature mitochondrial ThrRSs).

Figure 8. Aminoacylation activity of CmThrRS2. Aminoacylation of tRNA^{Thr}_1 (■) or tRNA^{Thr}_2 (▲) by CmThrRS2. Reaction without tRNA addition (●) was performed as a negative control.

not tRNA^{Thr}_1 (Figure 8). Therefore, our results indicated that only a ThrRS with both mitochondrial aminoacylation and C-terminal domains are capable of charging tRNA^{Thr}_1, suggesting that the two domains co-evolved to confer tRNA^{Thr}_1 aminoacylation activity.

DISCUSSION
Mitochondrial ThrRS deprived of the editing domain catalyzes tRNA-dependent pre-transfer editing

ThrRS is a class II synthetase with a unique modular structure containing three structural domains. The dimeric core consists mainly of the synthetic catalytic site and the C-terminal tRNA-anticodon binding domain. One extra domain on the N-terminal side of each monomer protrudes outside the core, forming the editing domains of the dimer (37). Such modular organization is conserved from bacteria (such as E. coli), to higher eukaryotes (such as humans) and in cytoplasmic and mitochondrial compartments. Among them, bacteria and eukaryotic cytoplasmic ThrRSs have been shown to predominantly use post-transfer editing reactions to prevent the synthesis of Ser-tRNA^{Thr} (19,30). In the archaeal kingdom, several ThrRSs (such as in Pyrococcus abyssi) use particular editing domains related to D-tyrosyl-tRNATyr deacylases to hydrolyze Ser-tRNA^{Thr} (38,39). Other archaeal ThrRSs (such as in Sulfolobus solfataricus) are devoid of editing domains; however, editing of Ser-tRNA^{Thr} is maintained and catalyzed by an unrelated free-standing editing domain (40). All these studies underline the crucial importance of post-transfer editing as a quality control mechanism of the tRNA^{Thr} aminoacylation reaction. Despite this evidence, the N-terminal editing domains of mitochondrial ThrRSs from several yeast species (such as S. cerevisiae, S. pombe and C. albicans) have been lost and these enzymes are defective in post-transfer editing of Ser-tRNA^{Thr}. It was previously shown that S. cerevisiae mitochondrial ThrRS (ScmtThrRS) harbored a tRNA-independent pre-transfer editing activity for hydrolysis of Ser-AMP (31). In the present study, we showed that ScmtThrRS also possesses a tRNA-dependent pre-transfer activity that is stimulated by tRNA^{Thr}_2 but not tRNA^{Thr}_1. Indeed, AMP formation of ScmtThrRS at the presence of tRNA^{Thr}_2 was ∼4-fold compared with that of without tRNA; however, the unusual tRNA^{Thr}_1 only induced AMP production very modestly. A similar tRNA synthetase, M. mobile LeuRS (MmLeuRS), which also naturally lacks edit-
ing domain, exhibits identical AMP formation activity at absence or presence of cognate tRNA_{Leu} (41). Furthermore, cognate tRNA is unable to stimulate any AMP formation for the editing domain-deprived E. coli LeuRS (EcLeuRS-MmLinker) (41). Therefore, the observed increase in AMP formation activity of ScmThrRS after tRNA^{Thr}2 addition is significant and really reflects the tRNA-dependent pre-transfer editing of ScmThrRS, which is defective in post-transfer editing. To our knowledge, this is the first report describing such tRNA-isoacceptor specificity at the pre-transfer editing level. However, as reported for EcThrRS (30), ScyThrRS (19) and other systems (42), pre-transfer editing alone is not sufficient to prevent synthesis of mis-charged tRNAs. Therefore, as an error-prone synthetase, editing alone is not sufficient to prevent synthesis of mis-incorporation provides evolutionary benefits to bacteria, yeast or humans (43,44).

Our study also showed that tRNA^{Thr}1 has the intrinsic capacity to stimulate tRNA-dependent pre-transfer editing activity according to the presence of the editing domain added in the chimeric enzyme CmThrRS. Indeed, it has been shown that the editing domain of bacterial ThrRS provides a binding interface for the minor groove of the tRNA acceptor stem and that deletion of the editing domain results in a dimeric enzyme that retains full activity in the activation step, while it is less efficient in the tRNA charging step (37). Similarly, we have previously found that deleting the N-terminal editing domain from yeast ThrRS results in an aminoacylation-impaired mutant; furthermore, amino acid alteration in the editing domain has an obviously negative effect on tRNA-dependent pre-transfer editing by yeast ScyThrRS (19). Collectively, these data indicate the critical contribution of the editing domain to aminoacylation and tRNA-dependent pre-transfer editing, possibly mediated by binding the acceptor stem of tRNA. The stimulation effect of chimeric CmThrRS observed here strongly suggests that interaction with the added editing domain may stabilize tRNA^{Thr}1 in a conformation that is suitable for pre-transfer editing.

For tRNA^{Thr}2-dependent pre-transfer editing, we found that both G35 and U36, but not A73 are key positive determinants. This is consistent with the cytosolic ScyThrRS, which depends critically on recognition of the anticodon bases for quality control (19). However, for the tRNA^{Thr}1-dependent pre-transfer editing catalyzed by the chimeric CmThrRS, we showed the critical importance of different bases in the anticodon loop, such as U33a and G36, which suggests differences in the anticodon loop-binding mode between the two tRNAs during editing.

tRNA-dependent pre-transfer editing is likely to occur at the aminoacylation active site

The location of the tRNA-dependent pre-transfer editing site has been debated. Preliminary evidence indicated that tRNA-dependent pre-transfer editing takes place in the editing domain, which is also the site of the post-transfer editing reaction. Indeed, fluorescence translocation-based assays combined with structure-directed mutagenesis in the C1 editing domain of class Ia isoleucyl-tRNA synthetase (IleRS) showed that the tRNA^{Ile}-dependent hydrolysis of Val-AMP occurs in the C1 domain (10–11,16). This observation was consistent with the X-ray crystal structures showing that both the substrate of pre- and post-transfer editing bind the C1 editing site with overlapping sites in LeuRS (12). In addition, a potential translocation channel was detected between the enzyme and tRNA, which could explain the migration of the adenylate molecules from the aminoacylation synthetic active site to the editing site (14,15). However, several reports indicated that tRNA-dependent pre-transfer editing occurs in the aminoacylation domain. This was first observed for GlnRS, a class I enzyme naturally devoid of a specialized editing domain, but able to catalyze tRNA-dependent aminoacyl-adenylate hydrolysis in the presence of a tRNA analog (17). Similarly, covalent inactivation of the E. coli LeuRS editing site by compound AN2690 did not reduce tRNA-dependent pre-transfer editing, indicating that the synthetic site was likely to be involved in tRNA-dependent pre-transfer editing (42). Furthermore, ScyThrRS-H151A/H155A, which harbored a defective editing domain, obviously catalyzed tRNA-dependent pre-transfer editing (19). However, these examples are subject to the criticism that analogs, inhibitors or mutations never mediate complete and definitive inactivation of the editing site, leading to careful and cautious interpretations. In the present study, we showed that ScmThrRS, a naturally occurring enzyme without a post-transfer editing domain, catalyzes significant tRNA^{Thr}2-dependent pre-transfer editing; therefore, representing a perfect model to study the mechanism of tRNA-dependent pre-transfer editing without contaminating post-transfer editing activity. In addition, it directly suggests that, at least for ScmThrRS, tRNA-dependent pre-transfer editing takes place in the aminoacylation domain where the cognate and non-cognate adenylate molecules are synthesized.

Specific binding mode of mitochondrial tRNA^{Thr}1 to ScmThrRS

As stated previously, many yeast mitochondrial ThrRSs lack editing domains, suggesting that the loss of the editing domain occurred before the divergence of these species. Strikingly, both S. pombe and C. albicans mitochondria have retained canonical tRNA_{Leu}^{CUN} (CUN) to decode CUN codons as Leu. S. cerevisiae mitochondria have lost tRNA_{Leu}^{CUN} (CUN) and evolved tRNA_{Thr}1 to decode CUN codons as Thr, yet, the advantage of this codon reassignment remains elusive. Despite high sequence similarity of ScmThrRS with SpmtThrRS and CmThrRS, the latter two ThrRSs failed to aminoacylate tRNA^{Thr}1 both in vitro and in vivo. Other ThrRSs, such as EcThrRS and ScyThrRS, are also unable to...
charge tRNAThr in vitro and in vivo. Furthermore, hcThrRS and hmtThrRS did not complement for the loss of ScmThrRS in vivo, which is likely to be due to an inability to charge tRNAThr. Therefore, ScmThrRS must have evolved tRNAThr-specific recognition elements. A crystal structure-based Ala-scanning mutagenesis strategy targeting all potential arginine or lysine residues has been employed to identify specific recognition sites for tRNAThr in the anticodon binding domain of ScmThrRS (29). Among them, mutant R434A displayed specifically reduced affinity for tRNAThr, suggesting that this residue is a critical element of tRNAThr discrimination. However, Arg634 is a highly conserved residue present in nearly all ThrRSs (Supplementary Figure S1), including EcThrRS, ScctThrRS, SpmtThrRS, CamtThrRS, hcThrRS and hmtThrRS, all of which were unable to charge tRNAThr. This suggests that Arg634 is only one element in a tRNAThr discrimination network, the whole process of which is probably more complex than expected. Our in vivo data generated with chimeric enzymes showed that the acquisition of tRNAThr aminoacylation required the presence of both yeast mitochondrial aminoacylation and tRNA binding domains, suggesting that both domains co-evolved to follow the CUN codon reassignment and recognition of the new anticodon loop. Therefore, the strategy of Ala-scanning of amino acid targets may be extended to the aminoacylation domain. In this study, we observed another remarkable difference characterizing the two tRNAThr isoacceptors. While tRNAThr2 spontaneously catalyzes tRNA-dependent pre-transfer editing, tRNAThr1 required the artificial presence of an editing domain to stimulate pre-transfer editing. As the editing and aminoacylation domains usually clamp the acceptor stem of tRNAThr, this strongly suggests differences in the interaction of the acceptor end of the two tRNAs with the aminoacylation domain. Further peptide swapping and site-directed point mutagenesis will be performed in this domain to identify residues that potentially interact with tRNAThr1 and may be part of the specific subset of amino acids involved in the recognition process.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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