Natural reassignment of CUU and CUA sense codons to alanine in Ashbya mitochondria

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Natural reassignment of CUU and CUA sense codons to alanine in Ashbya mitochondria

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ABSTRACT
The discovery of diverse codon reassignment events has demonstrated that the canonical genetic code is not universal. Studying coding reassignment at the molecular level is critical for understanding genetic code evolution, and provides clues to genetic code manipulation in synthetic biology. Here we report a novel reassignment event in the mitochondria of Ashbya (Eremothecium) gossypii, a filamentous-growing plant pathogen related to yeast (Saccharomycetaceae). Bioinformatics studies of conserved positions in mitochondrial DNA-encoded proteins suggest that CUU and CUA codons correspond to alanine in A. gossypii, instead of leucine in the standard code or threonine in yeast mitochondria. Reassignment of CUA to Ala was confirmed at the protein level by mass spectrometry. We further demonstrate that a predicted tRNA Ala UAG is transcribed and accurately processed in vivo, and is responsible for Ala reassignment. Enzymatic studies reveal that tRNA^Ala_{UAG} is efficiently recognized by A. gossypii mitochondrial alanyl-tRNA synthetase (AgAlaRS). AlaRS typically recognizes the G3:U70 base pair of tRNA^Ala; a G3A change in Ashbya tRNA^Ala_{UAG} abolishes its recognition by AgAlaRS. Conversely, an A3G mutation in Saccharomyces cerevisiae tRNA^Thr_{UAG} confers tRNA recognition by AgAlaRS. Our work highlights the dynamic feature of natural genetic codes in mitochondria, and the relative simplicity by which tRNA identity may be switched.

INTRODUCTION
When the genetic code was first deciphered in the 1960s, it was considered to be universal, with all organisms using the same standard code. Later it was shown that several codons have been recoded with different amino acids, thus creating non-standard genetic codes that are present in modern organisms (1). To date, 11 codon reassignment events have been reported in the nuclear genomes of bacteria, archaea and eukaryotes, and 16 have been found in mitochondria [reviewed in (1–4)]. Most recently, single-cell sequencing and biochemical analyses identified yet another. UGA tryptophan-to-glycine reassignment event in SR1 bacteria (5). These dogma-breaking discoveries suggest that the genetic code is evolvable in nature, and that it could be engineered in synthetic organisms. Enabled by genome engineering technologies, such as multiplex automated genome engineering (6), conjugative assembly genome engineering (7) and de novo genome synthesis (8), editing and rewriting the genetic code have emerged as an exciting topic in synthetic biology. Multiplex automated genome engineering, and conjugative assembly genome engineering have been used to change all 321 known UAG stop codons to the synonymous UAA stop codon. This will enable the abolition of UAG function, thereby permitting subsequent reassignment from ‘stop’ to any natural or non-natural amino acid (7).

Natural codon reassignment events may be explained by different evolutionary scenarios, depending on special circumstances. The codon capture mechanism (9) evokes that a specific set of codons and the corresponding tRNA completely disappear from a genome before a novel tRNA evolves to read such codons with a different specificity. In contrast, the ambiguous intermediate mechanism (10) posits that a codon does not need to disappear before reassignments and that it is ambiguously translated.

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The authors wish it to be known that, in their opinion, the first two authors should be regarded as Joint First Authors.

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Codon reassignment is facilitated in mitochondrial DNAs (mtDNAs) because they encode only a small set of proteins, and tend to be A+T rich, which introduces a strong codon bias. For instance, UAA stop codons are absent in mitochondrial genes of close relatives (23), and an 8- rather than 7-nt-long anticodon loop, which has evolved from a tRNA_His ancestor (21). Here, we report a second instance in which a tRNA closely related to tRNA^Thr reassigns CUU and CUA codons in the mitochondrial genome of the yeast *A. gossypii* to Ala. We further provide preliminary evidence for a third event in another yeast species (*Nakaseomyces bacillisporus*), in which CGA is read as histidine rather than arginine.

**MATERIALS AND METHODS**

**Cloning, mutagenesis and general methods**

The *A. gossypii* AlaRS gene was cloned into pET28a expression vector (Novagen) with an N-terminal six-His tag. Expression of recombinant proteins was induced at 37°C for 4 hours with 0.5 mM isopropyl β-D-1-thiogalactopyranoside in *Escherichia coli* strain BL21 codon plus in Luria–Bertani media. His-tagged proteins were purified according to the standard procedures. Mitochondrial tRNA genes were cloned into pUC18 vector (GenScript), and mutations were introduced using QuikChange Site-Directed Mutagenesis Kit (Stratagene).

**In vitro assays with tRNAs**

*In vitro* tRNA transcripts were obtained using the T7 RNA polymerase runoff procedure as described (24). Aminoacylation experiments were performed as described (25) in the presence of 100 mM Na-HEPES, pH 7.2, 30 mM KCl, 10 mM MgCl₂, 2 mM ATP, 25 μM[^14C] Ala or[^13C] Thr, 5 μM tRNA transcripts and 30-3000 nM aaRSs.

**Identification of mitochondrial tRNAs in RNA-Seq data**

* A. gossypii cells (ATCC 10895) were grown to an optical density of ~2.5 in a medium containing 1% yeast extract, 0.5% glucose and 3% glycerol, pH 5.5. Purification of a crude mitochondrial fraction followed previously published procedures (26), and RNA-Seq sequences (Illumina MiSeq; provided by the Genome Quebec Innovation Center) were generated from total, Trizol-extracted mitochondrial RNA, without size selection. Sequences in fastq format were quality-trimmed (phred 20, minimum sequence length 20 nt) and adapter-clipped using Seqtrimnext (http://rubygems.org/gems/seqtrimnext), tRNA sequences were analyzed by scanning the trimmed sequences with a 15-nt-long sequence window (using the basic Linux tools grep and wc).

**Identification of mitochondrial proteins by mass spectrometry**

Purified mitochondria were solubilized in a buffer containing 20 mM Heps/KOH, pH 7.4, 60 mM NH₄Cl, 10 mM MgCl₂, 0.5 mM ethylenediaminetetraacetic acid, 1 mM phenylmethylsulfonyl fluoride and digitonin (2 g/g of protein), followed by incubation on ice for 30 min and homogenization in a Potter homogenizer. After centrifugation at 18 000 g for 15 min, the supernatant was collected, and a small fraction (~150 μg protein) was separated for 30 min (4–14%) Blue Native Poly-Acrylamide Gel Electrophoresis (BN-PAGE); Hoefer apparatus with an 18 × 16 cm electrophoresis chamber; 140 V and 9 mA). The preparation of...
BN-PAGE gels, electrophoresis buffer and samples followed previously published procedures (27). The protein-containing zone was cut from the gel and submitted to liquid chromatography tandem mass spectrometry analysis (28,29), provided by a service platform at the Université de Montréal (Institute for Research in Immunology and Cancer). It includes destaining, reduction, alkylation, trypic digestion and functional annotation by Mascot (30).

Sequence alignments and identification of mitochondrial tRNAs

Derived mitochondrial protein sequences were aligned with Muscle version 3.6 (31). Mitochondrial tRNAs were identified with MFannot (http://megasun.bch.umontreal.ca/cgi-bin/mfannot/mfannotInterface.pl). It uses tool components of the Infernal package v1.1rc2 (32,33), notably embundle and cmcalibrate, to build a covariance search model from aligned tRNA training sets, followed by cmlsearch to screen genomic sequences. The tRNA sequences shown in Figures 2 and 6 were aligned with cmlsearch and the –A switch, using the standard tRNA model of MFannot. For visualization, editing and reformatting of sequence alignments, we used the Genetic Data Environment (GDE) sequence editor (34). A modified GDE version that functions with current 64-bit Linux versions, together with the appropriate libraries, is available on request.

Phylogeny of yeast species based on mtDNA-encoded protein sequences

Thirteen standard, mtDNA-encoded-derived protein sequences (Cob, Cox1,2,3, Atp6,9 and Nad1,2,3,4,5L,5,6) were aligned in two steps. Briefly, sequences were pre-aligned with Muscle (31) and then refined with HMMalign (S. Eddy; http://hmmer.janelia.org). Sequence positions that were not aligned with a posterior probability value of 1.0 are discarded, and alignments were concatenated. The final dataset includes 40 species and has 3583 amino acid positions. The phylogenetic analysis was performed with PhyloBayes (35), the CAT/GTR model, six discrete categories, four independent chains, 14000 cycles (corresponding to ~700000 generations) and the –dc parameter to remove constant sites. The first 10000 cycles were discarded as burn-in.

Phylogeny of yeast mitochondrial tRNAs

The phylogenetic analysis with PhyloBayes (CAT, GTR, six categories; four independent chains; 11000 cycles corresponding to ~1 800 000 generations) contained all tRNA sequences from the species presented in Figure 5. Only the section of the tRNA phylogeny covering the related tRNA\textsubscript{Thr} and tRNA\textsubscript{Htr} clusters is shown in Figure 3.

RESULTS

Bioinformatic analyses suggest that CUU and CUA codons are reassigned from Leu to Ala in mitochondria of \textit{A. gossypii}

Multiple sequence alignment of derived mitochondrial protein sequences reveals numerous positions where \textit{Ashbya} does not conform to otherwise highly conserved, or even invariant, amino acids. For instance, in the given example of a cytochrome oxidase Cox2 sequence alignment (Figure 1), three columns containing CUN-encoded amino acids (amino acid shown in lower case) are highlighted. In the first two marked sequence columns, the pattern of conservation is consistent with translation of CUN to Thr (indicated by a lower-case t) for the given species, as experimentally confirmed in \textit{S. cerevisiae} (21,22). In the third column, CUN corresponds to Ala in \textit{A. gossypii} (shown as a lower-case a). This trend applies to all eight regular mtDNA-encoded proteins in \textit{Ashbya} (49 CUU and 32 CUU codons; Supplementary Table S1), with most deviations in less well-conserved amino acid positions.

In the context of codon reassignment, the strict avoidance of CUG and CUC codons seems noteworthy. An analysis of overall mitochondrial codon usage reveals that \textit{Ashbya} is as biased in other codon families, with 24 sense codons unused, most of which with a C or G in the third position (Supplementary Table S1). In other yeast species such as \textit{S. cerevisiae}, overall codon bias is similar, although somewhat less extreme (Supplementary Table S1). A notable exception is in \textit{Kluyveromyces lactis}, a close relative of \textit{Ashbya}. This species avoids CUN codons altogether (Supplementary Table S1), and has no corresponding mtDNA-encoded tRNA with a UAG anticodon that would allow the recognition of this codon family.

Mass spectrometry confirms the identity of CUU and CUA codons in \textit{A. gossypii} mitochondrial proteins

To confirm the predicted CUU/CUU codon identity in \textit{A. gossypii} as Ala, trypic digests of proteins extracted from purified mitochondria were analyzed by mass spectrometry. To identify potential translation variants, results were analyzed based on three sets of inferred proteins in which CUA/CUU was translated as Leu, Thr or Ala. Among 475 identified proteins, two (Cox1 and Cox2) were mtDNA-encoded, with peptides covering gene regions with one CUA codon each. In both cases (experiment repeated three times), CUU was translated as Ala, tryptic digests of proteins extracted from purified mitochondria were analyzed by mass spectrometry. To identify potential translation variants, results were analyzed based on three sets of inferred proteins

\textit{In silico} identification of the \textit{A. gossypii} tRNA decoding CUU and CUA codons

Identification of yeast mitochondrial tRNAs is highly sensitive and without false positives when using covariance search models (32), which are used by our annotation tool MFannot (12). All known tRNA structures with a UAG anticodon (tRNA\textsubscript{UAG}) were identified throughout yeast species (e.g. Figure 2A), with the notable exception of \textit{K. lactis}, as mentioned earlier in the text. In distinction to the tRNA\textsubscript{Thr} in \textit{S. cerevisiae} and most other Saccharomycetaceae, the \textit{A. gossypii} tRNA\textsubscript{UAG} has a standard 7-nt anticodon loop (Figure 2A). A comparison of tRNA\textsubscript{UAG} across yeast species further reveals >70% sequence identity (e.g. Figure 2A and B), pointing to a
Figure 1. Alignment of derived Cox2 protein sequences and mass spectrometry at the protein level indicate that CUN decodes alanine in *A. gossypii*. The alignment corresponding to amino acids 141–195 of *A. gossypii* Cox2 is shown. Amino acids corresponding to CUN codons are in lower case, and translated into either Thr (most Saccharomycetaceae) or Ala (*A. gossypii*, confirmed by mass spectrometry of mitochondrial proteins). The sequence of the respective tryptic peptide is FIVTAaDVIHDFAVPSLGIK). Lower case m corresponds to AUA codons. This conservation pattern is valid for all mtDNA-encoded proteins of the shown species. Abbreviations: *Sacch.*., *Saccharomyces*; *Candi.*., *Candida*; *Klyv.*., *Kluveromyces*; *Lach.*., *Lachancea*; *Nakas.*., *Nakaseomyces*; and *Vande.*., *Vanderwaltozyma*.

recent common ancestry. A phylogenetic analysis of mtDNA-encoded tRNAs confirms this view, clustering tRNA\textsubscript{Thr} of Saccharomycetaceae with *A. gossypii* tRNA\textsubscript{UAG} (Figure 3). This analysis further confirms that tRNA\textsubscript{UAG} from yeast mitochondria was originally derived from a duplication of a histidine tRNA, as previously proposed (21). The tRNA phylogeny further reveals an unexpected clustering of *N. bacillisporus* mitochondrial tRNA(UAG) within tRNA\textsubscript{His} (Figure 3). A more detailed comparison with histidine tRNAs (Figure 6) reveals a shared recognition signal for histidyl-tRNA synthetase (HisRS) (17), a G residue at position −1 (the 5\textsuperscript{′} terminus of tRNA histidine) that pairs with a C at the 3\textsuperscript{′} discriminator position. This suggests that tRNA (UCG) might recognize the CGN codon family not as arginine (see Discussion).

To demonstrate that *A. gossypii* tRNA\textsubscript{UAG} is expressed, properly processed and matured with a 3\textsuperscript{′}-CCA terminus, RNA-Seq data from total RNA were produced and analyzed. This tRNA is expressed at about the same level as other mitochondrial tRNA species. The 5\textsuperscript{′} and 3\textsuperscript{′}-processing intermediates and mature tRNA (with CCA addition at the 3\textsuperscript{′}) were confirmed. The sequence of tRNA\textsubscript{UAG} is identical to that of the genomic DNA (including the anticodon), suggesting that the tRNA is not edited post-transcriptionally (36).

CUU/CUA-decoding tRNA in *A. gossypii* mitochondria is recognized by the mitochondrial alanyl-tRNA synthetase

The tRNA with a predicted UAG anticodon in *A. gossypii* mitochondria is closely related to *S. cerevisiae* mitochondrial tRNA\textsubscript{Thr} (Figures 2B and 3). Therefore, we tested whether the *A. gossypii* mitochondrial tRNA\textsubscript{UAG} is a substrate for ScMST1, which is the enzyme responsible for attaching Thr onto *S. cerevisiae* mitochondrial tRNA\textsubscript{Thr}. *In vitro* aminoacylation experiments show that the wild-type (WT) *A. gossypii* mitochondrial tRNA\textsubscript{UAG} is not recognized by ScMST1 (Figure 4). Previously we showed that the enlarged tRNA\textsubscript{Thr} anticodon loop is an important identity element for ScMST1 (21,37). In line with that, a U insertion (InsU31) in the anticodon loop of *A. gossypii* mitochondrial tRNA\textsubscript{UAG} converts it to a moderate substrate for ScMST1 in an aminoacylation experiment with Thr (Figure 4). To further validate the identity of this tRNA\textsubscript{UAG} species, we purified the recombinant *A. gossypii* mitochondrial AlaRS (AgAlaRS) and tested Ala acylation. The WT tRNA\textsubscript{UAG} from *A. gossypii* mitochondria turned out to be a good substrate for AgAlaRS, and was therefore named tRNA\textsubscript{Ala}.

The G3:U70 pair of tRNA\textsubscript{Ala} is critical for reassignment of CUU and CUA codons as Ala

The major identity element for AlaRS enzymes is the G3:U70 base pair (38,39). This pair is also present in *A. gossypii* mitochondrial tRNA\textsubscript{UAG}. A G3A change in tRNA\textsubscript{Ala} abolishes its recognition by AgAlaRS (Figure 4), suggesting that AgAlaRS recognizes its tRNA substrate in a similar manner as the characterized AlaRSs. As expected, the WT *S. cerevisiae* mitochondrial tRNA\textsubscript{Thr}, which contains an A3:U70 pair, is not a substrate for AgAlaRS. However, an A3G mutant of *S. cerevisiae* mitochondrial tRNA\textsubscript{Thr} gains 12% alanylation efficiency compared with the WT *A. gossypii* mitochondrial tRNA\textsubscript{Ala} (Figure 4 and Table 1). Further, deletion of U31 in the A3G/du31 mutant prevented the tRNA from recognition by MST1. These results suggest that *A. gossypii* mitochondrial tRNA\textsubscript{Ala} has evolved to an orthogonal Ala tRNA not recognized by ThrRS, either via duplication of tRNA\textsubscript{Thr} or its evolutionary precursor tRNA\textsubscript{His} (21). The emergence of a G3:U70 pair would be the defining evolutionary step during this reassignment process.

DISCUSSION

Reassignment of CUN codons in yeast mitochondria

The mitochondrial genetic code has been rapidly evolving across eukaryotes, including a relatively recent CUN codon reassignment close to the divergence of the
Saccharomycetaceae family (Figure 5). This group of yeast species has reduced mitochondrial gene numbers substantially (no nad genes, only 7–8 protein-coding genes are left in Saccharomycetaceae), which implies that codon families can be even more easily eliminated than in other mitochondrial systems. For example, K. lactis (a close relative of Ashbya) does not use CUN codons (Supplementary Table S1) and has no mtDNA-encoded tRNA with a UAG anticodon that would allow the recognition of this codon family. Based on the combined evidence, we favor the interpretation that CUN codon reassignment followed a codon capture mechanism, where CUN codons and the corresponding tRNA first vanished in the mitochondrial genome (completely, or more likely, reduced to a few codons that have little impact on protein structure and function), followed by...
the emergence of a tRNA with UAG anticodon that decodes CUN as alanine and the reappearance of more CUN codons (9,21). A short period of coding ambiguity cannot be ruled out if this new tRNA arose by duplication. However, a single mutation at the aaRS recognition site would suffice for an identity switch from threonine to alanine, without codon ambiguity. We favor this latter interpretation over other alternatives that may rather apply to more complex genetic systems [e.g. the nuclear genome of \textit{C. albicans} (3)] than to yeast mitochondria with much fewer protein-coding genes.

Our previous work reveals that in \textit{Saccharomyces}, tRNA\textsubscript{Thr} which is responsible for CUN codon reassignment from Leu to Thr, was derived from a mitochondrial tRNA\textsubscript{His} \((21)\). Loss of CUN codons (accompanied by loss of \textit{nad} genes) and evolution of tRNA\textsubscript{Thr} from tRNA\textsubscript{His} via gene duplication presumably occurred in a common ancestor of \textit{Saccharomyces} (Figure 5). Gene duplications are common in mtDNA. For example, among extant yeast species, the \textit{C. albicans} strain SC5314 mitochondrial genome encodes two copies of tRNA\textsubscript{His} within duplicated genome segments—the basis for neo-functionalization of one of the gene copies (40).

In the current work, we show that \textit{A. gossypii} mitochondria use CUA and CUU to decode Ala instead of Leu or Thr. tRNA\textsubscript{Ala} clearly clusters with yeast mitochondrial tRNA \textsubscript{Thr} from which it most likely also derived via gene duplication. This reassignment implies a reduction of the unusual 8-nt anticodon loop (the recognition site of threonyl-tRNA synthetase) to only seven nucleotides, and introduction of a G3:U70 base pair, which allows efficient recognition of CUN codons by \textit{A. gossypii} mitochondrial alanyl-tRNA synthetase (Figure 2).

**Evolution of mitochondrial tRNA\textsubscript{His} \textsubscript{UGU} from tRNA\textsubscript{His} \textsubscript{AGU} in \textit{N. bacillisporus}**

The tRNA phylogeny further reveals a divergence of a \textit{N. bacillisporus} mitochondrial tRNA(UCG) from within the tRNA\textsubscript{His} GUG cluster (Figure 3). According to the standard translation code, a tRNA with this anticodon is expected to recognize the CGN arginine codon family.

**Figure 3.** Phylogeny of yeast mitochondrial tRNAs. The phylogenetic analysis contains representatives from a broad selection of yeast species. Only the section of the tree in which relevant tRNA\textsubscript{Ala} and tRNA\textsubscript{Thr} cluster together is shown. The posterior probability support for the two tRNA groups is indicated. Green and blue indicate tRNA\textsubscript{Ala} and tRNA\textsubscript{Thr} families, respectively. Red indicates reassigned tRNAs. Note that phylogenetic analysis with tRNA sequences depends on only a few informative nucleotide positions, which does not allow resolving the branching order within these groups.

**Table 1.** Aminoacylation efficiency of tRNA variants by \textit{A. gossypii} AlaRS

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<td>0.65 ± 0.03</td>
<td>12</td>
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**Figure 4.** Aminoacylation of mitochondrial tRNA\textsubscript{Ala} and tRNA\textsubscript{Thr} variants by Ag\textsubscript{AlaRS} and Sc\textsubscript{MST1}. The reaction was performed at 37°C in the presence of 3 \(\mu\)M Ag\textsubscript{AlaRS} or Sc\textsubscript{MST1}, 5 \(\mu\)M tRNA transcript and 25 \(\mu\)M \([^{14}\text{C}]\text{Ala}\) or \([^{14}\text{C}]\text{Thr}\).
Yet, based on the following considerations, we predict instead that it most likely translates CGA as His: (i) tRNA\textsubscript{His}\textsuperscript{GUG} and tRNA\textsubscript{His}\textsuperscript{UCG} in this species are 86% identical at the primary sequence level (Figure 6), (ii) both tRNAs have a gene-encoded G at position –1, and a C in the discriminator position, forming a base pair that is the known recognition signal for HisRS (21), (iii) CGN codons do not exist in neighbor species of \textit{N. bacillisporus} (\textit{Nakaseomyces delphensis}, \textit{Candida glabrata} and \textit{Candida castellii}; Figure 5), preparing the way for CGN codon capture and (iv) \textit{N. bacillisporus} has a single CGA codon in the \textit{cox1} gene, at an overall poorly conserved amino acid position. Remarkably, its closest neighbor \textit{C. castellii} has a histidine in this sequence position that is overall not well conserved. An identity switch of the unique CGA codon from arginine to histidine would therefore have little, if any, functional bearing, but as \textit{N. bacillisporus} HisRS has to recognize the GUG anticodon of tRNA\textsubscript{His}\textsuperscript{GUG} (21), a specificity change of HisRS is required to also recognize CGA (or alternatively, by a duplicated and modified HisRS). Whether this implies a transition period with ambiguous codon recognition depends on the facility with which mutations become established. Further experimental evidence is needed to validate our prediction that CGA is reassigned from Arg to His in \textit{N. bacillisporus} mitochondria.
Natural evolution of orthogonal tRNAs

According to our interpretation, CUN codon identity in yeast mitochondria has evolved in the order Leu to Thr to Ala, with corresponding specific tRNAs for Thr and Ala deriving from duplicates of tRNA\textsubscript{His}GUG and tRNA\textsubscript{Thr}UAG, respectively (Figure 2B). The suggested complete reallocation of these codons requires that tRNAs are orthogonal to the corresponding aaRS (recognized by a single cognate aaRS). In other words, recognition of a tRNA by more than one aaRSs would result in ambiguous decoding, as observed in the nuclear genome of several \textit{Candida} species, where CUG is read by both Leu and Ser (16,41).

Experimental data and the presence of known tRNA identity signatures are consistent with our hypothesis. Mass spectrometry identified Ala (not Leu, His or Thr) in highly conserved positions of \textit{A. gossypii} mtDNA-encoded proteins, corresponding to CUA at the codon level and suggesting that tRNA\textsubscript{Ala}UAG is orthogonal to AlaRS. We further show experimentally that tRNA\textsubscript{Ala}UAG is not recognized by \textit{S. cerevisiae} MST1, in line with the previous observation that this enzyme recognizes the extended 8-nt-long anticodon loop of tRNA\textsubscript{Thr}AUG (37). Most decisively, \textit{A. gossypii} tRNA\textsubscript{Ala}UAG has a G3:U70 base pair, which is a known identity signature for AlaRS (38,42). Recognition of this tRNA by mitochondrial HisRS can be excluded, as it is known to recognize G\textsubscript{−1} (a nucleotide at position $−1$ according to standard nomenclature that is not present in other tRNAs), the anticodon GUG and the discriminator base C73 (21). \textit{A. gossypii} tRNA\textsubscript{Ala}UAG has all of these identity elements altered, and is therefore unlikely to be a substrate for HisRS. Finally, this tRNA has the same anticodon as mitochondrial tRNA\textsubscript{Leu} outside Saccharomycetaceae. However, leucyl–tRNA synthetases typically recognize A73 (not present in \textit{A. gossypii} tRNA\textsubscript{Ala}UAG) and not the anticodon (37). Thus, we conclude that CUA and CUU are decoded solely by Ala in \textit{A. gossypii} mitochondria.

Studying sense codon recoding is not only important for understanding the evolution of life, but also provides valuable insights into manipulation of the genetic code to create synthetic organisms. One roadblock of sense codon recoding is the orthogonality of the synthetic tRNA (Krishnakumar \textit{et al.}, submitted for publication), which requires that the synthetic tRNA is not recognized by any endogenous aaRS. Identifying naturally evolved orthogonal tRNAs would thus offer insights into the principles that have to be followed, and the translational components that need to be adapted, for recoding the translation machinery of synthetic organisms.
SUPPLEMENTARY DATA
Supplementary Data are available at NAR Online, including [43].

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Conflict of interest statement
None declared.

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