

Supplementary information S1 (table) | Genetic code flexibility in microorganisms

Organisms and organelles	Mechanism	References
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Biased codon usage

Synonymous codons	Most sequenced organisms	Mutational bias or natural selection	1
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Codon reassignment

AUA: Ile→Met	Mitochondria of most metazoa and yeasts	Loss of tRNA ^{Ile} _{CAU} and t ⁵ C modification of tRNA ^{Met} _{CAU}	2
CUN ^a : Leu→Thr	Mitochondria of <i>Saccharomyces</i> spp.	Loss of tRNA ^{Leu} _{UAG} ; evolution of tRNA ^{Thr} _{CAU} from tRNA ^{His}	3,4
CUA/CUU: Leu→Ala	Mitochondria of <i>Ashbya gossypii</i>	Loss of tRNA ^{Leu} _{UAG} ; evolution of tRNA ^{Ala} _{CAU}	5
UAG: Stop→Ala	Mitochondria of certain green algae	Unknown	6
UAG: Stop→Leu	Mitochondria of certain green algae	Evolution of tRNA ^{Leu} _{CUA}	6,7
UAG: Stop→Pyl	Archaea Methanosarcinales Methanomassiliicoccales Bacteria Clostridia Peptococcaceae, Halobacteroidaceae, Thermoanaerobacteraceae, Ruminococcaceae Negativicutes Sporomusa, unclassified δ-Proteobacteria Desulfospira, Bilophila, unclassified	Evolution of tRNA ^{Pyl} _{CUA} , pyrrolysyl-tRNA synthetase, and pyrrolysine biosynthesis genes <i>pylBCD</i> . Normally occurs as a gene cassette (<i>pylTSBCD</i>).	8-10
UAR ^b : Stop→Gln	Certain green algae and phages	Evolution of tRNA ^{Gln} with UUA and CUA anticodons	11
UCA: Ser→Stop	Mitochondria of <i>Scenedesmus</i>	Loss of tRNA ^{Ser} _{UGA}	12,13
UGA: Stop→Gly	SR1 bacteria, Gracilibacteria (ACD78, ACD80)	Evolution of tRNA ^{Gly} _{UCA} divergent D-arm and anticodon stem	14
UGA: Stop→Cys	<i>Euplotes</i> spp.	Evolution of tRNA ^{Cys} _{UCA} ; eRF1 does not recognize UGA	15,16
UGA: Stop→Trp	Certain Firmicutes; mitochondria of most eukaryotic microorganisms	Mutation of tRNA ^{Trp} _{CCA} to tRNA ^{Trp} _{CUA} or C-to-U editing of tRNA ^{Trp} _{CCA}	2,17,18

Codon recoding

Recoded UGA: Stop→Sec	<p>Bacteria Found in certain species from the phyla: Firmicutes, Proteobacteria, Acidobacteria, Aquificae, Chloroflexi, Spirochaetes, Actinobacteria</p> <p>Archaea Restricted to: <i>Methanopyrus kandleri</i>, Methanococcales</p> <p>Eukarya In most clades excluding higher plants and fungi.</p>	<p>Particular UGA codons are recoded by downstream adjacent SECIS (in bacteria and archaea) or SECIS in 3'UTR (eukaryotes).</p> <p>Requires tRNA^{Sec}_{UCA}, selenophosphate synthase (<i>seI/D</i>), Sec elongation factor (<i>seI/B</i> or EF-Sec), and Sec synthase (<i>seI/A</i>) in bacteria or phosphoseryl-tRNA^{Sec} kinase (PSTK) and Sep-tRNA^{Sec}:Sec-tRNA^{Sec} synthase (SepSecS) in archaea and eukaryotes.</p>	19-22
Recoded UGA: Cys→Sec	<i>Euplotes</i> spp.	SECIS elements in the 3'UTR recode certain UGA=Cys codons to Sec	15

Ambiguous decoding

ACN: Thr and Ser	<i>Escherichia coli</i> , <i>Mycoplasma</i> and likely other bacteria; yeast mitochondria	Loss of ThrRS editing due to oxidative stress or mutations	23-25
CUG: Leu and Ser	<i>Candida</i> and Ascomycetes	tRNA with CAG anticodon recognized by both leucyl- and seryl-tRNA synthetases	26-28
CUN, UUA, UUG: Leu, Ile, and Val	<i>Mycoplasma</i>	Loss of LeuRS editing	24
UUC, UUU: Phe, Tyr	<i>Mycoplasma</i> ; yeast mitochondria	Loss of PheRS editing	29
Mistranslation at all codons	Most microorganisms	Reduced ribosomal fidelity due to mutations, antibiotics, or starvation	30

^a N=A, U, G or C

^b R=A or G

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