The Ambiguous Genetic Code of Methanogenic Archaea that Grow on Methylamines

Katie E. Shalvarjian[1], Grayson L. Chadwick[2], Paloma I. Pérez[2], Philip H. Woods[3], Victoria J. Orphan[3,4], Dipti D. Nayak[1,2*]

[1]Department of Plant and Microbial Biology, University of California, Berkeley, CA, USA

[2]Department of Molecular and Cell Biology, University of California, Berkeley, CA, USA

[3]Division of Geological and Planetary Sciences, California Institute of Technology, Pasadena, CA, USA

[4]Division of Biology and Biological Engineering, California Institute of Technology, Pasadena, CA, USA

***Correspondence:** Dipti D. Nayak (dnayak@berkeley.edu), Department of Molecular and Cell Biology, 1 Barker Hall, University of California, Berkeley, CA 94720-3204; Tel +1-510-664-5267

Competing Interests Statement

The authors do not declare any competing interests.

Abstract – 150

Natural genetic code expansion is a phenomenon wherein an additional amino acid is encoded by a stop codon. These non-standard amino acids are beneficial as they facilitate novel biochemical reactions. However, code expansion leads to ambiguity at the recoded stop codon, which can either be read through or terminated. Pyrrolysine (Pyl) is encoded by the amber codon (TAG/UAG) and is widespread in archaea, where it is required for methylamine-mediated methanogenesis, an environmentally important metabolism. Mechanisms to conditionally suppress the amber stop codon for Pyl installation during protein synthesis have not been identified. Using the model methanogen, *Methanosarcina acetivorans,* we demonstrate that Pyl-encoding archaea maintain an ambiguous genetic code wherein UAG encodes dual meaning as stop and Pyl. Our data suggest that expression of Pyl biosynthesis and incorporation genes is tuned to the cellular demand for Pyl, which allows these archaea to navigate ambiguous stop decoding in response to environmental cues.

28 **Introduction – 585**

29 The genetic code is a core feature of life on Earth; through this triplet code, information
30 stored in the four nucleotides of mRNA are translated into the twenty standard amino acids found
31 in peptides/proteins. While initially proposed to be immutable[1], it is now well established that the
32 genetic code is flexible and subject to evolutionary pressure. At least 33 alternative genetic codes
33 have been identified across the tree of life—in ciliates[2], bacteria[3–5], archaea[6,7], fungi[8], and
34 phage[9]—where either a sense or a stop codon is reassigned to deviate from the standard genetic
35 code. Natural genetic code expansion is a distinct case of codon reassignment, wherein a stop
36 codon is recoded to an amino acid beyond the standard twenty amino acids[10]. Natural genetic code
37 expansion is beneficial because the non-standard amino acids can enhance reaction rates or
38 facilitate novel biochemistry[11–14]. But, it also presents a unique challenge due to the ambiguous
39 interpretation of the recoded stop codon: the ribosome can either read through the recoded stop
40 codon to add the non-standard amino acid to the peptide chain or terminate translation by recruiting
41 a release factor instead. This ambiguity likely leads to the production of two pools of proteins—
42 an extended form and a truncated form—for all transcripts containing the recoded stop codon. In
43 the case of Selenocysteine (Sec), the 21st amino acid, a Sec-tRNA^{Sec} specific elongation factor
44 called SelB directs the ribosome to incorporate Sec at a UGA codon contingent on the presence of
45 a proximal structural motif called SECIS (selenocysteine insertion sequence)[15,16]. In contrast,
46 neither a sequence motif nor a specialized elongation factor has been found for Pyrrolysine (Pyl),
47 the 22nd proteinogenic amino acid[17]. Thus, the molecular mechanisms that Pyl-encoding
48 microorganisms use (if at all) to tolerate ambiguous stop decoding remains unclear.

49 Pyl is biosynthesized from two molecules of lysine[18] and is installed in elongating
50 polypeptides using a dedicated UAG-decoding tRNA^{Pyl} that is charged by a cognate tRNA

51 synthetase (PylRS)[19]. Pyl was first identified in the active site of methylamine-specific
52 methyltransferases in methanogenic archaea (methanogens)[13], where it is hypothesized to play an
53 essential role during the methyltransfer reaction from methylamines to a corrinoid-containing
54 protein[14]. Since then, Pyl has been identified across both archaea[20–23] and bacteria[24,25]. However,
55 a mechanism for targeted insertion of Pyl is not known in any of these microorganisms.

56 Here, we address the conundrum of how Pyl-encoding archaea have evolved to navigate a
57 potentially ambiguous genetic code. First, we use an *in silico* approach to assess the distribution
58 of Pyl across archaea and identify features that are unique to Pyl^+ genomes. Although Pyl-encoding
59 archaea have lower TAG stop codon usage overall, it can vary substantially from 1 to 27%. Hence,
60 the pattern of stop codon usage is neither a universal solution for the ambiguous genetic code
61 created by Pyl nor is it a reliable predictor for its presence. Next, we engineer a heterologous
62 expression system in *Methanosarcina acetivorans*, a native Pyl user, to test the functionality of Pyl
63 systems from metabolically and taxonomically diverse archaea *in vivo*. Our functional assays add
64 a layer of nuance to computational predictions and demonstrate that the presence of the *pyl* genes
65 alone is not sufficient evidence for genetic code expansion. Finally, we provide conclusive
66 evidence that *M. acetivorans* has an ambiguous genetic code in which the amber codon can be
67 interpreted either as a stop codon or as Pyl. To this end, we describe possible mechanisms through
68 which *M. acetivorans* maintains an ambiguous genetic code without a detrimental impact to
69 organismal fitness.

70 **Results – 2070**

71 **Pyrrolysine is present in archaea that perform anaerobic methylamine and methane**
72 **metabolism**

To map the distribution of Pyl in archaea, we searched for genes involved in its biosynthesis and incorporation in reference genomes available in the Genome Taxonomy Database (n=4,416; GTDB 214.0)[26]. The biosynthesis genes for Pyl (*pylBCD*)[18] are typically encoded in an operon[27,28] and are generally found in close proximity to the incorporation genes, comprised of $tRNA^{Pyl}$ (*pylT*)[29] and its cognate aminoacyl tRNA synthetase (*pylRS*, denoted as *pylS* hereafter)[19,20,28] (**Fig 1**). We observe a strong correlation between the presence of the biosynthesis (*pylBCD*) and incorporation (*pylTS*) modules (p=1.4e-273, χ^2=1249, **Table S1**); genomes encoding both sets of genes were annotated as Pyl^+ (putative Pyl users) and the remainder as Pyl^-. The Pyl^+ genomes are broadly distributed across archaea (**Fig S1, Table S2**) but can be discontinuous at the Genus level. For instance, among the *Asgardarchaeota*, only a few strains within the Genus *Borrarchaeum* are Pyl^+ (**Fig S1, S2A**). Likewise, even though 92% of *Methanosarcina* genomes are Pyl^+ (**Table S3**), a few strains have lost Pyl (**Fig S1, S2B**).

The Pyl machinery (i.e. PylBCD and PylTS) strongly co-occurs with two markers of methane metabolism in archaea: methyl-coenzyme M reductase (MCR) and component A2[30] (p=3.1e-49, χ^2=218, **Table S1**). If we survey only methanogens, the co-occurrence metric strengthens (p=1.1e-51, χ^2=288 **Table S1**), a trend that does not hold true for **an**aerobic **met**hanotrophic archaea (ANME) (p=1.0, Fisher's exact test). Pyl also co-occurs with genes encoding methylamine methyltransferases (p= 2.9e-231, χ^2=1054, **Table S1**), although some Pyl^+ archaea with these methyltransferases lack markers for methanogenesis (**Fig S2**) and are instead likely to perform acetogenesis[21]. Often, genes involved in methylamine metabolism[31] are in close genomic proximity to the Pyl machinery (**Fig 1C, Fig S3**), which further corroborates their functional association.

95 *Methanosarcinaceae* from diverse environments commonly encode genes for
96 methylamine-mediated methanogenesis and, thus, can be used to investigate fine-scale
97 evolutionary events associated with Pyl-mediated genetic code expansion. To this end, we
98 compared the gene trees for *pylS* and *pylBCD* to the 16S rRNA tree for this Family. While the
99 *pylBCD* tree is in strong agreement with vertical inheritance (**Fig S4A**), the *pylS* tree diverges
100 substantially (**Fig S4B, S5**). These data suggest that the Pyl biosynthesis and incorporation
101 modules can have distinct evolutionary histories despite being functionally interlinked.

102 **Pyl-mediated genetic code expansion does not lead to universal patterns of stop codon**
103 **compensation**

104 Given that Pyl incorporation relies on read through of the TAG codon, we examined
105 differences in stop codon usage between Pyl^+ and Pyl^- genomes. As expected, TAG usage is
106 significantly lower in Pyl^+ genomes (median=5.0%) compared to Pyl^- genomes (median=22.0%)
107 (Welch's t-test, p=5.6e-47) (**Fig 2A**). However, taxon-specific features, like GC content[32], can be
108 major confounders in these global trends. To control for these biases, we analyzed the distribution
109 of stop codon usage and GC content within the *Methanosarcinaceae* and the
110 *Methanomethylophilaceae*, two groups that have a relatively high distribution of Pyl^+ and Pyl^-
111 genomes. Despite a large difference in GC content, TAG usage in Pyl^+ genomes from
112 *Methanosarcinaceae* (median=4.9%) and *Methanomethylophilaceae* (median=4.1%) is similar
113 (**Fig 2B**). Further, within *Methanosarcinaceae,* we observe a marked increase in TAG stop codon
114 usage for Pyl^- strains to their Pyl^+ counterparts (Pyl^-: 13.5%; Pyl^+: 7.8%) (**Fig 2C, Table S2**).

115 We did not detect a global pattern of compensation for decreased TAG usage in the Pyl^+
116 genomes. While there are significant differences in TGA and TAA usage between Pyl^+ and Pyl^-
117 genomes across archaea (Welch's t-test, p=8.3e-7 and p=5.9e-5, respectively) (**Fig 2A**), these are

118 likely driven by taxon-specific factors. For instance, the Pyl$^+$ genomes in
119 *Methanomethylophilaceae* have higher TGA usage relative to *Methanosarcinaceae*, likely due to
120 their heightened GC content (**Fig 2B)**. Hence, even though reduced TAG usage correlates with the
121 presence of Pyl, there is no global compensation pattern. Rather, changes in TAA and TGA usage
122 are contingent on factors like GC content.

123 Although TAG codon usage is substantially lower in Pyl$^+$ genomes, it can be highly
124 variable, from 1% to 27% (**Table S2**). We hypothesized that differences in TAG codon usage might
125 impact the fraction and function of putative Pyl-containing proteins Pyl$^+$ genomes. Hence, we
126 predicted ORFs with internal TAG codons and measured their putative readthrough lengths within
127 each Pyl$^+$ genome (**Table S4**). Overall, we observe that heightened TAG usage (>15%) is
128 associated with an increase in the density of putative Pyl-containing proteins, whereas low TAG
129 usage (<5%) is associated with an increase in readthrough length of TAG-containing ORFs (**Fig**
130 **2D, Fig S6**).

131 **Genetic studies of diverse Pyl systems defy computational predictions**

132 Although Pyl is broadly distributed in archaea, its role in genetic code expansion has only
133 been studied in the context of a few methanogens[7,33,34]. To broaden our functional understanding
134 of Pyl across the domain, we expressed the Pyl machinery from two non-methanogens in the
135 genetically tractable model organism, *Methanosarcina acetivorans.* The first strain, *Borrarchaeum*
136 *weybense*, is an *Asgardarchaeon* hypothesized to use Pyl to perform methylamine-mediated
137 acetogenesis[21]. The second strain, ANME-3 S7, contains Pyl despite lacking methylamine
138 metabolism[22,35]. Axenic cultures are currently unavailable for both these strains, which prevents
139 attempts to investigate their Pyl machinery in its native context. Moreover, these strains are

140 unusual because they break from the strong co-occurrence patterns shown in (**Fig S1, Table S1**)
141 and thus might offer additional insights into the role of Pyl in archaea.

142 To develop *M. acetivorans* as a heterologous host, we generated deletion mutants lacking
143 either the biosynthetic operon (Δ*pylBCD*) or the incorporation genes (Δ*pylTS*) using our well-
144 established CRISPR-Cas9 editing system[36]. Neither mutant had off-target effects or suppressor
145 mutations based on whole genome resequencing (**Table S5**). We observed that both mutants have
146 a mild growth defect (slower by 15%; **Fig 3A, Table S6**) when Pyl is not essential (i.e., on
147 methanol) and are unable to grow when Pyl is essential [i.e., on trimethylamine (TMA)].
148 Complementation of each deletion mutant with the native locus *in trans* restored growth across all
149 conditions (**Fig 3A, Fig S7, Table S6**), indicating that no extragenic effects stem from the
150 chromosomal deletions. To validate the proposed catalytic role for Pyl in methylamine
151 methyltransferases[13,14,28,37], we generated a suite of non-synonymous point mutations at the Pyl
152 residue in the TMA-specific methyltransferase, *mttB1.* We expressed these point mutants *in trans*
153 from a tetracycline-inducible promoter[38] in the Δ*pylBCD* background, where the chromosomal
154 copy of *mttB1* would be prematurely truncated at the TAG codon (**Fig 3B)**. If Pyl (O) is
155 catalytically essential, then the mutant alleles of *mttB1* will not be able to rescue growth on TMA
156 (**Fig 3A, Table S6**). Indeed, neither the $mttB1_{O334A}$ nor the $mttB1_{O334K}$ mutants restored growth on
157 TMA (**Fig 3C, Fig S7, Table S6**). To control for polar effects caused by premature translational
158 termination of chromosomal *mttB1,* we jointly expressed $mttB1_{O334K}$ with its cognate corrinoid
159 containing protein, *mttC1*, and observed the same lethal phenotype (**Fig 3C, Fig S7, Table S6**).
160 Together these data affirm the hypothesis that Pyl is essential for the activity of methylamine
161 methyltransferases, which underlies the lethal phenotype for the Δ*pyl* mutants on TMA.

162 Next, to test the functionality of non-native Pyl machinery, we complemented each deletion
163 mutant with the *pyl* genes from *B. weybense* or ANME-3 S7 under the control of a tetracycline-
164 inducible promoter. Even when fully induced, *pylTS*, *pylBCD* or *pylTS*+*pylBCD* from *B. weybense*
165 were unable to restore growth on TMA (**Fig 3D**). Given that *pyl* genes from archaea have been
166 successfully expressed in bacteria[39], these data suggest that the *B. weybense* Pyl system is likely
167 non-functional. In contrast, *pylBCD* from ANME-3 S7 could restore growth of the Δ*pylBCD*
168 mutant on TMA (**Fig 3D, Table S6**). We tested both copies of the *pylT* locus (*pylT1* and *pylT2*)
169 from ANME-3 S7 with their cognate synthetase, and neither could support growth of the Δ*pylTS*
170 mutant on TMA (**Fig 3D**). In an alignment of ANME-3 S7 *pylT* sequences with *M. acetivorans*
171 *pylT,* we identified a 3bp insertion at the 3' end of the tRNA that could alter its secondary structure
172 and disrupt its function (**Fig 3E**). To test this hypothesis, we generated Δ3bp deletions of *pylT1*
173 and *pylT2* from ANME-3 S7 (**Fig 3D**) and introduced it with its cognate synthetase in *M.*
174 *acetivorans*. However, we were still unable to rescue growth on TMA. Altogether, our
175 heterologous expression platform suggests that only the Pyl biosynthetic machinery derived from
176 ANME-3 S7 is functional in *M. acetivorans*. However, despite retaining the capacity to produce
177 Pyl, it seems unlikely that ANME-3 S7 can incorporate it into proteins.

178 **The amber codon can be read as a stop or as a Pyl residue in *Methanosarcina acetivorans***

179 Although Pyl$^+$ genomes have lower TAG usage, it is not clear if this codon has been
180 obligately recoded to Pyl. Our genomic analyses show that *M. acetivorans* exists at an inflection
181 point on the spectrum of Pyl$^+$ genomes (**Fig 2D**), which uniquely positions it as a model system to
182 experimentally test for TAG recoding. To this end, we evaluated readthrough versus translational
183 termination at the TAG codon in RdmS, a non-essential Pyl-containing sensor kinase[34,40]. We fused
184 a 1xFLAG tag at the N-terminus of *rdmS* and expressed it *in trans* in either a Δ*rdmS* or a Δ*pylBCD*

185 background. In the latter, RdmS would be obligately truncated at the TAG codon located in its
186 second PAS domain (**Fig 4A**). As expected, we only detected this "short-form" protein of
187 approximately 25 kDa by α-FLAG western blot in the Δ*pylBCD* mutant (**Fig 4B, Fig S8**). In
188 contrast, both the "long -form" and "short -form" of FLAG-tagged RdmS were detected in the Pyl^+
189 Δ*rdmS* background (**Fig 4B, Fig S8**). Since a UAG codon retains the ability to recruit a release
190 factor for translation termination, even in the presence of Pyl-$tRNA^{Pyl}$, we searched for genes that
191 might use it as a bona fide stop codon in *M. acetivorans* (see Methods). One candidate is *rnfA*, a
192 membrane integral subunit of the energy conservation complex RNF[41,42]. If TAG is read as Pyl in
193 lieu of a stop, RnfA would have a putative 28 AA C-terminal extension. Yet, *rnfA* homologs across
194 *Methanosarcinaceae* lack the 28 AA C-terminal extension and use either TAA or TGA as a stop
195 codon instead (**Fig S9, Table S7**), supporting a stop interpretation for TAG in *rnfA* from *M.*
196 *acetivorans*. Taken together, these data support the hypothesis that the amber codon encodes a dual
197 meaning in *M. acetivorans*.

198 In the absence of any sequence-specific cues for conditional suppression of the amber
199 codon, we hypothesized that *M. acetivorans* might use the environmental context to dynamically
200 tune the expression of the *pyl* genes i.e. produce more *pyl* transcripts in the presence of
201 methylamines. Indeed, when we compare the global transcriptome, we observe that all *pyl* genes
202 are substantially upregulated on TMA compared to methanol (**Fig 4C**, **Table S8**). Interestingly,
203 even in the absence of TMA, *pylTS* is upregulated in the Δ*pylBCD* mutant and vice versa (**Fig 4C,**
204 **Table S8**). These transcriptional profiles suggest that the *pyl* genes are dynamically expressed
205 based on the cellular demand for Pyl in both a substrate-dependent and substrate-independent
206 manner.

207 **Archaeal release factor copy number is not correlated with Pyl**

208 Besides the expression of the *pyl* genes, the abundance and/or specificity of the archaeal
209 release factor, aRF1, could, in principle, bias translation termination of the amber codon. A
210 previous study showed that *Methanosarcina barkeri* has two copies of aRF1 and that one of them
211 recognizes all three stop codons *in vitro*[43]. *M. acetivorans* also encodes two copies of aRF1, aRF1-
212 1 (MA_RS00215) and aRF1-2 (MA_RS05270), but their functions have not been investigated.
213 Thus, we reasoned that Pyl^+ archaea might encode more than one aRF1, perhaps with distinct
214 affinities for stop codons and expression levels, which could bias how UAG is decoded. We
215 mapped the distribution of aRFs across all archaea and found that 4.3% of sampled genomes
216 encode two copies of aRF1 (n=81, **Table S9**). However, most Pyl^+ genomes with two copies of
217 aRF1 belong to the Genus *Methanosarcina* (**Table S9**). Thus, it is likely that the additional aRF1
218 copy in *Methanosarcina* spp. arose from gene duplication due to lineage-specific genome
219 expansion. Accordingly, we found that aRF1 copy number increases with genome size in archaea
220 (p=2e-21, **Fig S10A**), independent of predicted Pyl use (**Fig S10B**). Finally, our transcriptomics
221 analyses indicate that the aRF1 genes are constitutively expressed in *M. acetivorans* across all
222 tested conditions (**Fig S10C**). While our data do not rule out the possibility for post-transcriptional
223 regulation or differing affinities of aRF1s, it seems unlikely that aRF1 duplications play a universal
224 role in streamlining an ambiguous code in Pyl^+ archaea.

225 **Discussion – 971**

226 Pyl-based code expansion is a double-edged sword: the Pyl residue enables methylamine-
227 metabolism but also leads to ambiguous interpretation of the amber codon. Here, we outline two
228 co-occurring processes that allow Pyl^+ archaea to maintain Pyl in their proteome. First, the
229 acquisition of *pyl* genes selects for the genome-wide redistribution of stop codons to lower TAG
230 usage (**Fig 2**). This process is relatively swift and can be observed in archaea that have recently

231 gained Pyl, like *Hydrothermarchaeum profundi* (**Fig S1**), or in archaea that have recently lost Pyl,
232 like ANME-3 S7, which encodes partially functional *pyl* genes (**Fig 3D**), or the *Methanosarcina*
233 *spp.* that have entirely lost *pyl* genes (**Fig 2C**). Given the speed and ease at which this process
234 occurs, lowering TAG usage is likely the first step in maintaining Pyl.

235 Once TAG usage stabilizes, the ability to tolerate ambiguous decoding at all remaining
236 amber codons is essential to maintaining Pyl homeostasis. Using RdmS, a gene with an in-frame
237 TAG codon, we provide evidence that, at least in *M. acetivorans,* the amber codon can be
238 simultaneously read as both a sense and nonsense codon *in vivo* (**Fig 4**). These data reinforce
239 previous findings that show the co-existence of the extended and truncated forms of the Pyl-
240 containing monomethylamine-methyltransferases (MtmB) in *Methanosarcina barkeri* MS[33].
241 Hence, unlike Sec, an ambiguous code is not an evolutionary intermediate but an endpoint in Pyl-
242 mediated genetic code expansion.

243 To address how an ambiguous code might be tolerated, we present a heuristic model for *M.*
244 *acetivorans* using our transcriptome data. In the absence of a sequence-specific suppression
245 mechanism, we assume that the likelihood of readthrough and truncation are equal for all UAG-
246 containing transcripts in the cell. Hence, we can define readthrough efficiency for a given UAG-
247 containing transcripts as the ratio of the readthrough rate to the truncation rate, which is
248 proportional to the ratio of Pyl supply and demand in the cell, respectively (see Methods). We can
249 estimate Pyl supply by measuring the abundance of transcripts for the *pyl* genes, and Pyl demand
250 by measuring the total number of UAG-containing transcripts (Eq. 1, see methods, FPKM:
251 fragments per kilobase per million mapped reads):

252 $$readthrough\ efficiency = \frac{readthrough\ rate}{truncation\ rate} \propto \frac{Pyl\ supply}{Pyl\ demand} \propto \frac{FPKM_{Pyl\ transcripts}}{\sum FPKM_{UAG\ transcripts}} \quad (1)$$

253 Based on equation 1, the readthrough efficiency is *ca.* two-times higher on methanol than on TMA
254 i.e. there is a higher fraction of the long-form of the protein for all UAG-containing transcripts on
255 methanol than on TMA (**Table S10**). At first glance, this outcome might seem counterintuitive, as
256 the cells needs to produce Pyl-containing methylamine methyltransferases on TMA. However, a
257 4.0-fold increase in expression of the *pyl* genes (i.e. Pyl supply) is far surpassed by the dramatic
258 increase in UAG-containing transcripts (i.e. Pyl demand) on TMA, *ca.* 188.0-fold, primarily due
259 to the upregulation of methylamine methyltransferases (**Fig 4C, Table S8**). Hence, even though
260 Pyl supply increases during growth on TMA, its demand far outpaces its supply, leading to lower
261 readthrough efficiency (**Fig. 5**).

262 In our Δ*pylBCD* and Δ*pylTS* knockouts, we eliminate Pyl supply and effectively reduce the
263 readthrough efficiency to zero. Under this regime, we observe that *pylBCD* is upregulated in the
264 absence of *pylTS*, and vice versa, on methanol (**Fig 3C**). While the cue(s) leading to an
265 upregulation of the complementary *pyl* genes in the knockout mutants is unknown, we rule out
266 sensing of free Pyl, as the transcriptomes of Δ*pylBCD* and Δ*pylTS* are nearly overlapping (**Table**
267 **S8**). Instead, we hypothesize that these transcriptional changes stem from an inability to
268 incorporate Pyl in a UAG-containing transcript, i.e. by sensing a diminishingly low readthrough
269 efficiency. This artificially low readthrough efficiency, and its resulting transcriptional response,
270 is likely akin to what occurs in wildtype cells upon initial exposure to TMA. Here, the rapid
271 increase in demand for Pyl (due to expression of methylamine methyltransferases) results in a
272 transiently low readthrough efficiency, which is partially recovered by increased expression in *pyl*
273 genes (**Fig 5**).

274 Given the enrichment of TAG codons in genes with proposed regulatory function, one
275 hypothesis for how cells sense readthrough efficiency is through a Pyl-containing repressor that is

active when there is readthrough and inactive in its truncated form. In this scenario, high readthrough efficiency on methanol maintains the repressor in its elongated form and partially represses *pyl* genes. In contrast, during growth on TMA, the repressor is prematurely truncated at its UAG site, which results in de-repression of *pyl* genes (**Fig 5**). Therefore, when we impose a readthrough efficiency of zero through deletion of either *pylTS* or *pylBCD,* the repressor is fully inactive. This leads to a TMA-like transcriptional response on methanol, complete with upregulation of the remaining *pyl* genes and methylamine methyltransferases (**Fig 4C, Table S8**). Alternately, other mechanisms like attenuation or transcript stability may play a role in regulation too. It is worth noting that *pylB* has an in-frame TAG codon at the C-terminus. While the functional consequence (if at all) of Pyl in $PylB^{34}$ is unknown, it is tempting to hypothesize that it plays a role in tuning Pyl biosynthesis.

Our model also explains the counterintuitive growth data wherein overexpression of the *pyl* genes is tolerated on methanol but leads to a growth defect on TMA (**Fig 3A**). An increase in Pyl supply likely elevates the readthrough efficiency across all growth conditions. This is tolerated on methanol since the readthrough efficiency is already high. In contrast, on TMA, where the readthrough efficiency is low, elevated Pyl incorporation in some UAG-containing transcripts might lead to a buildup of the "long form" of certain proteins that are detrimental to growth.

Altogether, we propose that Pyl^{+} archaea, like *M. acetivorans,* are expert funambulists that navigate the tightrope of Pyl homeostasis through transcriptional regulation of Pyl supply and demand. While we cannot rule out unknown mechanisms for sequence-specific Pyl insertion, we show that the ambiguity imposed by its presence can be tolerated successfully.

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Author contributions

KS was involved in conceptualization, data curation, formal analysis, methodology, investigation, validation, visualization, writing – original draft preparation, and writing – review and editing.

GLC was involved in conceptualization, methodology, investigation, writing – original draft preparation, and writing – review and editing.

PIP was involved in conceptualization, methodology.

PHW and VJO provided resources.

319 DDN was involved in conceptualization, data curation, funding acquisition, investigation,
320 methodology, project administration, resources, supervision, validation, writing – original draft
321 preparation, and writing – review and editing.

322 **Data availability statement**

323 Sequencing data have been deposited in the Sequencing Reads Archive and the BioProject number
324 will be made available upon publication. All other data generated in this study are provided in the
325 manuscript.

326 **Declaration of interests**

327 The authors declare no competing interests.

328 **Methods**

329 **Bioinformatic screen for Pyl and Pyl-associated genes**

330 All archaeal genomes from GTDB Release 214.0[44] were annotated with Prokka[45] v.1.14.6 using
331 the prokaryotic genetic code 11 to identify homologs of the Pyl biosynthetic genes (*pylBCD*), Pyl
332 incorporation gene (*pylS*), methyl-coenzyme M reductase catalytic subunits (*mcrABG*),
333 component A2, and methylamine-specific methyltransferases (*mttB, mtbB,* and *mtmB*). The Pyl-
334 $tRNA^{Pyl}$ sequences (*pylT*) were predicted in the Prokka pipeline using Aragorn[46], and hits were
335 counted for each genome using a custom script that can be found at https://github.com/kshalv/pyl.
336 Gene identification was performed using a command line tool developed for automated gene
337 searching with profile HMM's (accessions can be found in **Table S12**) using the 'hmm' option, as
338 previously described in [47] and can be found at: https://github.com/kshalv/hmm_tools. Pyl^+
339 genomes were strictly defined as those containing a full suite of biosynthetic genes (*pylBCD*) and
340 incorporation genes (*pylS*, *pylT*). In principle, a genome with just *pylTS* (0.2% of genomes) could
341 be Pyl^+ but there are no known Pyl transporters, so we also classified this group as Pyl^-.

342 **Phylogenetic analyses**

343 Phylogenetic trees depicted in **Fig 1C**, **Fig S1**, **Fig S2**, and **Fig S3** were generated using ete3 and
344 a custom python script to parse the ar53_r214.tree available through Genome Taxonomy Database
345 (GTDB). Genomes with a checkM ≥90% were used for all trees except for Fig S1 for which
346 genomes with a checkM completeness scores of ≥80% were used. The CheckM score was
347 calculated using a concatenated biomarker set described in [44]. The trees depicted in all figures,
348 except for Fig S3-S5, were visualized using iTol v7.1[48]. Genomic neighborhood diagrams for genes
349 +/- 7.5 kb up and downstream of *pylB* in Fig. S3 were generated using BioPython and overlaid on
350 the GTDB tree using a custom script found at https://github.com/kshalv/pyl. Amino acid sequences
351 used to generate gene trees for the Pyl biosynthetic and incorporation machinery within the Family
352 *Methanosarcinaceae* were extracted from the corresponding GTDB 214.0 genomes (code 11)
353 using the 'seq' option of the hmm_tools CLI described above with the 'trusted cutoff' threshold.
354 Sequences were aligned using MAFFT and trimmed to 90% with TrimAl. The trimmed alignments
355 were then concatenated using a custom script (https://github.com/kshalv/pyl). Gene trees were
356 generated using the Geneious RAxML plug-in 8.2.11 and GAMMA BLOSUM62 substitution
357 matrix with n_bootstraps=100. The 16S rRNA tree for the Family *Methanosarcinaceae* was
358 generated using an alignment provided in GTDB r214.0 and assembled using the Geneious
359 RAxML 8.2.11 plug-in. Tanglegrams were visualized using Dendroscope 3.5.9[49]. Sequences used
360 to generate methyltransferase gene trees were extracted using the protocol described above from
361 GTDB 214.0 genomes (annotated to code 15, with TAG recoding to Pyl using a custom script
362 (https://github.com/kshalv/pyl). Sequences were dereplicated to 90% sequence identity using
363 MMSeqs2[50] easy-cluster. The tree was built using the Geneious RAxML 8.2.11 plug-in and was
364 rooted to the methanol-specific methyltransferase family in iTol (v 7.1).

365 **Evaluation of stop codon usage and GC content**

366 Stop codon usage was calculated for all genomes available in GTDB 214.0 using BioPython to
367 extract the last three nucleotides of each annotated open reading frame (i.e., "CDS" designation)
368 in the corresponding code 11 Genbank files generated by Prokka's annotation pipeline. Usage for
369 each stop codon was calculated as a fraction of the total number of predicted stop codons and was
370 recorded for each genome. The GC content for each genome was derived from GTDB r214.0
371 metadata. Taxonomic groups were classified by binning accessions in accordance with the
372 taxonomy designated by GTDB 214.0. All genomes used in this analysis exceeded a checkM
373 genome completeness score of ≥90%. A Welch's t-test was performed for each comparison group
374 depicted in Figure 2 using the scipy.stats Python package.

375 **Identification of putative Pyl-containing proteins**

376 Predictions for putative Pyl containing proteins were performed for each genome predicted to be
377 Pyl^+ based on the presence of 2/3 Pyl biosynthetic genes, the presence of *pylS,* and *pylT*. Each Pyl^+
378 genome was reannotated using the Blepharisma Nuclear Code (code 15) in Prokka v1.14.6,
379 effectively recoding each TAG codon to Glutamine (Gln, Q). For each genome, we identified
380 putative Pyl proteins using a custom script, where CDS's containing an in-frame 'TAG' codon
381 were defined as putative Pyl proteins. For each Pyl protein, extension length was calculated as the
382 difference between total length of the protein and the 'TAG' position and recorded in a genome-
383 specific CSV file. We recorded the total number of putative Pyl proteins, the average and median
384 extension lengths, and the density of putative Pyl proteins (i.e., normalized Pyl hits per Mb) for
385 each genome. A CDS containing the TAG codon as putative stop codon was identified as a
386 sequence where TAG readthrough results in a >5 AA extension for which there is 1) no predictable
387 domain, and 2) is absent in sequence homologs.

388 **Media and culture conditions**

389 All *Methanosarcina acetivorans* strains were grown without shaking at 37°C in bicarbonate-
390 buffered high salt (HS) liquid medium containing either 50 mM trimethylamine hydrochloride
391 (TMA) or 125 mM methanol as growth substrates. All growth substrates were added to the medium
392 prior to sterilization, along with NH_4Cl, Cysteine-HCl, and $Na_2S.9H_2O$ to final concentrations of
393 19 mM, 2.8 mM, and 0.4 mM, respectively. Each strain was grown in a hermetically sealed Balch
394 tube with N_2/CO_2 (80%/20%) in the headspace at 8-10 psi. All *Escherichia coli* strains were grown
395 in lysogeny broth (LB) with antibiotic concentrations of 20 µg/mL chloramphenicol and/or 25
396 µg/mL kanamycin.

397 **Plasmid construction**

398 Plasmids for Cas9-mediated genome editing were designed using the method previously described
399 in [36]. PCR fragments containing the promoter (P_{mtaCB1}), scaffolds, and terminator (T_{mtaCB1}), were
400 amplified with overhangs containing single guide RNAs (sgRNAs) that target Pyl genes
401 (Δ*pylBCD,* MA_RS00820-MA_RS00810; Δ*pylTS* MA_RS00815). All sgRNAs were designed
402 using the CRISPR site finder tool in Geneious Prime version 2023.2.1 and are provided in **Table**
403 **S12**. PCR fragments containing the sgRNA scaffold were assembled into pDN201 linearized with
404 *AscI* using the Gibson assembly method described previously in [51]. The repair template was
405 assembled into the sgRNA containing derivative of pDN201 at the *PmeI* site. All complementation
406 constructs were built using either pJK027A or pJK029A as described in **Table S12**. PCR fragments
407 containing the genes of interest and if applicable, affinity-purification tags, were fused to the
408 appropriate tetracycline-inducible promoter (**Table S12**) by linearizing pJK027A or pJK029A with
409 *NdeI* and *HindIII*. Cointegrates of all plasmids with pAMG40 for expression in *M. acetivorans*
410 were obtained using the Gateway BP Clonase II Enzyme Mix (Thermo Fisher, Waltham, MA,

411 USA) and verified by restriction endonuclease digest. All cloning was performed in WWM4489[52],
412 a DH10B derivative, which was transformed by electroporation at 1.8 kV using an *E. coli* Gene
413 Pulser (Bio-Rad, Hercules, USA), and the growth medium was supplemented with 10 mM
414 Rhamnose to induce copy number as previously described [52]. All plasmids were extracted using
415 Zyppy Miniprep Kit (Zymo Research, Tustin, CA, USA) and verified by Sanger sequencing at the
416 UC Berkeley DNA Sequencing Facility. All primers and plasmids used in this study are listed in
417 **Table S12** and **Table S13**, respectively.

418 ***Methanosarcina acetivorans* mutant generation**

419 Liposome-mediated transformation was used to generate *M. acetivorans* mutants as previously
420 described in [53]. Briefly, 20 mL cultures of *M. acetivorans* were grown in HS-Methanol (MeOH)
421 medium until they reached mid-late exponential phase and were harvested for transformation.
422 Transformants were plated and selected for on agar-solidified HS medium with 125 mM MeOH
423 and 2 µg/mL puromycin. Plates were incubated in an intra-chamber anaerobic incubator
424 maintained at 37°C with $N_2/CO_2/H_2S$ (1000 ppm/20%/balance) in the headspace. For all
425 complementation strains, plasmids were screened by PCR and resulting products were verified by
426 Sanger sequencing at the UC Berkeley DNA Sequencing Facility. For deletion mutants, individual
427 colonies were picked and screened at the chromosomal locus using primers designated in **Table**
428 **S12** for the desired mutation. Colonies that were positive for the desired mutation were then
429 streaked on solid HS-MeOH medium with 20 µg/mL 8ADP (Carbosynth, San Diego, CA, USA)
430 to cure the plasmid; single plasmid cured colonies were screened for the absence of the *pac* gene
431 on the mutagenic plasmid with PCR. Chromosomal deletion mutants were sent for whole genome
432 re-sequencing (described below) to screen for the deletion and suppressor mutations elsewhere on
433 the chromosome. All strains used and generated in this study are listed in **Table S14**.

434 **DNA extraction and sequencing**

435 Genomic DNA for whole genome re-sequencing of deletion strains was extracted from 10 mL of
436 stationary phase culture of the *M. acetivorans* strain using the Qiagen blood and tissue kit
437 following the manufacturer's instructions (Qiagen, Hilden, Germany). Genomic DNA was sent to
438 SeqCenter (Pittsburgh, PA) where it was further processed using the Illumina DNA Prep kit and
439 sequenced (150 bp paired end reads). Sequencing reads were mapped to the *M. acetivorans* C2A
440 reference genome using breseq[54] version 0.35.5 using default parameters. All mutations identified
441 through this analysis are listed in **Table S5**. Illumina sequencing reads for DDN121 (Δ*pylBCD*),
442 and DDN146 (Δ*pylTS*) have been deposited in the Sequencing Reads Archive (SRA) and the
443 project number will be made available upon publication.

444 **Cultivation for growth assays**

445 All growth curves generated for this work were performed by pre-culturing strains in 10 mL HS-
446 MeOH media at 37°C without shaking (HeraTherm General Protocol Microbiological Incubator,
447 Thermo Fisher Scientific, Waltham, MA, USA) in hermetically sealed Balch tubes with N_2/CO_2
448 (80%/20%) in the headspace at 8-10 psi. All growth experiments were inoculated with 500 µl of
449 the pre-culture at late exponential phase (OD_{600} ~0.9-1.0). Growth of three independent biological
450 replicates was measured by monitoring the optical density of cultures at 600 nm using a UV-Vis
451 Spectrophotometer (Genesys 50, Thermo Fisher Scientific, Waltham, MA, USA) with an
452 uninoculated "blank" containing 10 mL HS medium with the appropriate growth substrate. All
453 strains harboring a plasmid for gene expression *in trans* also contained 2 µg/mL puromycin in the
454 medium for plasmid maintenance and 100 µg/mL tetracycline for promoter induction. All cultures
455 with tetracycline were wrapped in aluminum foil to prevent degradation over time. Growth rates

456 were calculated as the slope of the linear fit of the log-transformed optical density versus time plot
457 with a minimum five points with the highest R^2 value (minimum cut-off ≥0.95).

458 **RNA extraction, sequencing, and analysis**

459 10 mL cultures of WWM60 (parental strain), DDN121 (Δ*pylBCD*), and DDN146 (Δ*pylTS*) were
460 grown in triplicate on HS + 125 mM MeOH at 37˚C; an additional triplicate set of WWM60 was
461 grown on HS+ 50 mM TMA at 37˚C. When cultures reached mid-exponential phase (OD_{600}~ 0.45-
462 0.65), 1 mL culture was removed for RNA extraction and mixed 1:1 with Trizol (Life Technologies,
463 Carslbad, CA, USA) that was pre-warmed to 37˚C. After a five-minute incubation at room
464 temperature, 2 mL of 100% ethanol was added to each sample and RNA extraction was performed
465 according to the manufacturer's instructions using the Qiagen RNeasy Mini Kit (Qiagen, Hilden,
466 Germany). RNA concentration was determined using Nanodrop One UV Spectrophotometer
467 (Thermo Fisher Scientific, Waltham, MA, USA) before storage at -80˚C. Samples were sent to
468 SeqCenter (Pittsburg, PA) where each replicate underwent DNase treatment, rRNA depletion,
469 library preparation, and Illumina paired-end sequencing (600 bp read length). Transcriptome
470 analysis was performed using the KBase bioinformatics platform. Raw transcript reads (in FastQ
471 format) were used as an input for read alignment to the *M. acetivorans* C2A reference genome
472 using HISAT2 (v.2.1.0). The resulting read alignment was assembled using Cufflinks (v.2.2.1) and
473 fold changes, significance values were calculated using DESeq2 (v.1.20.0). We considered changes
474 in transcript abundance between pairwise comparison to be significantly differentially expressed
475 if they exceeded a $\log_2$ fold change of ±2.0 and a *q*-value of ≤0.05. All DESeq2 data is recorded
476 in **Table S7**. Raw transcript reads for DDN121 and DDN146 have been deposited in Sequencing
477 Read Archive (SRA) and the project number will be made available upon publication; raw
478 transcript reads for WWM60 grown on MeOH and on TMA have been deposited in the SRA.

479 **Immunoblotting of FLAG-tagged proteins**

480 Immunoblotting was performed with cell lysates from a 10 mL culture in HS medium + 125 mM
481 MeOH grown to late-exponential phase (OD600 ~0.9-1.0). For strains harboring plasmids with
482 tetracycline inducible genes, 2 µg/mL puromycin was added to maintain the plasmid and 100
483 µg/mL tetracycline was added to induce gene expression. Crude cell lysates were prepared from
484 cultures using the method described in [51, 55]. Briefly, the culture was spun down at 5,000 x *g* at
485 4˚C for 10 minutes using the Sorvall Legend XTR centrifuge (Thermo Fischer Scientific, Waltham,
486 MA, USA). The culture supernatant was decanted, and the pellets were resuspended in 200 µL
487 lysis buffer (50 mM Na_2HPO_4) and kept on ice for ten minutes prior to adding 1 µL of DNase
488 along with 12 µl 5M NaCl. After mixing gently, the lysate was stored at room temperature for two
489 minutes prior to centrifugation at 14,000 x *g* for ten minutes twice to obtain cleared lysate. Near-
490 equal loading of 30 µg of protein was estimated using Bradford reagent (Sigma-Aldrich, St Louis,
491 MO) with bovine serum albumin (BSA) standards per the manufacturer's instructions. Cell lysates
492 were run on a 12% mini-Protean TGX Gels (Bio-Rad, Hercules, USA) and transferred to a Trans-
493 Blot Turbo Mini 0.2 µM PVDF membrane using the Bio-Rad Trans-Blot Turbo Transfer System
494 (Bio-Rad, Hercules, USA). FLAG-tagged proteins were probed by immunoblotting using
495 monoclonal anti-FLAG M2-Peroxidase (HRP) antibody (Sigma-Aldrich, St Louis, MO, USA) at
496 a 1/50,000x dilution. Subsequent signal detection was performed using Immobilon Western
497 Chemiluminescent HRP Substrate (Millipore, Burlington, MA, USA). Imaging was performed
498 with ChemiDoc MP Imaging System (Bio-Rad, Hercules, CA, USA) with a 1 second exposure
499 time. Imaging was also performed with a 13.5 second exposure time and a paper towel occluding
500 the high molecular weight portion of the gel to gain better resolution of the short form RdmS bands
501 in **Fig 4**. Coomassie blue dye (Thermo Fisher, Waltham, MA, USA) was used to evaluate near-

502 equal loading of all cell lysates. All blots and Coomassie stained gel images are available in **Fig**
503 **S8**.

504 **Readthrough efficiency calculation**

505 We generated Eq. 1 by representing the rates of readthrough and truncation for the cellular
506 proteome assuming second order kinetics as described in Eqs. 2 and 3. The rate of readthrough of
507 any UAG codons in the cell depends on the concentration of Pyl-tRNA^{Pyl}, the number of UAG-
508 containing transcripts, and the rate constant $k_{readthrough}$ as shown in Eq. 2. The rate of truncation of
509 any UAG codon is a function of archaeal release factor (aRF1) concentration, the number of UAG-
510 containing transcripts, and the rate constant $k_{truncation}$ as shown in Eq. 3.

511 $$\frac{d[readthrough]}{dt} = k_{readthrough}[Pyl \cdot tRNA^{Pyl}][UAG\ transcript] \quad (2)$$

512 $$\frac{d[truncation]}{dt} = k_{truncation}[aRF1][UAG\ transcript] \quad (3)$$

513 The rate of change of Pyl-tRNA^{Pyl} can be described by:

514 $$\frac{d[Pyl \cdot tRNA^{Pyl}]}{dt} = k_{production}[Pyl][tRNA^{Pyl}] - k_{readthrough}[Pyl \cdot tRNA^{Pyl}][UAG\ transcript] \quad (4)$$

515 Where the first term on the right side of Eq. 4 represents the rate of production of Pyl-tRNA^{Pyl} and
516 is dependent on the concentration of free pyrrolysine [Pyl], the uncharged tRNA^{pyl} [tRNA^{pyl}] and
517 the rate constant $k_{production}$. The second term on the right represents the rate of consumption of Pyl-
518 tRNA^{Pyl} due to readthrough of a UAG codon (i.e. the readthrough rate, Eq. 2). If we assume steady
519 state concentrations of Pyl-tRNA^{Pyl} during growth on a given substrate then the production and
520 consumption of Pyl-tRNA^{Pyl} are balanced, i.e.:

521 $$k_{production}[Pyl][tRNA^{Pyl}] = k_{readthrough}[Pyl \cdot tRNA^{Pyl}][UAG\ transcript] \quad (5)$$

522 To determine the readthrough efficiency, we take the ratio of the readthrough rate—equivalent to
523 the production rate in steady state (Eq. 5)—over the truncation rate (Eq. 3), yielding Eq. 6.

$$readthrough\ efficiency = \frac{readthrough\ rate}{truncation\ rate} = \frac{Production\ rate}{k_{truncation}[aRF1][UAG\ transcript]} \quad (6)$$

Since we observe that aRF1 transcription does not significantly change between MeOH and TMA growth conditions (**Fig S10C**, **Table S8**), we assume $k_{truncation}$[aRF1] remains constant and find that:

$$\frac{readthrough\ efficiency\ (MeOH)}{readthrough\ efficiency\ (TMA)} \propto \left(\frac{Production\ rate\ MeOH}{Production\ rate\ TMA}\right) \times \left(\frac{[UAG\ transcript]\ TMA}{[UAG\ transcript]\ MeOH}\right) \quad (7)$$

We refer to the Pyl-tRNA^{Pyl} production rate as the "Pyl supply" and estimate this value to be proportional to the FPKM (fragments per kilobase per million mapped reads) of the *pyl* genes for a given condition. We refer to the concentration of UAG transcripts as the "Pyl demand" and estimate it as the sum FPKM values for transcripts containing a UAG, using gene IDs identified in our Pyl ID script, for a given condition. This leads us from Eq. 7 to the relationship represented in Eq. 1 and illustrated in **Fig. 5**. This heuristic model for readthrough efficiency allows us to compare the ratio of Pyl-containing proteins to their truncated counterparts without quantifying the precise proportion of readthrough to truncation in any single condition. All FPKM values can be found in **Table S10**, along with the calculations used to determine ratio of readthrough efficiencies between substrates.

Data and code availability

Raw Illumina reads associated genome-wide DNA and RNA sequencing have been deposited to the Sequencing Reads Archive (SRA) and the project number will be made available upon publication. All custom scripts described can be found at the following repository: https://github.com/kshalv/pyl.

References

1. Crick, F. H. C. The origin of the genetic code. *J. Mol. Biol.* **38**, 367–379 (1968).
2. Preer, J. R., Preer, L. B., Rudman, B. M. & Barnett, A. J. Deviation from the universal code shown by the gene for surface protein 51A in Paramecium. *Nature* **314**, 188–190 (1985).

3. Yamao, F. *et al.* UGA is read as tryptophan in Mycoplasma capricolum. *Proc. Natl. Acad. Sci.* **82**, 2306–2309 (1985).
4. Shulgina, Y. & Eddy, S. R. A computational screen for alternative genetic codes in over 250,000 genomes. *eLife* **10**, e71402 (2021).
5. Campbell, J. H. *et al.* UGA is an additional glycine codon in uncultured SR1 bacteria from the human microbiota. *Proc. Natl. Acad. Sci.* **110**, 5540–5545 (2013).
6. Meng, K., Chung, C. Z., Söll, D. & Krahn, N. Unconventional genetic code systems in archaea. *Front. Microbiol.* **13**, 1007832 (2022).
7. Kivenson, V. *et al.* Sporadic distribution of a new archaeal genetic code with all TAG codons as pyrrolysine. 2024.09.30.615893 Preprint at https://doi.org/10.1101/2024.09.30.615893 (2024).
8. Santos, M. A., Keith, G. & Tuite, M. F. Non-standard translational events in Candida albicans mediated by an unusual seryl-tRNA with a 5′-CAG-3′ (leucine) anticodon. *EMBO J.* **12**, 607–616 (1993).
9. Borges, A. L. *et al.* Widespread stop-codon recoding in bacteriophages may regulate translation of lytic genes. *Nat. Microbiol.* **7**, 918–927 (2022).
10. Ling, J., O'Donoghue, P. & Söll, D. Genetic code flexibility in microorganisms: novel mechanisms and impact on physiology. *Nat. Rev. Microbiol.* **13**, 707–721 (2015).
11. Evans, R. M. *et al.* Selective cysteine-to-selenocysteine changes in a [NiFe]-hydrogenase confirm a special position for catalysis and oxygen tolerance. *Proc. Natl. Acad. Sci.* **118**, e2100921118 (2021).
12. Kim, H.-Y. & Gladyshev, V. N. Different Catalytic Mechanisms in Mammalian Selenocysteine- and Cysteine-Containing Methionine-R-Sulfoxide Reductases. *PLOS Biol.* **3**, e375 (2005).
13. Hao, B. *et al.* A New UAG-Encoded Residue in the Structure of a Methanogen Methyltransferase. *Science* **296**, 1462–1466 (2002).
14. Li, J. *et al.* Insights into pyrrolysine function from structures of a trimethylamine methyltransferase and its corrinoid protein complex. *Commun. Biol.* **6**, 1–10 (2023).
15. Berry, M. J. *et al.* Recognition of UGA as a selenocysteine codon in Type I deiodinase requires sequences in the 3′ untranslated region. *Nature* **353**, 273–276 (1991).
16. Leibundgut, M., Frick, C., Thanbichler, M., Böck, A. & Ban, N. Selenocysteine tRNA-specific elongation factor SelB is a structural chimaera of elongation and initiation factors. *EMBO J.* **24**, 11–22 (2005).
17. Zhang, Y., Baranov, P. V., Atkins, J. F. & Gladyshev, V. N. Pyrrolysine and selenocysteine use dissimilar decoding strategies. *J. Biol. Chem.* **280**, 20740–20751 (2005).
18. Gaston, M. A., Zhang, L., Green-Church, K. B. & Krzycki, J. A. The complete biosynthesis of the genetically encoded amino acid pyrrolysine from lysine. *Nature* **471**, 647–650 (2011).
19. Polycarpo, C. *et al.* An aminoacyl-tRNA synthetase that specifically activates pyrrolysine. *Proc. Natl. Acad. Sci.* **101**, 12450–12454 (2004).
20. Guo, L.-T. *et al.* Ancestral archaea expanded the genetic code with pyrrolysine. *J. Biol. Chem.* **298**, 102521 (2022).
21. Sun, J. *et al.* Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. *ISME Commun.* **1**, 30 (2021).
22. Woods, P. H. *et al.* Convergence and horizontal gene transfer drive the evolution of anaerobic methanotrophy in archaea. 2024.05.23.595608 Preprint at https://doi.org/10.1101/2024.05.23.595608 (2024).

23. Brugère, J.-F., Atkins, J. F., O'Toole, P. W. & Borrel, G. Pyrrolysine in archaea: a 22nd amino acid encoded through a genetic code expansion. *Emerg. Top. Life Sci.* **2**, 607–618 (2018).
24. Kivenson, V., Paul, B. G. & Valentine, D. L. An Ecological Basis for Dual Genetic Code Expansion in Marine Deltaproteobacteria. *Front. Microbiol.* **12**, 680620 (2021).
25. Prat, L. *et al.* Carbon source-dependent expansion of the genetic code in bacteria. *Proc. Natl. Acad. Sci.* **109**, 21070–21075 (2012).
26. Rinke, C. *et al.* A standardized archaeal taxonomy for the Genome Taxonomy Database. *Nat. Microbiol.* **6**, 946–959 (2021).
27. Srinivasan, G., James, C. M. & Krzycki, J. A. Pyrrolysine Encoded by UAG in Archaea: Charging of a UAG-Decoding Specialized tRNA. *Science* **296**, 1459–1462 (2002).
28. Krzycki, J. A. The direct genetic encoding of pyrrolysine. *Curr. Opin. Microbiol.* **8**, 706–712 (2005).
29. Blight, S. K. *et al.* Direct charging of tRNA(CUA) with pyrrolysine in vitro and in vivo. *Nature* **431**, 333–335 (2004).
30. Borrel, G. *et al.* Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. *Nat. Microbiol.* **4**, 603–613 (2019).
31. Galagan, J. E. *et al.* The Genome of M. acetivorans Reveals Extensive Metabolic and Physiological Diversity. *Genome Res.* **12**, 532–542 (2002).
32. Li, J., Zhou, J., Wu, Y., Yang, S. & Tian, D. GC-Content of Synonymous Codons Profoundly Influences Amino Acid Usage. *G3 GenesGenomesGenetics* **5**, 2027–2036 (2015).
33. James, C. M., Ferguson, T. K., Leykam, J. F. & Krzycki, J. A. The Amber Codon in the Gene Encoding the Monomethylamine Methyltransferase Isolated from Methanosarcina barkeri Is Translated as a Sense Codon *. *J. Biol. Chem.* **276**, 34252–34258 (2001).
34. O'Donoghue, P. *et al.* Reducing the genetic code induces massive rearrangement of the proteome. *Proc. Natl. Acad. Sci.* **111**, 17206–17211 (2014).
35. Chadwick, G. L. *et al.* Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. *PLOS Biol.* **20**, e3001508 (2022).
36. Nayak, D. D. & Metcalf, W. W. Cas9-mediated genome editing in the methanogenic archaeon Methanosarcina acetivorans. *Proc. Natl. Acad. Sci.* **114**, 2976–2981 (2017).
37. Mahapatra, A. *et al.* Characterization of a Methanosarcina acetivorans mutant unable to translate UAG as pyrrolysine. *Mol. Microbiol.* **59**, 56–66 (2006).
38. Guss, A. M., Rother, M., Zhang, J. K., Kulkkarni, G. & Metcalf, W. W. New methods for tightly regulated gene expression and highly efficient chromosomal integration of cloned genes for Methanosarcina species. *Archaea* **2**, 193–203 (2008).
39. Longstaff, D. G. *et al.* A natural genetic code expansion cassette enables transmissible biosynthesis and genetic encoding of pyrrolysine. *Proc. Natl. Acad. Sci.* **104**, 1021–1026 (2007).
40. Fiege, K. & Frankenberg-Dinkel, N. Thiol-based redox sensing in the methyltransferase associated sensor kinase RdmS in Methanosarcina acetivorans. *Environ. Microbiol.* **21**, 1597–1610 (2019).
41. Downing, B. E. & Nayak, D. D. Innovations in the electron transport chain fuel archaeal methane metabolism. *Trends Biochem. Sci.* **50**, 425–437 (2025).
42. Kumar, A. *et al.* Molecular principles of redox-coupled sodium pumping of the ancient Rnf machinery. *Nat. Commun.* **16**, 2302 (2025).

43. Alkalaeva, E. *et al.* Translation termination in pyrrolysine-utilizing archaea. *FEBS Lett.* **583**, 3455–3460 (2009).
44. Parks, D. H. *et al.* GTDB: an ongoing census of bacterial and archaeal diversity through a phylogenetically consistent, rank normalized and complete genome-based taxonomy. *Nucleic Acids Res.* **50**, D785–D794 (2022).
45. Seemann, T. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* **30**, 2068–2069 (2014).
46. Laslett, D. & Canback, B. ARAGORN, a program to detect tRNA genes and tmRNA genes in nucleotide sequences. *Nucleic Acids Res.* **32**, 11–16 (2004).
47. Chadwick, G. L., Williams, M. C., Shalvarjian, K. E. & Nayak, D. D. Methanogenesis marker 16 metalloprotein is the primary coenzyme M synthase in Methanosarcina acetivorans. *PLOS Genet.* **21**, e1011695 (2025).
48. Letunic, I. & Bork, P. Interactive Tree of Life (iTOL) v6: recent updates to the phylogenetic tree display and annotation tool. *Nucleic Acids Res.* **52**, W78–W82 (2024).
49. Huson, D. H. *et al.* Dendroscope: An interactive viewer for large phylogenetic trees. *BMC Bioinformatics* **8**, 460 (2007).
50. Steinegger, M. & Söding, J. MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. *Nat. Biotechnol.* **35**, 1026–1028 (2017).
51. Nayak, D. D. & Metcalf, W. W. Genetic techniques for studies of methyl-coenzyme M reductase from Methanosarcina acetivorans C2A. in *Methods in Enzymology* vol. 613 325–347 (Elsevier, 2018).
52. Kim, S. Y. *et al.* Different Biosynthetic Pathways to Fosfomycin in Pseudomonas syringae and Streptomyces Species. *Antimicrob. Agents Chemother.* **56**, 4175–4183 (2012).
53. Metcalf, W. W., Zhang, J. K., Apolinario, E., Sowers, K. R. & Wolfe, R. S. A genetic system for Archaea of the genus Methanosarcina: Liposome-mediated transformation and construction of shuttle vectors. *Proc. Natl. Acad. Sci.* **94**, 2626–2631 (1997).
54. Deatherage, D. E. & Barrick, J. E. Identification of mutations in laboratory evolved microbes from next-generation sequencing data using breseq. *Methods Mol. Biol. Clifton NJ* **1151**, 165–188 (2014).
55. Chadwick, G. L., Dury, G. A. & Nayak, D. D. Physiological and transcriptomic response to methyl-coenzyme M reductase limitation in Methanosarcina acetivorans. *Appl. Environ. Microbiol.* **90**, e02220-23.
56. Bose, A., Kulkarni, G. & Metcalf, W. W. Regulation of putative methyl-sulphide methyltransferases in Methanosarcina acetivorans C2A. *Mol. Microbiol.* **74**, 227–238 (2009).

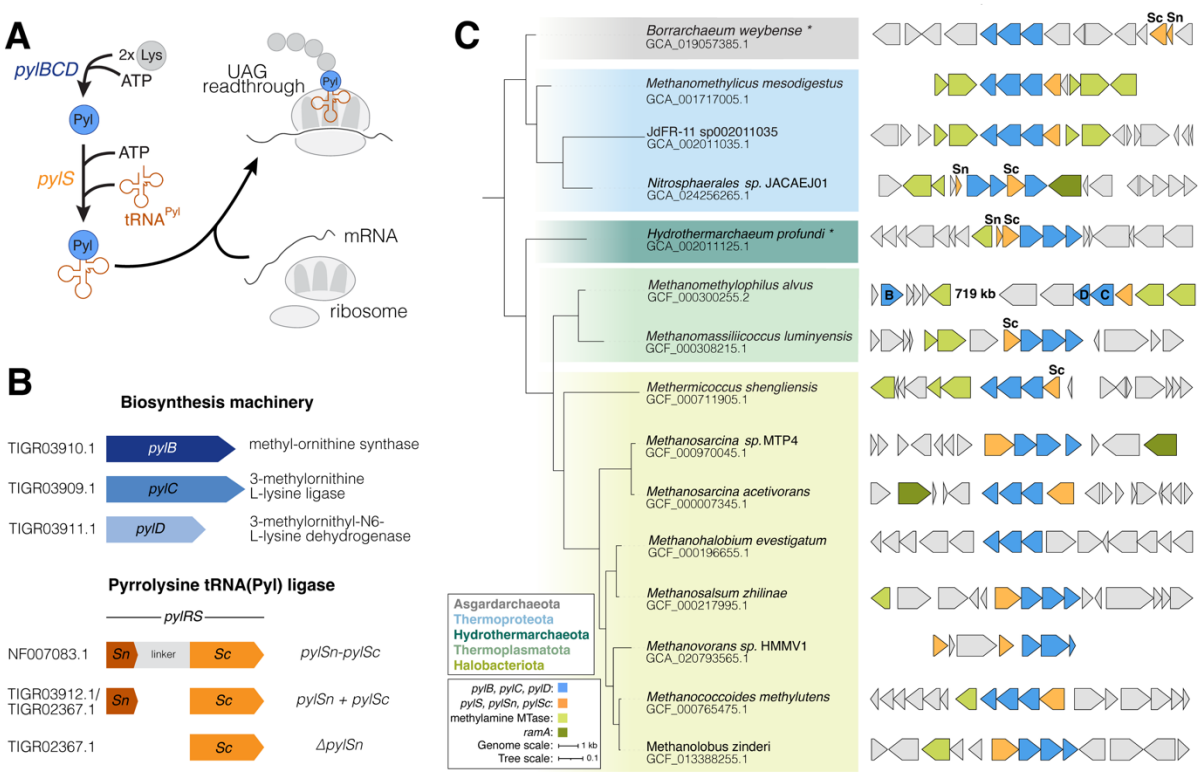

Figure 1. Distribution of Pyrrolysine (Pyl) in archaea. **A)** Proposed mechanism for Pyl biosynthesis (blue), and incorporation (orange) into elongating polypeptides by a Pyl-tRNA^{Pyl} charged by its cognate aminoacyl tRNA synthetase (PylS). **B)** Pyl^{+} archaea were annotated based on the presence of the biosynthesis genes encoded by *pylBCD* (in blue) and the Pyl aminoacyl tRNA synthetase (PylS; in orange). Genes and their corresponding Hidden Markov Models (HMM's) accessions used for the bioinformatic survey are shown. Domain architecture and class distinctions are noted for each of the *pylS* classes. **C)** Pyrrolysine biosynthesis (blue) and incorporation (orange) genes and their genome neighborhood (±7.5 kb of *pylB,* unless otherwise noted) across different Phyla of Pyl^{+} archaea. The genome accession number is provided below the strain names. The corrinoid reductive activase *ramA* (dark green) and methylamine methyltransferases (light green) that often co-occur with the *pyl* genes are indicated. Strains denoted with an asterisk lack genes involved in methane metabolism. **Pyl:** pyrrolysine; **MTase**: methyltransferase; ***pylB****:* methyl-ornithine synthase; ***pylC****:* 3-methylornithine L-lysine ligase; ***pylD****:* 3-methylornithyl-N6-L-lysine dehydrogenase; ***pylS***: pyrrolysine tRNA(pyl) ligase; ***ramA****:* corrinoid protein reductive activase.

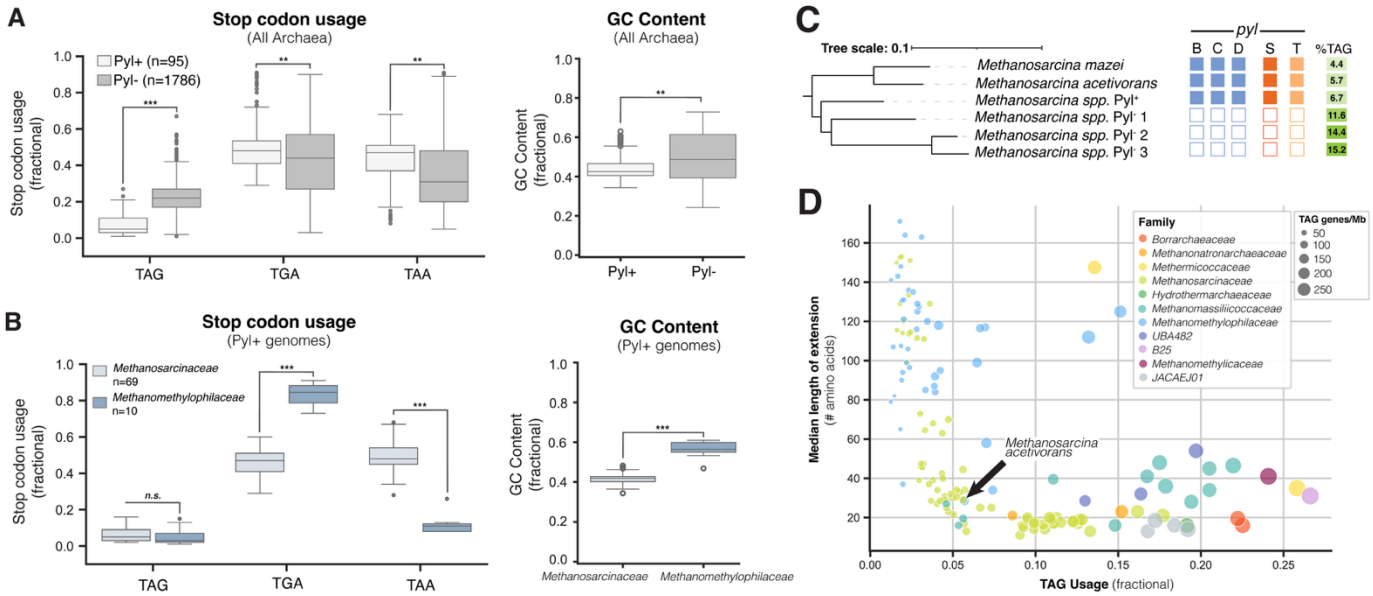

Figure 2. Stop codon usage in response to Pyl-mediated genetic code expansion. **A)** Box and whisker plots of stop codon usage and GC content in Pyl^+ (light gray) and Pyl^- (dark gray) genomes within the archaea. **B)** Box and whisker plots of stop codon usage and GC content in Pyl^+ genomes within the *Methanosarcinaceae* (light blue) and *Methanomethylophilaceae* (dark blue). Stop codon usage was calculated as fraction of total stop codons in protein encoding genes. All statistical tests for panels A and B were performed using Welch's t-test (***p<1.0e-10, **p<1.0e-5, ***n.s.*** not significant). **C)** TAG usage in select *Methanosarcina* strains. The presence of a given gene is indicated by a filled-in square corresponding to the gene noted above the box; %TAG usage is indicated by the opacity of green box and denoted numerically. *Methanosarcina spp.* accessions are as follows: Pyl^+: GCA_00171414685.2; Pyl^-1: CA_017883485.1; Pyl^-2: GCA_003157235.1; Pyl^-_3: GCA_003164755.1 **D)** Genome-specific traits of Pyl^+ archaea. A graph showing the relationship between the fractional TAG usage and the median extension length (# of amino acids) of putative Pyl-encoding proteins. The size of the genome dot indicates the relative abundance of putative Pyl containing genes (genes/Mb). The Family-level taxonomy is indicated by the color of the genome dot, and *Methanosarcina acetivorans* is indicated with the black arrow.

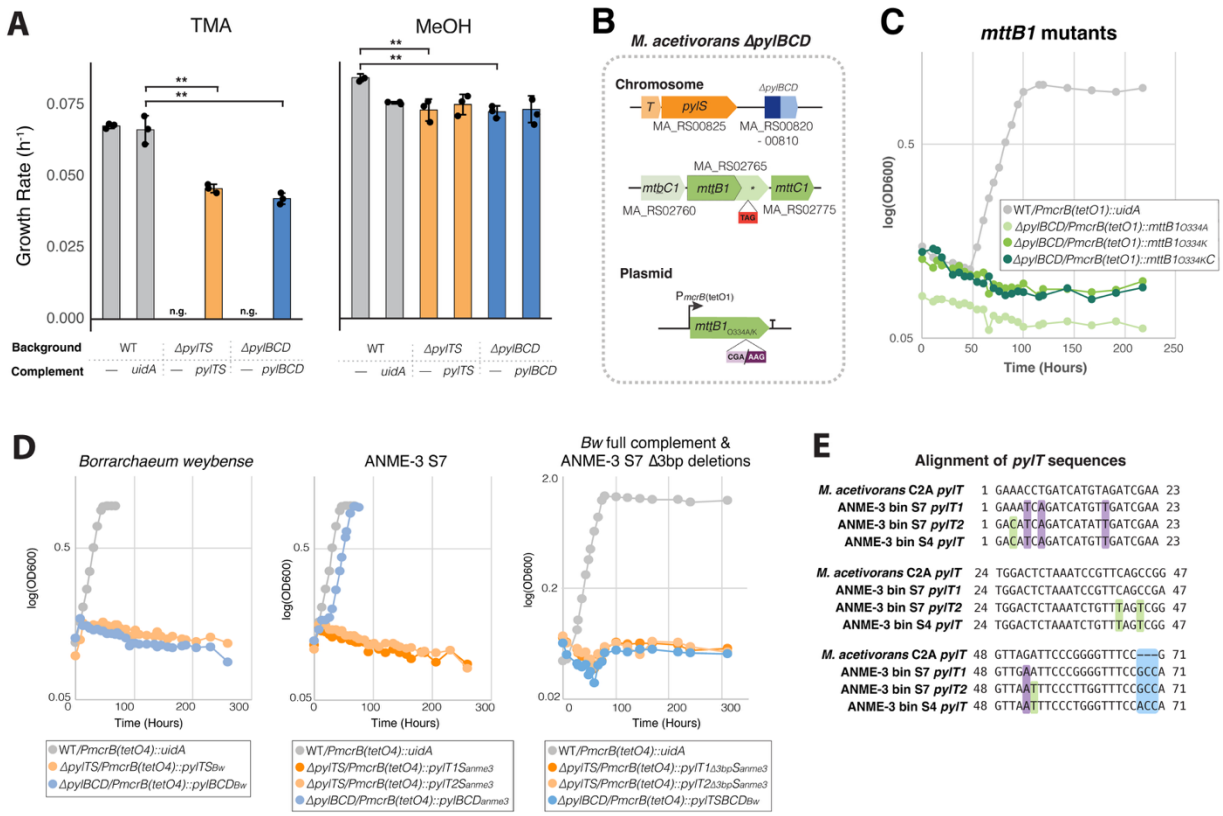

Figure 3. Heterologous expression of *pyl* genes from uncultivated archaea in *Methanosarcina acetivorans*. **A)** Growth rates of the parent strain (WWM60, denoted as wildtype or WT; in gray), the Δ*pylTS* (in orange), Δ*pylBCD* (in blue) mutants and the corresponding complementation strains in minimal media with either trimethylamine (TMA) or methanol (MeOH). In the WT strain, a control gene (*uidA)* was expressed from the tetracycline inducible promoter (P*mcrB*(*tetO1*)) on a plasmid like the genes complemented in *trans.* A two-sided t-test with unequal variances was used to compare mean growth rate from three biological replicates (**p<0.005). Error bars represent the standard deviation of three replicates. **B)** Diagram representing the genomic background for *mttB1* point mutation experiments. In the Δ*pylBCD* background, the chromosomal copy of *mttB1* is maintained, but TAG is obligately read as a stop codon due to the absence of Pyl biosynthesis machinery. A point mutated form of *mttB1* is complemented *in trans* under the control of the tetracycline inducible promoter, P*mcrB*(*tetO1*). **C)** Representative growth of triplicate curves for WT with a control gene (*uidA*; in gray) or the Δ*pylBCD* strain with the *mttB1* point mutants (in green) after transferring MeOH-grown cells into minimal medium with TMA. **D)** Representative growth of triplicate curves for the *pyl* genes from *Borrarchaeaum weybense* or ANME-3 bin S7 (including Δ3bp deletion in *pylT).* Complements were expressed *in trans* under a tetracycline-inducible promoter (P*mcrB*(*tetO4*)) in a *M. acetivorans* Δ*pylTS* (orange) or Δ*pylBCD* (blue) mutant as indicated. All growth curves were performed by transferring MeOH-grown cells into medium with TMA. WT with a control gene (*uidA*) are shown in gray. **E)** Alignment of *pylT* sequences from two members of ANME-3 (bin S7 and bin S3) with *M. acetivorans*. Blue box highlights the 3 bp insertion identified and deleted in panel D. Purple box highlights point mutations shared amongst all ANME *pylT* sequences. Green box highlights point mutations shared between S7 *pylT2* and S3 *pylT.* In panels A, C, and D, all strains bearing a plasmid for expression were

732 cultivated with puromycin to maintain the plasmid and 100 μg/ml tetracycline to induce full
733 expression of the complement from the tetracycline-inducible promoter.

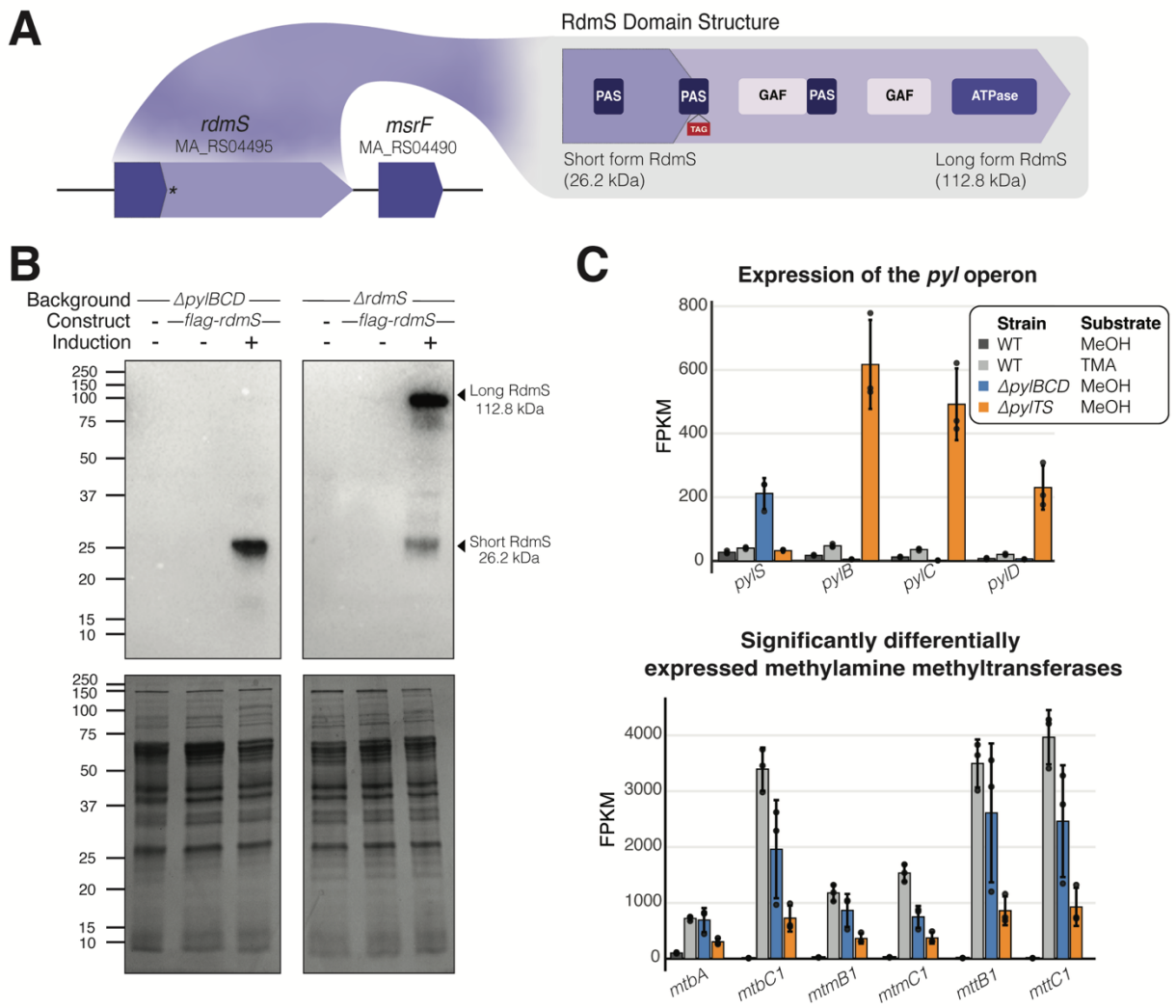

Fig 4. The amber codon can be interpreted as a stop codon or Pyl in *Methanosarcina acetivorans*. **A)** Diagram of RdmS domain structure and genomic organization. RdmS is a predicted sensor kinase located upstream of *msrF*[56], a Msr (methanol-specific regulator) family protein likely involved in the regulation of methylsulfide methyltransferases. Asterisk and TAG box indicate the location of the Pyl residue, where truncation would result in a ~26.2 kDa protein. **PAS: P**er-**A**rnt-**S**im domain; **GAF:** c**G**MP-specific phosphodiesterases, **A**denylyl cyclases and **F**hlA; **ATPase**: **ATP** hydrolyzing domain. **B)** α-FLAG western blot for a N-terminal 1xFLAG translational fusion of *rdmS* expressed *in trans* from tetracycline inducible promoter, P*mcrB*(*tetO4*). Each blot represents a different genetic background, where induction of the 1xFLAG translational fusion of *rdmS* is indicated as no induction (-) at 0 µg/ml tetracycline or maximum induction (+) at 100 µg/ml tetracycline. Predicted molecular weights for the long form RdmS protein (where Pyl is incorporated at TAG) and the short form RdmS protein (where TAG is read as a stop) are indicated on the right side of the gel. Coomassie stained SDS-PAGE gels shown beneath western blot as loading control. **C)** Fragment per kilobase per million reads (FPKM) values of the *pyl* genes (top) and methylamine methyltransferase genes (bottom) in the Δ*pylBCD* mutant on methanol (MeOH) (blue), Δ*pylTS* mutant on MeOH (orange), WWM60 (parent strain also referred to as wildtype or WT) on MeOH (light gray) or trimethylamine (TMA) (dark gray). Error bars represent the standard

752 deviation amongst plotted FPKM values for three replicates. The DESeq2 data can be found in
753 Table S8.

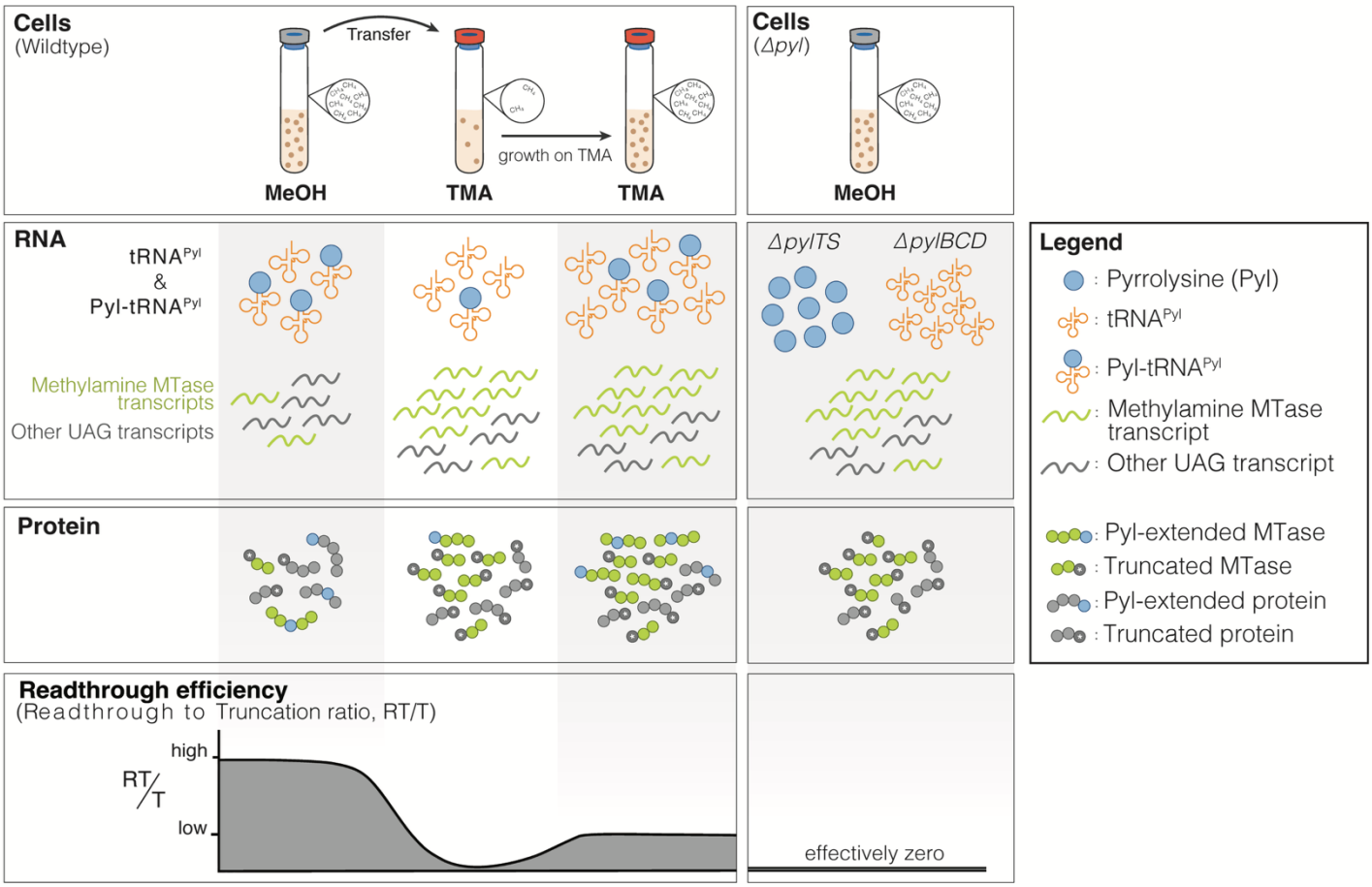

Fig 5. A model for Pyrrolysine (Pyl) homeostasis in *Methanosarcina acetivorans*. During growth on methanol (MeOH), the pool of UAG-containing transcripts is lower, leading to the higher readthrough efficiency (RT/T, bottom panel). We hypothesize that as cells switch from MeOH to trimethylamine (TMA), they encounter a transient state wherein the expression of methylamine methyltransferases (MTase) increases rapidly and Pyl demand outpaces its production. As a result, the readthrough efficiency transiently decreases. This decrease in RT/T likely leads to an increase in expression of *pyl* genes, and methylamine MTases, however, because the MTases have an outsized contribution to the total UAG transcript pool, MTase transcripts effectively outcompete other UAG transcripts for Pyl. We suggest our *pyl* knockouts have a readthrough efficiency that is close to zero and that they respond to this by upregulating the *pyl* genes as well as the methylamine-specific MTases as seen in **Fig 4C**.