

1 **Title: Chloroplast-localized translation for protein targeting in *Chlamydomonas reinhardtii***

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15 **Abstract:** Translation is localized within cells to target proteins to their proper locations. We asked
16 whether translation occurs on the chloroplast surface in *Chlamydomonas* and, if so, whether it is
17 involved in co-translational protein targeting, aligned spatially with localized translation by the
18 bacterial-type ribosomes within this organelle, or both. Our results reveal a domain of the
19 chloroplast envelope which is bound by translating ribosomes. Purified chloroplasts retained
20 ribosomes and mRNAs encoding two chloroplast proteins specifically on this “translation
21 domain”, but not a mRNA encoding a cytoplasmic protein. Ribosomes clusters were seen on this
22 domain by electron tomography. Activity of the chloroplast-bound ribosomes is supported by
23 results of the ribopuromycylation and puromycin-release assays. Co-translational chloroplast
24 protein import is supported by nascent polypeptide dependency of the ribosome-chloroplast
25 associations. This cytoplasmic translation domain aligns localized translation by organellar
26 bacterial-type ribosomes in the chloroplast. This juxtaposition the dual translation systems
27 facilitates the targeting and assembly of the polypeptide products.

28

29 **One-Sentence Summary:** Translation is localized to a domain of the chloroplast envelope for
30 co-translational protein targeting in *Chlamydomonas*.

31

32 **Introduction**

33 Translation is localized in cells to ensure that the protein products get to the proper compartment,
34 are integrated into membranes or assembled into complexes (1). Cytoplasmic ribosomes (cyto-
35 ribosomes) on the ER synthesize polypeptides undergoing either co-translational import or
36 insertion into the ER membrane. Mitochondria in yeast and human cells are bound by cyto-
37 ribosomes which synthesize mitochondrial proteins, of which many undergo co-translational
38 import (2, 3). Mitochondria and chloroplasts contain bacteria-type ribosomes, “mito-ribosomes”
39 and “chloro-ribosomes”, respectively, for the synthesis of proteins encoded by the small genomes
40 in these semiautonomous organelles (4). Chloroplast proteins that are encoded by nuclear genes
41 are widely believed to be synthesized at random cytoplasmic locations and undergo
42 posttranslational import (4, 5). This is based on the ability of purified chloroplasts to import *in*
43 *vitro* synthesized chloroplast pre-proteins (i.e. still having their N-terminal localization sequence)
44 and EM images of chloroplasts lacking the arrays of bound cyto-ribosomes seen on the rough ER
45 and mitochondria (4). Some of the bacterial-type ribosomes within chloroplasts translate on
46 thylakoid membranes as their nascent polypeptides undergo co-translational import (6). While
47 translation on the cytoplasmic surface of a chloroplast has not been demonstrated, this possibility
48 was raised by images from TEM and fluorescence microscopy of the unicellular green alga
49 *Chlamydomonas reinhardtii* showing that chloroplast is adjacent to cytoplasmic region enriched
50 in cyto-ribosomes and the mRNA encoding a chloroplast-localized protein (7, 8). .

51 Here, we show that cyto-ribosomes translated on a “translation domain” of the chloroplast
52 envelope in *Chlamydomonas*. These associations are demonstrated by 1) the retention of cyto-
53 ribosomes by chloroplasts during their purification from free cyto-ribosomes and organelles
54 known to bind them, 2) immunofluorescence (IF) microscopy images of a marker cyto-ribosomal

55 protein (cyL4) on the chloroplast surface and 3) high resolution electron tomography images
56 showing ribosome clusters on the outer envelope membrane. Translational activity of these
57 chloroplast-bound cyto-ribosomes is demonstrated by results of the ribopuromylation (RPM)
58 and the puromycin-release assays (9–12). A proportion of these chloroplast-bound cyto-ribosomes
59 were tethered by their nascent polypeptides, evidence that their nascent polypeptides were
60 undergoing co-translational import *in vivo*. Synthesis of chloroplast-localized light-harvesting
61 proteins and the small subunit of Rubisco (RBCS1 and RBCS2) on the translation domain of the
62 chloroplast envelope is supported by results of fluorescence *in situ* hybridization (FISH) showing
63 that purified chloroplast retained mRNAs encoding chloroplast-localized light-harvesting complex
64 proteins (LHCPs) and the small subunits of ribulose bis-phosphate carboxylase-oxygenase
65 (Rubisco) RBCS1 and RBCS2, but not the mRNA encoding the cytoplasmic protein β 2-tubulin.
66 Finally, the translation domain of the envelope is spatially aligned with domains of the envelope
67 enriched in the protein translocons of the inner/outer membrane of the chloroplast envelope (TIC
68 and TOC) and the translation zone (T-zone), an intraorganellar compartment where chloro-
69 ribosomes translate subunits of photosystem I (PSI) and photosystem II (PSII) of the
70 photosynthetic electron transport chain (8, 13–15) (Fig. 1A). Therefore, our results reveal evidence
71 of an elaborate spatial coordination of translation of the dual translation system for photosystem
72 biogenesis.

73

74 **RESULTS**

75 **Cyto-ribosomes are bound to a translation domain of the chloroplast envelope.**

76 To explore the possibility that translation is localized to the outer envelope membrane of
77 the chloroplast in *Chlamydomonas*, we asked whether cyto-ribosomes copurify with chloroplasts

78 during their isolation from away from cyto-ribosomes that are free or bound to contaminating ER
79 and mitochondria. Isolated chloroplast retained more cyto-ribosomes than can likely be explained
80 by contamination by mitochondria and ER (Fig. 1B). To determine whether cyto-ribosomes were
81 bound to the purified chloroplasts, we imaged the ribosomal protein cyL4 by IF microscopy. On
82 purified chloroplasts, the cyL4 IF signal was seen adjacent to the chloroplast envelope, which was
83 co-IF-stained for the envelope marker protein LCIA (*16*). The cyL4 signal was strongest at a region
84 of the chloroplast envelope bordering the central nuclear-cytosolic region (Fig. 1A and C). This
85 localization pattern can be seen in a representative chloroplast and in the average signal distribution
86 in all chloroplasts of the data set, but not in images of whole cells, where the signal was throughout
87 the cytoplasm (Fig. 1C and D, Fig. S1A). This chloroplast-localized cyL4 IF signal was not from
88 cyto-ribosomes bound to ER or mitochondria that were retained by these chloroplasts because
89 marker proteins for these organelles did not show the same pattern as cyL4 (Figs 1D, S2A and B).
90 These results support associations of cyto-ribosomes with a translation domain of the chloroplast
91 envelope which spatially aligns with the T-zone within this organelle (Fig. 1A).

92 **Cyto-ribosomes on the translation domain of the chloroplast envelope were imaged by high-**
93 **resolution electron tomography.**

94 The evidence cited against chloroplast-localized translation includes EM images of
95 chloroplast envelope devoid of bound ribosomes and chloroplasts surrounded by a cyto-ribosome-
96 free zone (*17–19*). Therefore, to determine whether cyto-ribosomes can be visualized on the
97 chloroplast envelope, and to validate the cyL4 IF signal as a marker for them, we imaged cells
98 with three-dimensional high-resolution electron tomography (Fig. 2). For reference, we imaged
99 the envelope of chloroplast lobes, which did not strongly IF-stain for cyL4. The results show the
100 presence of cyto-ribosome clusters on the chloroplast envelope domain where we observed the

101 localized cyL4 IF signal (Compare Figs. 1C and 2C-F). Cyto-ribosome density was lower on other
102 regions of the chloroplast envelope, e.g., of the chloroplast lobe (Fig. 2F and G). This illustrates
103 that, cyto-ribosomes are on the chloroplast envelope, thereby, corroborating the results of IF
104 microscopy.

105 **Chloroplast-bound cyto-ribosomes are active.**

106 We used two methods to determine whether the chloroplast-bound cyto-ribosomes are
107 translationally active. The RPM method takes advantage of the conjugation of puromycin to the
108 nascent polypeptide when it terminates translation by imaging the IF signal from the resulting
109 puromycin-conjugated nascent polypeptides as markers *in situ* for locations of translation *in vivo*
110 (12). Routing of the puromycin-conjugated nascent polypeptides from sites of their synthesis, a
111 concern when live cells are treated prior to fixation and IF-staining (20), is unlikely because we
112 treated isolated chloroplasts with puromycin.

113 Chloroplasts were isolated, treated with puromycin, IF-stained with an antibody specific to
114 puromycin, and imaged by epifluorescence microscopy. (Specificity of the puromycin signal is
115 demonstrated in Fig S2C). Isolated chloroplasts showed the strongest IF-signal of puromycin-
116 conjugated nascent polypeptides at the envelope domain marked by the localized cyL4 IF-signal
117 (Fig. 3A). Localization of the puromycin signal on the cytoplasmic side of the chloroplast envelope
118 (LCIA) demonstrates that these nascent polypeptides were from cyto-ribosomes and not chloro-
119 ribosomes (Fig. 3B). Moreover, this puromycin-nascent polypeptide localization pattern was seen
120 in the average signal distribution in maximal intensity projection of all chloroplasts in the data set
121 (Fig. 3C). These results support translational activity of the chloroplast-bound cyto-ribosomes *in*
122 *vivo*.

123 The puromycin-release assay tests for organelle-localized translation by exploiting the
124 specificity of puromycin for releasing translating ribosomes from their nascent polypeptides (9).
125 Puromycin-induced release of cyto-ribosome from an isolated organelle is evidence that the
126 ribosomes were translating and tethered by nascent polypeptides undergoing co-translational
127 passage via the protein translocons in the organellar membrane (9, 21). In addition, ribosomes on
128 the ER, mitochondria and thylakoid membranes required high-ionic strength (300-750 mM KCl)
129 to be released, because they are bound to ribosome receptors on the organelle surface (10, 22, 23).
130 When chloroplasts were incubated in the high ionic strength condition (750 mM KCl), a significant
131 proportion of cyL4 was released (32%, $p=0.037$) (Fig. 3D). Therefore, this proportion of the cyto-
132 ribosomes on the translation domain of the chloroplast envelope were bound by non-covalent
133 bonds alone. Treatments with both puromycin and high ionic strength released 49% of cyL4 ($p=$
134 0.012), 17% more than were released during treatment with high ionic strength alone ($p=0.023$).
135 Therefore, these cyto-ribosomes were bound by both non-covalent bonds and their nascent
136 polypeptides. This result confirms that some of the chloroplast-bound cyto-ribosomes were
137 translationally active *in vivo*. It also reveals that at 17% of the ribosomes were associated by their
138 nascent polypeptides. Similar results revealed previously that nascent polypeptides undergo co-
139 translational import into the ER and mitochondria (10, 22, 23). Moreover, the retention of the
140 puromycin-conjugated nascent polypeptides by the chloroplast envelope domain is consistent with
141 their being anchored in the chloroplast envelope, for example, possibly reflecting co-translational
142 import. (Fig. 3A-C). Finally, puromycin alone did not release a significant proportion of cyL4
143 ($p=0.603$), revealing that few, if any, cyto-ribosomes were associated with the chloroplast by
144 nascent polypeptides alone. That approximately 50% of the cyto-ribosomes were not dissociated
145 by any of the treatments could reflect high affinity ribosome-chloroplast associations, ribosomes

146 trapped within contaminating unbroken cells or both. Together, these results reveal the chloroplast
147 bound cyto-ribosomes are active and bound to the chloroplast by both non-covalent bonds and
148 their nascent polypeptides.

149 **The translation domain of the chloroplast envelope is bound by mRNAs encoding**
150 **chloroplast-localized LHCB and RBCS proteins.**

151 The results above support localized translation by chloroplast-bound cyto-ribosomes for
152 protein import into the T-zone within the chloroplast (Fig. 1A). This predicts that the translation
153 domain of the chloroplast envelope is associated with mRNAs encoding chloroplast proteins, but
154 not mRNAs encoding non-chloroplast proteins. We used FISH to test this prediction (24). The
155 imported chloroplast proteins include subunits of the light harvesting complexes (LHCs), which
156 each have three hydrophobic transmembrane domains and are embedded in the membranes of
157 photosynthetic thylakoid vesicles where they associate with PSI and PSII (25, 26). One might
158 expect LHCPs to be synthesized by chloroplast-bound cyto-ribosomes and undergo co-
159 translational import and membrane insertion because the vast majority of such hydrophobic
160 integral membrane proteins use this targeting mechanism to prevent their misfolding and
161 aggregation in the aqueous cytoplasm and, consequentially, impaired import and toxicity (2, 3,
162 27). Therefore, we asked whether chloroplasts released from cells retain mRNAs encoding LHCPs
163 (28). Our FISH probe sequences are complementary to the mRNAs of *LHCBM2* (Cre12.g548400)
164 and *LHCBM7* (Cre12.g548950), highly similar paralogues in the *LHCB* gene family (Table S1).
165 The mRNAs detected by these probes are referred to collectively as “*LHCBM*” here. In cells, the
166 *LHCBM* FISH signal was detected from the cytosol, where it was enriched near the chloroplast, as
167 was reported previously (Fig. 4E and Fig S1B) (8). Chloroplasts retained 96% of average cellular
168 signal, and individual chloroplasts showed localized signal closely adjacent to, but not

169 overlapping, the chloroplast-localized cyL4 IF signal (Fig. 4A and B). Consistency of this
170 localization pattern across all chloroplasts imaged was seen in a display of the average *LHCBM*
171 mRNA FISH signal distribution (Fig. 4E). While the translation domain extends along the
172 envelope between opposing lobes, the strongest average *LHCBM* mRNA FISH signal was
173 localized at the center of this domain (contrast cyL4 in Fig. 1D versus *LHCBM* and *RBCS* in Fig.
174 4E, illustrated in Fig. 1A). These results reveal a physical association of *LHCBM* mRNAs with the
175 translation domain of the chloroplast envelope. We also imaged the mRNAs of *RBCS1* and *RBCS2*,
176 which encode the small subunits of Rubisco, a chloroplast-localized enzyme (Cre02.g120100 and
177 Cre02.g120150). We refer to these mRNAs as “*RBCS*” because our FISH probes hybridize to both
178 (Table S1). In cells, localization of the *RBCS* mRNAs in the cytosol was not evident in most
179 images, as was reported previously (Fig. S1C) (8). However, the average *RBCS* FISH signal from
180 all cells imaged revealed localization to the approximate location of the cyto-ribosomes on the
181 translation domain of the chloroplast envelope (Fig. 4E). Moreover, an association of the *RBCS*
182 mRNAs with the chloroplast was revealed by our findings that free chloroplasts retained 80% of
183 the cellular *RBCS* FISH signal and that individual chloroplasts showed this signal localized at the
184 middle of the translation domain (marked by cyL4), like the localization of the *LHCBM* mRNA
185 FISH signal (Fig. 4A and C). A heatmap of the average *RBCS* FISH signal confirmed this
186 localization pattern and revealed that more of the *RBCS* mRNA FISH signal was around the entire
187 basal (posterior) region of the chloroplast, than was the *LHCBM* FISH signal (Fig. 4E). These
188 results support the translation of at least a few cytoplasmic mRNAs encoding chloroplast proteins
189 by the cyto-ribosomes in the center of the translation domain of the chloroplast envelope.

190 To assess for specificity of chloroplast localization of mRNAs encoding chloroplast
191 proteins, we visualized the FISH signal from the *TUB2* mRNA, which encodes β 2-tubulin, a

192 protein of the cytoplasm and cilia (Cre12.g549550) (29). In cells, strong *TUB2* FISH signal was
193 detected throughout the cytosol, as reported previously (Fig. 4E, Fig. S1D) (7). Chloroplasts
194 retained 2% of this signal (Fig. 4A) which was not enriched at or near the translation domain (Fig.
195 4D and E). These results support chloroplast-localized translation specifically of mRNAs encoding
196 proteins of the chloroplast.

197 **DISCUSSION**

198 Our results reveal localized translation of mRNAs encoding chloroplast proteins at a domain of
199 the chloroplast envelope in *Chlamydomonas*. This translation domain contradicts the long-
200 standing model that all chloroplast proteins are synthesized throughout the cytoplasm (4). In
201 addition, the nascent polypeptide dependency of cyto-ribosome associations with the chloroplast
202 supports co-translational import of chloroplast proteins (Fig. 3D). In this mechanism, the emerging
203 nascent polypeptide passes through the chloroplast envelope via the TOC/TIC translocons during
204 its synthesis, thereby tethering the cyto-ribosome to the chloroplast. Translation localization at the
205 ER and mitochondria, in addition to tethering by nascent polypeptides, involves cyto-ribosome
206 receptors on the organellar surface. These receptors were revealed by requirements for high ionic
207 strength for ribosome dissociation from these organelles *in vitro* (23, 30–32). The possibility that
208 cyto-ribosomes bind to receptors on the chloroplast surface is suggested by our finding that high
209 ionic strength is required for their dissociation (Fig. 3D).

210 Our results reveal that chloroplast protein synthesis and import are organized spatially in a
211 fashion analogous to mitochondrial protein synthesis in *Saccharomyces cerevisiae* and humans (33–
212 37). Mito-ribosomes synthesize subunits of the complexes of the respiratory electron transport
213 system and ATP synthase into the inner membrane where it invaginates to form cristae, i.e. cristae
214 junctions (36–38). Cristae junctions are also preferential sites of the early steps of respiratory

215 complex assembly (36–38). As such, cristae junctions are analogous to the T-zone of the chloroplast
216 (15). The translation domain of the chloroplast envelope is analogous to patches of mitochondrial
217 outer membrane located outside cristae junctions, which are bound by translating cyto-ribosomes
218 and enriched in the mitochondrial protein import translocons (21, 33, 36, 39). Therefore, spatial
219 coordination of translation on and within each of the semiautonomous organelles might be a
220 fundamental aspect of their biogenesis. This localized co-translational import of mitochondrial inner
221 membrane proteins is hypothesized to facilitate their integration into the membrane and assembly
222 with the locally synthesized protein products of mito-ribosomes (32, 40–42). Similarly, we
223 hypothesize that LHCPs, and possibly other chloroplast proteins, are synthesized at the translation
224 domain of the chloroplast envelope and undergo co-translational import into the T-zone to facilitate
225 their insertion into developing thylakoid membranes and their assembly with subunits synthesized
226 by chloro-ribosomes. In this model, the homologues of the chloroplast SRP system, cpSRP43 and
227 cpSRP54, engage the nascent polypeptide as it emerges from the TIC translocon and direct it to the
228 translocon for co-translational insertion into developing thylakoid membranes in the T-zone,
229 thereby obviating the proposed post-translational roles of the chloroplast SRP system.

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358 Writing – review & editing: YS, SB, WZ, KHB.

359 **Competing interests:** Authors declare that they have no competing interests.

360 **Data and materials availability:** All data, code, and materials used in the analysis must be
361 available in some form to any researcher for purposes of reproducing or extending the

362 analysis. Include a note explaining any restrictions on materials, such as materials transfer
363 agreements (MTAs). Note accession numbers to any data relating to the paper and deposited
364 in a public database; include a brief description of the data set or model with the number. If
365 all data are in the paper and supplementary materials, include the sentence “All data are
366 available in the main text or the supplementary materials.”

367 **Supplementary Materials**

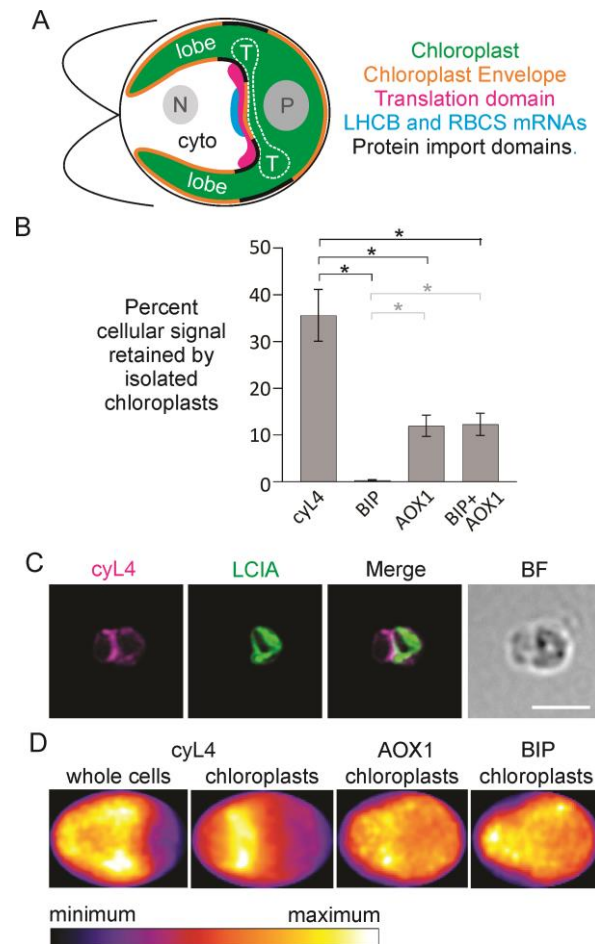
368 Materials and Methods

369 Figs. S1 to S4

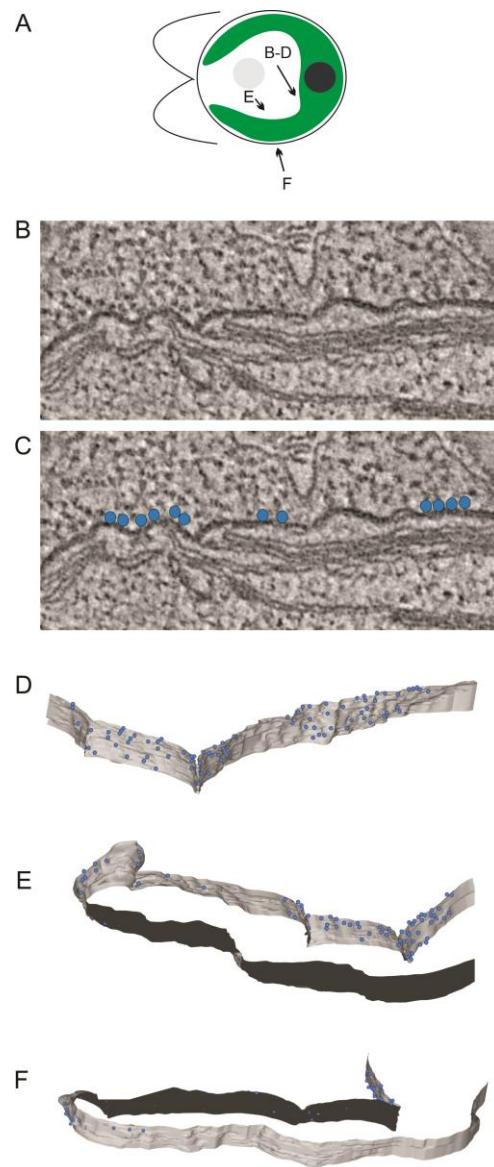
370 Table S1

371

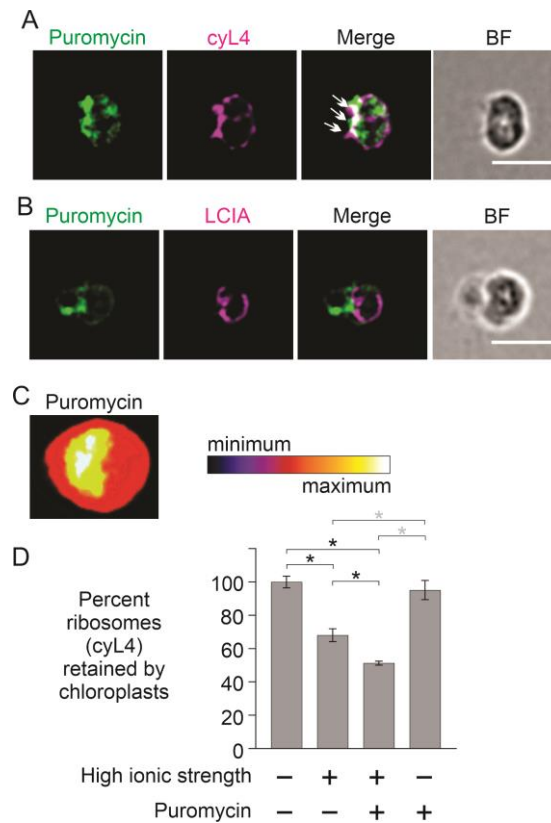
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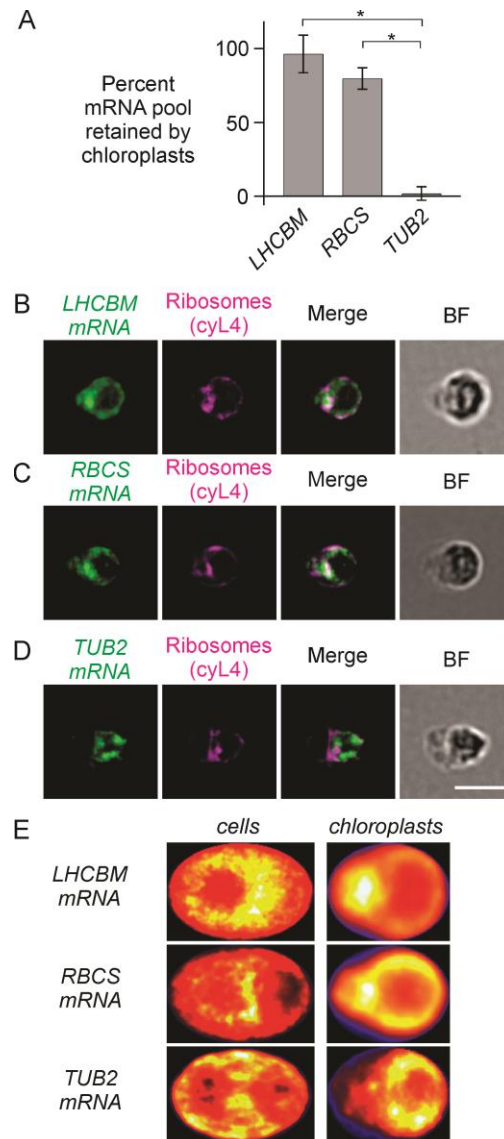
373 **Fig. 1. Cyto-ribosomes are bound to a domain of the chloroplast envelope.** (A) An illustration
 374 shows a *Chlamydomonas* cell with the nucleus (grey sphere), cytosol (cyto) and chloroplast
 375 (green). The chloroplast has lobes which enclose the nucleus (grey sphere), and cytosol (cyto),
 376 pyrenoid (black sphere), the T-zone (T) and it is surrounded by a dual membrane envelope
 377 (orange). The translation domain of the envelope (magenta) is adjacent to the mRNA-enriched
 378 region (cyan) and overlaps envelope domains shown previously to be enriched in the TOC/TIC
 379 protein import translocons (black) (14). (B) Results of immunoblot analyses of marker proteins in
 380 extracts of whole cells versus isolated chloroplasts reveal that cyto-ribosomes (cyL4) preferentially
 381 copurify with chloroplasts (AtpB) relative to the organelles known to be bound by cyto-ribosomes;
 382 ER (BIP), mitochondria (AOX1). (Immunoblot results are in Fig. S4. Error bars= 1.0 SEM, n=3
 383 biological replicates from independent cultures). (C) IF-microscopy images of purified
 384 chloroplasts show cyL4 localized to a domain of the envelope (LCIA). The absence of LCIA signal
 385 from the lobes of the chloroplast does not reflect a change in chloroplast morphology during
 386 isolation (Fig. S3). (BF, bright field, size bar, 5.0 μ m) (D) Heat maps show average IF signals of
 387 cyL4, AOX1, and BIP from all cells or chloroplasts in representative data sets (CyL4, n= 32
 388 chloroplasts or n= 102 cells; AOX1, n=22 chloroplasts; BIP48, n=48 chloroplasts).



389 **Fig. 2. Electron tomograms show cyto-ribosomes on the outer membrane of the chloroplast**
390 **envelope.** (A) The illustration shows the regions where the tomographs were acquired for B-E. (B)
391 A tomographic slice showing the region of chloroplast envelope bound by cyto-ribosomes as seen
392 by IF microscopy (Fig. 1C). (C) The image in B with blue dots marking the cyto-ribosomes that
393 are on the envelope. (D-E) Models of chloroplast envelope (grey, cytoplasmic face of the outer
394 membrane; black, stromal face of the inner membrane) and bound cyto-ribosomes (blue dots) as
395 seen from the angles shown in Panel B.



396 **Fig. 3. The cyto-ribosomes on the chloroplast are translationally active and tethered by**
397 **nascent polypeptides.** (A and B) Results of the RPM method show IF signal of the puromycin-
398 conjugated nascent polypeptides (green), as markers of translation, localized to (A) the cyto-
399 ribosome (cyL4) IF signal (B) on the cytoplasmic side of the chloroplast envelope (LCIA) (size
400 bar, 5.0 μm). Arrows indicate sites of colocalization of puromycin-conjugated nascent
401 polypeptides and cyto-ribosomes. The green IF signal is specific to puromycin (Fig S2C). (C) A
402 heat map of the average IF signal from the puromycin-conjugated nascent polypeptides from all
403 chloroplasts in this data set (n= 30) shows that the individual chloroplasts are representative. (D)
404 Bar heights indicate the average proportion of cyto-ribosomes (cyL4) retained by isolated
405 chloroplasts following the treatments indicated. (Immunoblot results represented by this graph are
406 presented in Fig S4.) High ionic strength was 750 mM KCl. (Error bars= 1.0 SEM, n= 3 biological
407 replicates from independent cultures).



408 **Fig. 4. FISH results reveal that mRNAs encoding specifically chloroplast-localized proteins**
409 **are bound to isolated chloroplasts.** (A) Bar heights represent percentages of the average FISH
410 signal intensities of whole cells that were retained by chloroplasts for the mRNAs indicated. (Error
411 bars= 1.0 SEM). (B-D) Chloroplasts IF-stained for cyto-ribosomes (cyL4) and FISH-probed for
412 the mRNAs encoding chloroplast-localized proteins of (B) the *LHCBM* mRNAs or (C) the *RBCS*
413 mRNAs. (D) Chloroplast FISH-probed for the *TUB2* mRNA as a control mRNA encoding a non-
414 chloroplast protein. Size bar, 5.0 μ m. (E) Heat maps show the distributions of the average FISH
415 signals in maximal intensity projections of image stacks from all cells or chloroplasts in each data
416 set ($n \geq 30$ cells or chloroplasts per data set).