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Review

Translational regulation in chloroplasts for development and homeostasis☆

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ABSTRACT

Chloroplast genomes encode 100–200 proteins which function in photosynthesis, the organellar genetic system, and other pathways and processes. These proteins are synthesized by a complete translation system within the chloroplast, with bacterial-type ribosomes and translation factors. Here, we review translational regulation in chloroplasts, focusing on changes in translation rates which occur in response to requirements for proteins encoded by the chloroplast genome for development and homeostasis. In addition, we delineate the developmental and physiological contexts and model organisms in which translational regulation in chloroplasts has been studied. This article is part of a Special Issue entitled: Chloroplast biogenesis.

1. Introduction

Chloroplasts contain a few thousand proteins which function in photosynthesis, the biosynthesis of fatty acids, amino acids, hormones, vitamins, nucleotides, secondary metabolites, and intracellular signaling [1]. Most of these proteins are encoded by the nuclear genome, synthesized by cytosolic eukaryotic-type ribosomes, imported into the chloroplast, and targeted to a specific compartment of the chloroplast where they function. Chloroplast genomes encode 100–200 of these proteins, most of which function in photosynthesis and the organellar genetic system. These proteins are synthesized by the chloroplastic translational machinery, which is "bacterial-type" reflecting the evolutionary origin of plastids; a cyanobacterial endosymbiont in the ancient common ancestor of plants and algae. Hence, chloroplastic ribosomes are more like bacterial ribosomes than those of the eukaryotic cytoplasm [2].

A variety of model organisms are used in studies of translational regulation in chloroplasts. The dicot *Arabidopsis thaliana* (hereafter "Arabidopsis") is the most widely used model plant, largely due to its amenability to genetic analyses and the many resources and tools that have been developed by a large research community [3]. Maize is advantageous as a model organism because essential chloroplast processes, like translation, can be dissected with genetic analyses because zygotic lethal mutant seedlings provide sufficient quantities of tissue for analyses of translation defects at the molecular level [4]. Maize and barley seedlings present a developmental gradient of green tissue allowing characterizations of developmental profiles of chloroplast gene expression (Fig. 1A) [5–8]. Lateral sections from seedling leaves have cells in essentially the same stage of differentiation for molecular analyses of chloroplast gene expression [5–8]. Tobacco is the only vascular plant in which the chloroplast genome can be routinely transformed with exogenous DNA, allowing analyses of the effects of site-directed mutagenesis or gene disruptions of translational components, and the use of chimeric reporter gene constructs to monitor translation rates in vivo [9]. The unicellular green alga *Chlamydomonas reinhardtii* (hereafter Chlamydomonas) is used as a model in chloroplast biology because it is amenable to diverse experimental approaches [10]. For example, one can readily monitor translation rates by in vivo radioisotopic pulse labeling, transform the chloroplast genome with exogenous DNA, obtain and study viable mutants deficient in the translation of chloroplast mRNAs encoding photosynthesis proteins [11].

Chloroplast compartments and components are mentioned throughout this review. The chloroplast stroma is the aqueous–proteinaceous compartment that is functionally analogous to the cytoplasm of a cell. The chloroplast envelope transports metabolites, imports chloroplast proteins encoded by the nuclear genome, and synthesizes various chloroplast lipids [12]. Thylakoids are a network of membranous vesicles which carry out the light-dependent reactions of photosynthesis and ATP synthesis

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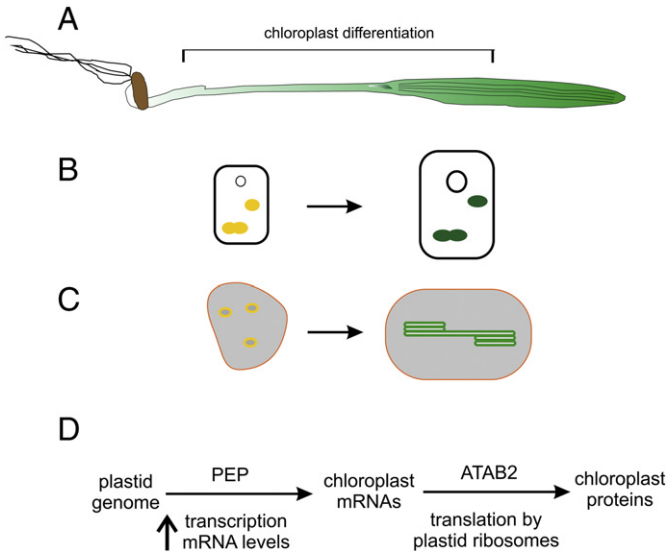

Fig. 1. Translational regulation in chloroplast development from the proplastid. (A) Chloroplast differentiation occurs in cells near the base of the monocot leaf, where meristematic tissue develops into photosynthetic green tissue. (B) In these cells, proplastids (yellow ovals) differentiate to chloroplasts (green ovals). The nucleus is shown as a circle. (C) During proplastid to chloroplast development, prothylakoid vesicles (yellow) differentiate to the thylakoid vesicles (green). (D) This is accompanied by increased chloroplast transcription and mRNA levels. Photosynthesis genes are transcribed primarily by the plastid-encoded RNA polymerase (PEP) [163]. ATAB2 activates the translation of mRNAs encoding subunits of PSI and PSII in Arabidopsis (Section 2) [27].

[13]. Embedded in thylakoid membranes are the multi-subunit complexes of the photosynthetic electron transport system; photosystem I (PSI), photosystem II (PSII), and the cytochrome b6/f complex, as well as the ATP synthase. The CO_2-fixing step in the Calvin cycle is carried out by ribulose bis-phosphate carboxylase–oxygenase (Rubisco); as a multi-subunit "holoenzyme" complex in the chloroplast stroma. Most studies of translational regulation in chloroplasts have focused on genes encoding proteins in photosynthesis.

Translation in chloroplasts has been covered by excellent reviews recently. Some are comprehensive [14–16] while others focus on specific themes; translational regulation by light and redox poise [17,18], translation factors with repeated amino acid sequence motifs (pentatricopeptide repeats (PPR) or octotricopeptide repeats (OPRs)) [17,19], evidence that translation is localized to "biogenesis centers" in chloroplasts and cyanobacteria [20,21], co-translational roles of molecular chaperones [22,23], small regulatory RNAs (sRNAs) [24], and the essentiality of translation in plastids for plant development [25].

Here, we focus on translational regulation in chloroplasts as responds to changing requirements for proteins encoded by the chloroplast genome. We also delineate the different contexts in which this regulation occurs. For example, translational regulation is required for the biogenesis that occurs in chloroplasts as they differentiate from proplastids during the early development of stem and leaf tissues (Section 2). Translational regulation has been studied in chloroplasts differentiating from etioplasts in de-etiolating monocot seedlings (Section 3). Mature chloroplasts regulate translation for the biogenesis that underlies their growth for division in the expanding cells of green tissues and in growing algal populations (Section 4). Translational regulation in chloroplasts also occurs in response to changing environmental conditions, for example, repair the photosynthesis machinery (Section 5). Thus, this review highlights how translational regulation in chloroplasts meets developmental and physiological requirements for proteins encoded by the plastid genome and we discuss the underling regulatory mechanisms.

2. Translational regulation in differentiating chloroplasts in developing green tissues

Proplastids of meristematic cells differentiate to photosynthetic chloroplasts in developing photosynthetic tissues of leaves and stems [26]. This involves the bulk synthesis of most of the polypeptides that function in chloroplasts. Transcriptome profiling of a developmental gradient along the longitudinal axes of the seedling leaves in monocots, e.g., maize and barley (Section 1), revealed drastic increases in chloroplast mRNA levels early in differentiation (Fig. 1) [5–8]. These increases reflect the activation of the plastid-encoded-RNA-polymerase and increased transcription of photosynthesis genes of the plastid genome. However, little is known about translational regulation during proplastid-to-chloroplast differentiation, apart from the role of the RNA-binding protein ATAB2 (Section 2.2).

2.1. ATAB2 is a translational regulator in Arabidopsis

In Arabidopsis, ATAB2 was proposed to regulate translation of chloroplast mRNAs encoding subunits of both photosystems early in proplastid-to-chloroplast differentiation, based on several findings [27]. *ATAB2* expression is induced early in seedling development when proplastid-to-chloroplast differentiation occurs. This induction involves the photoreceptors that initiate development; the cryptochromes. ATAB2 is required for loading the *psaA/B and psbD/C* polycistronic mRNAs on polysomes. Finally, the ATAB2 homologue in Chlamydomonas, Tab2, is required for the translation of the chloroplast *psaB* mRNA [27,28]. Future research of ATAB2 and TAB2 could provide a valuable avenue to elucidate the activation of translation during these earliest stages of chloroplast development, a challenging endeavor considering the tremendous increases in chloroplast mRNA levels and transcription of the chloroplast genome which occur during then (Section 2.1).

3. Translational regulation occurs during etioplast-to-chloroplast differentiation

In angiosperm seedlings that have germinated in the dark, the proplastid differentiates to an etioplast (Fig. 2). Etioplasts lack chlorophyll-binding proteins due to a strict light-requirement for chlorophyll biosynthesis in this phylogeny group [29] and are poised to undergo rapid differentiation to chloroplasts upon illumination and the onset of chlorophyll synthesis, a process called de-etiolation or "greening". Pioneering studies examined translational regulation of plastid gene expression during greening of etiolated seedlings because one can obtain desired amounts of chloroplasts in defined stages of differentiation for molecular and biochemical analyses. Isolated etioplasts were often used because they readily take up exogenous radiolabelled amino acids, allowing determinations of protein synthesis rates (in in organello radioisotope pulse-labeling experiments). Translation rate was inferred from the synthesis rate of a polypeptide normalized to the level of the mRNA encoding it (determined with Northern blot analysis). Translation rates were also determined by the degree of polysome loading of specific mRNAs (determined by sucrose density gradient ultracentrifugation).

3.1. Translational regulation during de-etiolation

De-etiolation activates expression of the chloroplast genes encoding chlorophyll-binding apoproteins of PSII (D1, D2, CP43, CP47) and PSI (PsaA and PsaB) and the LSU of Rubisco [30–33] via translational regulation based on the following. Drastic increases in the rates of radioisotope pulse-labeling of PsbA, PsaA, PsaB, and the LSU of Rubisco were observed in isolated etioplasts as they underwent greening, while levels of the mRNAs encoding these proteins changed less [31–33]. This could be due to repression of the elongation phase of translation in the dark because ribosome occupancy on the initiation

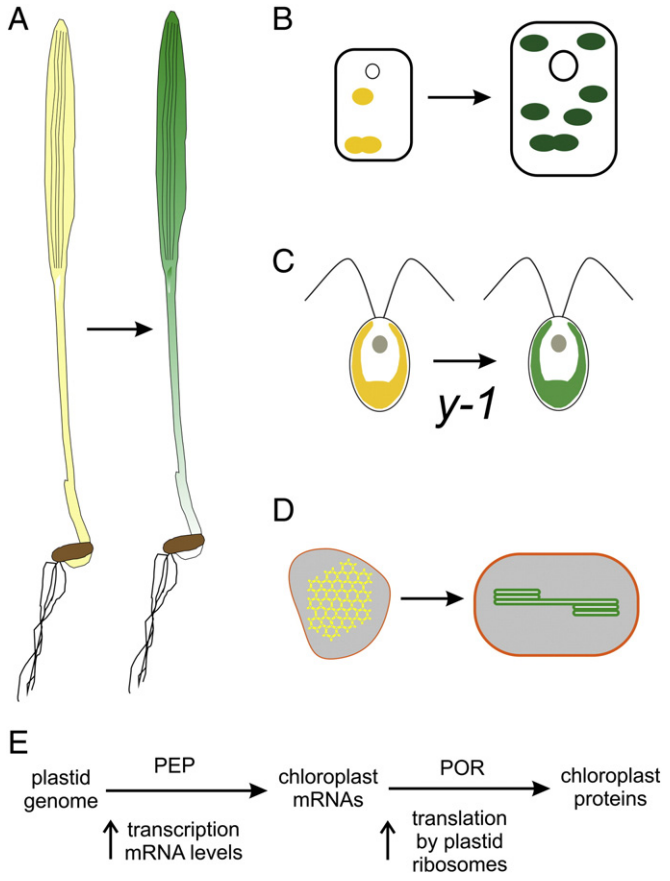

Fig. 2. Translational regulation in chloroplast development from the etioplast. (A) A monocot seedling germinated in the dark is etiolated; it lacks photosynthetic green tissue because light is required for chlorophyll synthesis in angiosperms. Illumination (arrow) initiates chlorophyll synthesis whereupon the seedling undergoes uniform development to photosynthetic green tissue. (B) In these de-etiolating cells, etioplasts (yellow) differentiate to chloroplasts (green). (C) The *y-1* mutant of Chlamydomonas cannot synthesize chlorophyll in the dark and has an undifferentiated yellow plastid (left). Upon illumination (arrow), this plastid differentiates to the chloroplast (right). (D) Within the etioplast (left), upon illumination and the onset of chlorophyll synthesis (arrow), the prolamellar body differentiates to photosynthetic thylakoid membranous vesicles of the chloroplast (right). (E) De-etiolation in maize is accompanied by increased transcription by PEP and mRNA levels. De-etiolation in all organisms studied to date also involves enhanced translation of the chloroplast mRNAs encoding photosynthesis proteins (Section 3). Light is perceived by protochlorophyllide oxidoreductase (POR).

codons of the mRNAs of *psaA*, *psbA*, and *rbcL* was essentially constant immediately prior to and during early greening [31,34] while the *psaA/B* mRNA was loaded on the membrane-bound polysomes in the dark to the same extent as in the light [35]. In addition, activation of translation initiation of the chlorophyll-binding apoproteins was supported by several findings. First, ribosome occupancy on the *psbA* mRNA translation initiation codon increased upon the induction of de-etiolation, at least in one study [36]. Second, pharmacological inhibition of the initiation of protein synthesis prevented this induction [37]. Third, in greening tobacco, regulation of the initiation of *psbA* mRNA translation in differentiating plastids was supported by in vivo light regulation of chimeric reporter genes under the control of the *psbA* 5′ untranslated region (UTR) [38,39]. The biochemical factors and mechanisms underlying this translational regulation have yet to be determined. The constant levels of chloroplast mRNAs during de-etiolation in Barley [31–33] contrasts that drastic increases in plastid transcription and mRNA levels in maize [6–8].

It was proposed that newly synthesized chlorophyll stimulates translation of the abovementioned chlorophyll-binding apoproteins of PSII and PSI during de-etiolation, based on the following evidence. The activation of chlorophyll-binding apoprotein synthesis and the accumulation of chlorophyll were concurrent [37,40]. Exogenous chlorophyll *a* activated translation of these chlorophyll-binding apoproteins in isolated etioplasts. Pharmacological inhibition of chlorophyll synthesis or genetic deficiency for enzymes in the pathway prevented the activation of chlorophyll-binding apoprotein synthesis [37,41]. Activation of apoprotein synthesis was attribute to POR because this response lacked a characteristic of the red light photoreceptor, phytochrome; reversal by a subsequent pulse of far-red light [42]. By contrast, the expression of nuclear genes encoding chloroplast proteins is regulated by photoreceptors [43]. The role of metabolic signals in the regulation of translation in chloroplasts is reviewed in Section 4.

3.2. Translational regulation during greening in a Chlamydomonas mutant that cannot synthesize chlorophyll in the dark

The Chlamydomonas *yellow-in-the-dark* mutant *y-1* has been used to study chloroplast gene expression during chloroplast differentiation. This mutant lacks the light-independent POR and, like in barley and maize, has only the light-dependent POR. Consequently, *y-1* mutant cells have an undifferentiated plastid in the dark which, upon illumination, undergoes differentiation to a chloroplast [44–46]. This differentiation involves the enhanced synthesis of several chlorophyll-binding apoproteins encoded by chloroplast genes, which was attributed to translational regulation because it occurred in the absence of corresponding changes in the levels of the mRNAs encoding these proteins [47]. Similar results were also obtained in *Euglena gracilis* [48].

4. Translational regulation in mature chloroplasts for their growth and division

Chloroplast biogenesis also occurs in the development of young photosynthetic green tissues, as cells expand during plant growth (Fig. 3) [49]. In these cells, mature chloroplasts undergo division by binary fission. Each round of chloroplast division requires the doubling of all organellar components and, hence, the regulated expression of chloroplast genes.

4.1. Translational regulation predominates in mature chloroplasts

The regulation of plastid gene expression in mature chloroplasts is believed to occur mostly at posttranscriptional steps for several reasons. First, chloroplastic mRNAs generally have half-lives on a time scale of hours, much longer than the minute time scale of half-lives of mRNAs in bacteria [50–52]. Long mRNA half-lives suggest that transcriptional regulation alone cannot effectively regulate protein levels. Secondly, in the chloroplast of Chlamydomonas, protein synthesis rates were not diminished by severe reductions of the levels of the mRNAs encoding them, suggesting the intervention of translational activation [53,54]. Third, many *trans*-acting factors are known to be required for translation with single chloroplast gene specificity. This specificity suggests regulatory rather than general translation functions of these factors, as has been confirmed for several of these factors (reviewed by [55,56]). Finally, other evidence pointing to translational control, the levels of chloroplast mRNAs encoding photosynthesis proteins show only moderate changes of a few fold in mature, dividing chloroplasts [5–8]. Diurnal mRNA level changes in mature chloroplasts of 2–3 fold have been documented [57,58]. These relatively constant mRNA levels allow for the detection of translational control because translation rates are generally determined as the synthesis rate of a protein normalized to the level of mRNA encoding it (see below). This section reviews modes of translational regulation in mature chloroplasts, with the few documented cases in vascular plants and several in the Chlamydomonas chloroplast.

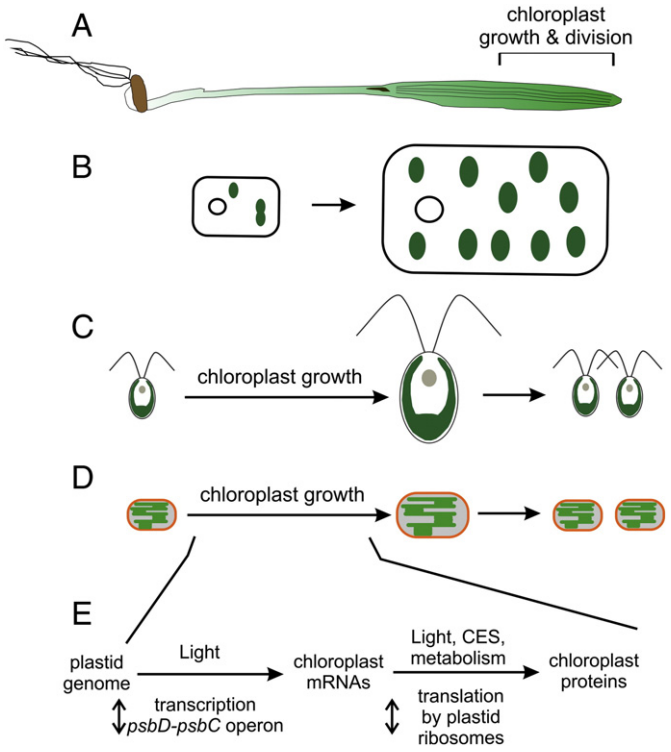

Fig. 3. Translational regulation in mature chloroplasts for their growth and division. (A) The illustration of a monocot seedling shows the distal leaf where (B) cells are expanding and their chloroplasts are increasing in size and number [26]. (C) In Chlamydomonas, the mature chloroplast grows along with the cell prior to mitosis. (D) Mature chloroplasts grow and divide by binary fission. (E) Chloroplast gene expression is regulated primarily at the levels of translation and in response to light, acetate metabolism, and the CES for complex assembly (Section 4). Transcription of the *psbD-psbC* operon is regulated by light in vascular plants.

4.2. Light regulates translation in mature chloroplasts

Translation in mature chloroplasts is regulated by light, presumably in order to coordinate this energetically costly process with photosynthesis. This section covers translational regulation by light of moderate intensity for the biogenesis of the photosynthesis complexes, primarily PSII and the Rubisco holoenzyme. This regulation is distinct from the light-regulation of *psbA* translation for the repair of photodamaged PSII complexes (Section 5).

In vascular plants, there are only a few examples of light-regulated translation in mature chloroplasts under physiological, non-stress conditions. Two studies found that illumination of isolated barley chloroplasts increases the synthesis rates of the D1 subunit of PSII and the LSU of Rubisco and that these effects result from enhanced translation elongation on the *psbA* and *rbcL* mRNAs, respectively [59,60]. Another report described the light stimulation of *psbA* and *rbcL* translation in mature chloroplasts of *Spirodela oligorrhiza*, an aquatic angiosperm [61,62].

Chlamydomonas has been used in most studies of light-regulation of translational regulation in chloroplasts. Results of transmission electron microscopy and subcellular fractionation observed that chloroplast ribosomes were recruited to thylakoid membranes within the first 10 min of the light phase of a diurnal light–dark cycle and they were released in the first 10 min of the dark phase, supporting translational regulation of unidentified thylakoid membrane proteins by light [63]. Light regulated synthesis of chloroplast genome-encoded proteins was also revealed by the results of radioisotope pulse-labeling experiments as light-dependent changes of the synthesis rates of specific polypeptides (in the chloroplast) in the absence of corresponding changes of their mRNA levels [32,47,58,64]. For example, in Chlamydomonas cells cultured in a diurnal light–dark regime or comparisons of light vs dark conditions, several photosynthesis proteins were synthesized in the light but not in the dark [32,47,58,64]. These were the major subunits of the PSII reaction center: D1, encoded by *psbA*; D2, encoded by *psbD*; CP43, encoded by *psbC*; CP47, encoded by *psbB*; the major subunits of the PSI reaction center: PsaA, encoded by *psaA*; and PsaB, encoded by *psaB*; the LSU of Rubisco, encoded by *rbcL*. Translation was concluded to be a major regulated step because mRNA level changes were minor compared to the changes in protein synthesis rates [32,47,58,64] see also [57]. The converse was revealed for the translation of the *tufA* mRNA, encoding the translation elongation factor EF-Tu; it was higher in the dark than in the light [64]. Another measure of translation is the proportion of a chloroplast mRNA pool that is associated with polysomes. Polysomes from cells in the light, but not those from cells in the dark, were shown to synthesize D1 and LSU in in vitro radioisotope pulse-labeling translation run-off assays [58–60]. The *psbA* mRNA shifted from the free (non-translated) pool to the polysomal (translated) pool during a transition from dark to moderate light conditions [65]. Translation of the *chlL* mRNA is higher in the dark than in the light, as revealed by comparisons of the distributions of the *chlL* mRNA between large polysomes and free mRNA pool from cells under these two conditions [66]. The *trans*-acting factors involved in *chlL* translational control could be encoded by one or more of six nuclear *YELLOW-IN-THE-DARK* (*y*) genes: *y-1*, *y-5*, *y-6*, *y-7*, *y-8*, and *y-10*, because each is required for CHLL accumulation in the dark. Indeed, in the *y-1* mutant, the *chlL* mRNA was not on polysomes in the dark (or in the light) [67].

4.3. Translational regulation involves mRNA localization in the Chlamydomonas chloroplast

A common mechanism of translational regulation involves the localization of mRNAs to a specific intracellular location where their translation is either activated or repressed [20]. Results of in situ localization experiments revealed that the activation of translation of PSII subunits and the LSU of Rubisco by light correlates with the localization of the mRNAs encoding at least two PSII subunits and the LSU to a specific region of the Chlamydomonas chloroplast around the pyrenoid called the translation (T)-zone [68]. Chloroplast ribosomes and translation factors also localized to this T-zone under these conditions. This localization occurred independently of translation and, hence, any targeting signals in the nascent chains, suggesting that these signals are within the mRNA sequences and ribosome subunits [69]. Results of subcellular fractionation revealed "chloroplast translation membranes" which are enriched in marker proteins for the T-zone and, therefore, are proposed to function in this cytological region as a platform for the synthesis and assembly of PSII subunits because they have chloroplast ribosomes, two translational activator proteins, and intermediates in PSII assembly [70,71]. Evidence that chloroplast nucleoids are a privileged location of translation was provided by the presence of chloroplast ribosomal proteins in nucleoid-enriched fractions in a proteomics study of maize [72].

4.4. Light perception and signaling in translational regulation in mature chloroplasts

In plants and algae, specialized photoreceptors and signal transduction pathways control many processes, including gene expression [73,74]. For example, cryptochrome 1, cryptochrome 2, and phytochrome A mediate light activation of the transcription of the chloroplast *psbD-psbC* operon and several nuclear genes [75–78]. As reviewed in Section 2, crytochromes activate the translation of chloroplast mRNAs encoding subunits of photosystems I and II via the translation factor ATAB2 in early Arabidopsis development

[27]. It remains to be determined whether or not ATAB2 regulates translation in mature chloroplasts.

However, the available data do not support a role of photoreceptors in translational control in mature chloroplasts. Rather, light is perceived through its effects on specific biochemicals which serve as light proxies; termed here "biochemical light proxies" (BLPs). BLPs can be biochemical intermediates in photosynthesis or other light-modulated pathways (Fig. 4). For example, in the model reviewed in Section 3 (Fig. 2), during de-etiolation the light sensor that activates translation is POR and the BLP is chlorophyll, which activates translation via unknown regulatory factors [37,40,41]. Other BLPs are intermediates of photosynthesis; e.g., reduced plastoquinone, reduced thioredoxin, the stromal ADP concentration, the trans-thylakoid membrane H^+ gradient, and NADPH (Fig. 4) [79–82]. Regulatory factors respond to specific BLPs by controlling chloroplast gene expression at the levels of transcription [83], RNA splicing [165], mRNA stability [84] and translation [65,85,86].

Light perception and signaling by BLPs is supported by findings that pharmacological inhibition of the photosynthetic electron transport chain or dissipation of the electrochemical H^+ gradient across the thylakoid membrane abolished light-dependent *psbA* translation in Chlamydomonas [85]. Similarly, in isolated barley chloroplasts, light stimulation of *psbA* translation at the level of translation elongation requires ATP and the electrochemical H^+ gradient across the thylakoid membrane [59,60]. These authors proposed that a pH-sensitive factor regulates translation elongation on the *psbA* mRNA. In intact chloroplasts isolated from spinach, the rate of translation elongation on the *psbA* mRNA was oppositely affected by oxidizing and reducing agents, supporting control by the redox states of one or more components of the photosynthetic electron transport chain [87]. A comprehensive study of proteins and complexes in mustard seedlings under oxidizing and reducing conditions revealed an elevated level of the translation elongation factor EF-Tu in the chloroplast under a light regime that oxidizes the photosynthetic electron transport chain, the major difference between oxidizing and reducing conditions [88]. The repression of *chlL* translation by light (covered in Section 4.2) is mediated by biochemical cues within photosynthesis because inhibitors of specific steps in the photosynthetic electron transport chain induced CHLL accumulation in the light [67]. The sensors could be the ADP/ATP ratio or the redox state(s) of an electron acceptor located downstream of the cytochrome b6/f complex. Finally, the ability of isolated chloroplasts to light-regulate translation suggests that the light sensor(s) and the signaling molecules involved are none of the photoreceptors that are known to control gene expression because they are not in chloroplasts [89,90]

Other evidence of light perception and signaling by BLPs was provided by demonstrations that the diurnal regulation of D1 and D2 translation in Chlamydomonas (Section 4.2) is not mediated by a circadian clock. The diurnal translational oscillations in the chloroplast were

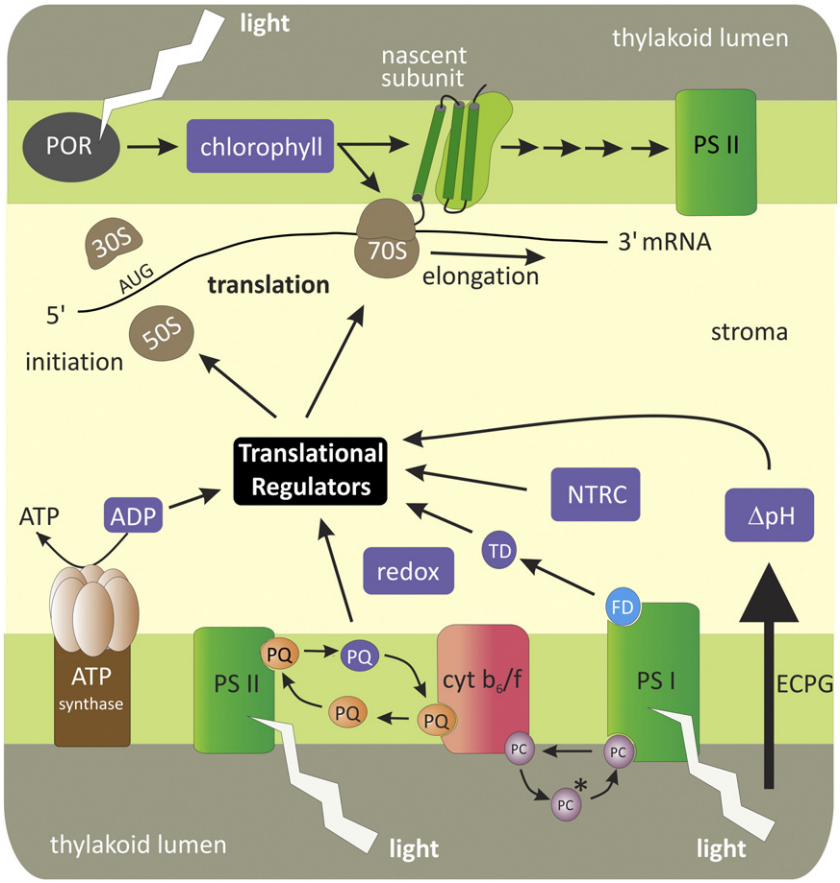

Fig. 4. Light regulates translation in chloroplasts for their biogenesis. The illustration shows the membranes of two neighboring thylakoid vesicles, containing lumen (top and bottom) and separated by chloroplast stroma. Translation of the *psbA* or *psbD* mRNA is shown. During initiation, 30S and 50S ribosome subunits assemble on the AUG start codon to form a translation competent 70S ribosome. During elongation, the 70S ribosome translates the coding sequence to synthesize the polypeptide subunit. The nascent polypeptide assembles for the de novo biogenesis of photosystem II. Light regulates translation by changing the concentrations or redox states of specific biochemical light proxies (purple) which, in turn, control translational regulatory factors. Light activates POR to generate chlorophyll, it stimulates ATP synthase to decrease the ADP concentration of the stroma, and it drives photosynthetic electron transport to reduce plastoquinol (PQ) and thioredoxin (TD) and generate the electrochemical [H^+] gradient (ΔpH; ECPG, large arrow). Dark-activated NTRC represses *psbD* translation. Other abbreviations are photosystem II (PSII) cytochrome b6/f complex (cyt b6/f), photosystem I (PSI), and plastocyanin (PC).

abolished when light was sustained into a subjective dark phase [64]. Because a circadian clock would continue to regulate translation for several cycles in sustained 24 h light, it was concluded that other mechanisms are involved. Secondly, in the dark phase, exogenous acetate (an energy source) induces the synthesis of the major photosynthesis proteins (e.g., D1, D2, and LSU) and hence mimics the effect of light [91]. Acetate did not alter the protein synthesis rates when it was added in the light phase. These results suggest that acetate metabolism and photosynthesis activate translation through a common BLP. For example, a BLP could be the stromal concentration of ATP or ADP based on three findings. First, ADP inhibits a translational activator complex in the Chlamydomonas chloroplast [92] (Section 4.6). Second, isolated pea chloroplasts in the dark were shown to activate translation of D1 and D2 in response to exogenous ATP [93]. Third, light and acetate increased the ATP concentration of the chloroplast stroma during dark phase and both ATP synthesis and the light-induced translation require the trans-thylakoid membrane electrochemical H^+ gradient [64,94]. Therefore, diurnal translation rate changes are cued to one or more BLPs, which are probably intermediates in energy metabolism such as ADP and ATP.

4.5. Light regulation of psbD translation for de novo PSII biogenesis in Chlamydomonas

Light regulates the translation of the chloroplast *psbD* mRNA for the de novo biogenesis of PSII in Chlamydomonas [47,64,94]. This was shown to involve a redox switch acting on a complex with factors that bind to sequences near the translation initiation region on the *psbD* 5′ UTR; RBP40 and NAC2 [95]. RBP40 was initially identified by affinity chromatography with the *psbA* 5′ UTR as ligand and called RB38 [96]. RBP40 regulates specifically *psbD* translation based on three findings. First, results of in vitro RNA-binding experiments revealed RBP40 binding preferentially to the 5′ UTR of the *psbD* mRNA over others [97]. Second, RBP40 depletion, in RNAi-mediated knock-down lines, resulted in failure to load the *psbD* mRNA on polysomes, while the loading of two other chloroplast mRNAs was unaffected [97]. Third, the restoration of photosynthesis by *psbD* 5′ UTR suppressor mutations revealed that *psbD* is the primary chloroplast mRNA requiring RBP40 for its translation [98].

The redox mechanism underlying the activation of *psbD* translation by light involves the formation of an intermolecular disulfide bond between NAC2 and RBP40 [95]. According to the model, the complex with covalently bound NAC2 and RBP40 activates *psbD* translation by melting a repressive secondary structure containing the translation initiation region with the AUG initiation codon [98–100]. In the dark, this secondary structure hinders the binding of the small ribosomal subunit to the translation initiation region and, thereby, represses *psbD* translation. This mechanism is supported by the finding that abovementioned cis-acting suppressor mutations restore *psbD* translation in the absence of bound RBP40 and are predicted to destabilize this secondary structure [98]. Evidence that RBP40 also directly recruits the chloroplast ribosome was provided by results of co-immunoprecipitation experiments [97]. RBP40 probably acts only during initiation steps of translation because it cosedimented with monosomes and not with polysomes [97]. In the dark, the disulfide bond linking NAC2 and RBP40 is reduced (broken) whereupon RBP40 loses its ability to activate *psbD* translation. To explain how this reduction occurs specifically in the dark—we normally think that reducing equivalents are produced in the light by photosynthetic electron transport—these authors propose the involvement of NADPH-dependent thioredoxin reductase C (NTRC) using NADPH produced by the oxidative pentose phosphate pathway in the dark [95]. Support of this hypothesis was provided by the demonstration that NTRC reduces the disulfide bond linking NAC2 and RBP40 in vitro, thereby mimicking the effect of darkness in vivo.

4.6. Light regulation of psbA translation for de novo PSII biogenesis in mature chloroplasts

The activation of *psbA* translation by light of moderate intensity (Section 4.2) has been reported to involve a complex that was identified and purified by affinity chromatography using *psbA* 5′ UTR as the ligand and characterized by in vitro RNA-binding assays. This “RB complex” was shown light-dependent RNA-binding activity in vitro with some specificity for the *psbA* 5′ UTR [101]. Two proteins of the RB complex have been characterized; RB47 and RB60. Results of in vitro assays assigned the RNA binding activity to RB47 and this was substantiated by the identification of RB47 as a poly(A)-binding protein [102]. Based on these results, the RB complex was proposed to specifically bind the 5′ UTR of the *psbA* mRNA to activate D1 synthesis (reviewed by [103]).

RB60 is a protein disulfide isomerase (PDI) [104]. It was proposed to mediate the light regulation of the *psbA* mRNA-binding by the RB complex by redox control [65,85,101]. This conclusion was based on results of in vitro and in organello assays in which reducing conditions (e.g., reduced thioredoxin) activated the complex while oxidizing conditions inactivated it [65,86]. Therefore, the BLP was proposed to be reduced thioredoxin generated by the photosynthetic electron transport (Fig. 4). Modulation of RB60 activity by thioredoxin is consistent with the identification of RB60 as a thioredoxin target [105]. Activation of the RB complex by light was proposed to involve the RB60-catalyzed reduction (under reducing conditions associated with photosynthetic electron transport) of an intramolecular disulfide bond in RB47, between cysteine residues in adjacent RNA-binding domains. This would relieve steric inhibition of RNA-binding by RB47 [106,107]. Effects of light and photosynthetic electron transport on the stromal pH were proposed to fine tune this redox control [107]. A distinct mechanism was proposed to inactivate the RB complex in the dark, based on the inability of reducing agents to activate it in extracts of dark-grown cells [65]. This primary repression could be signaled by an oxidized plastoquinone pool, elevated stromal ADP levels (e.g., via ADP-dependent phosphorylation of RB60 [92]), or both [65]. In the light, photosynthesis could reverse these effects and relieve dark-induced inhibition of RB60 [65]. This “priming” step was proposed to allow RB60 to respond to the redox state of thioredoxin and modulate the RNA-binding activity of RB47 according to variable light. In Arabidopsis, the chloroplast-localized protein disulfide isomerase (PDI6) controls D1 synthesis in response to high-intensity light during a stress condition called photoinhibition (Section 5) [108]. These studies of *psbA* translational regulation by the RB complex examined effects of physiological intensity light, which activate the synthesis of several chloroplast genome-encoded subunits of PSII, and therefore, the de novo biogenesis of the complex [65,85] see also [47,68]. Section 5 reviews a distinct mode of *psbA* translational regulation by light to produce the D1 subunit for repair the photodamaged PSII complexes.

4.7. DLA2/RBP63 regulates psbA translation in response to acetate metabolism in Chlamydomonas

Thylakoid membrane biogenesis requires the de novo bulk synthesis of membrane lipids and polypeptide subunits of the photosynthesis complexes [15]. These processes have been proposed to be coordinated in response to the presence or absence of acetate metabolism by the E2 subunit of the plastid pyruvate dehydrogenase complex, DLA2, aka RBP63 [15,70,109]. This enzyme complex synthesizes acetyl-CoA, the precursor for fatty acids and, hence, is early in the biosynthesis of the glycerol lipids of the thylakoid membrane bilayer (reviewed by [110]. A moonlighting function of DLA2 in the regulation of *psbA* translation by acetate and light (reviewed in Section 4.4 [91]) was demonstrated recently [70,109]. DLA2 is required for *psbA* translation; RNAi-mediated knock-down lines for DLA2 showed defects in both [70]. This translational role is specific for *psbA* translation; the synthesis of other proteins was not affected in the RNAi lines and DLA2 showed

in vitro binding specificity for the *psbA* 5′ UTR [70,109]. DLA2 and the *psbA* mRNA were found together in a high molecular mass complex specifically in cells metabolizing acetate. DLA2 localizes in situ to the aforementioned T-zone and cofractionates with chloroplast translation membranes proposed to be privileged sites of translation in the chloroplast for de novo photosystem II biogenesis (Section 4.3). Inverse regulation of lipid synthesis and *psbA* translation in response to acetate metabolism was proposed to involve the redistribution of DLA2 between pyruvate dehydrogenase and the high molecular weight complex, based on formation of the later specifically in the presence of acetate and light, and the ability of *psbA* mRNA to inhibit pyruvate dehydrogenase activity in vitro, e.g., by sequestering DLA2 [70].

4.8. Translational regulation in the biogenesis of the multisubunit complexes of photosynthesis

"Control by Epistasis of synthesis" (CES) is a mode of translational regulation that has several functions in the biogenesis of the photosynthesis complexes. CES adjusts the translation rate of a chloroplast gene-specific mRNA according to the requirement for the encoded subunit in the de novo assembly of the complex in which it functions (reviewed by [111]). As a result, the chloroplast genome-encoded subunits are synthesized in the correct stoichiometry. CES also prevents the accumulation of unassembled subunits, which are highly prone to aggregate due to their hydrophobicity. Finally, CES ensures that certain subunits are synthesized and incorporated into an assembling complex in a specific order.

In Chlamydomonas, CES involves autoregulatory repression of translation in the biogenesis of PSI, PSII, and the cytochrome b6/f complex. When a subunit of one of these complexes is present in excess of what is needed for complex assembly, it represses translation of the mRNA encoding it, thereby preventing the synthesis of additional unassembled copies [112–119]. In Chlamydomonas, CES in the biogenesis of the chloroplast ATP synthase involves translational activation; the β subunit *trans*-activates the translation of mRNA encoding the α subunit [120]. The details of this regulation were reviewed by [111].

Translation is considered to be the regulated step in CES because, in each case, no alteration in the level of mRNA of the regulated gene was detected and the 5′ UTR (a region of mRNAs involved predominantly in translation initiation) can confer CES regulation to a reporter gene in vivo (in chloroplast genome transformants) [114,115,117,118,121].

Specific components in the CES regulation of *petA* translation have been identified. In this case, the *petA* product, cytochrome f, induces autoregulatory feedback repression of *petA* translation for the biogenesis of the cytochrome b6/f complex. Results of site-directed mutagenesis revealed that the initial signal of this translational repression is a tetrapeptide motif near the cytochrome f C-terminus [122]. These authors proposed that this motif in the properly assembled cytochrome f is embedded within the complex where it cannot trigger the autoregulatory repression. By contrast, this motif is exposed in the unassembled cytochrome f, and signals the translational repression via sequences within the *petA* 5′ UTR [121,123]. However, the topology and physicochemical properties of the C-terminal repressor motif do not favor a direct interaction with the 5′ UTR [123]. This suggests that the exposed motif is recognized by *trans*-acting factors that mediate the translational control via the *petA* 5′ UTR [123]. Such a factor was identified as TCA1p, based on the following [124]. First, *TCA1* is required for translation of the *petA* mRNA; *tca1* mutants failed to synthesize cytochrome f while the *petA* mRNA accumulated. Second, both TCA1p and the repressor motif control translation via the *petA* 5′ UTR, a feature of CES (covered earlier in this section). Finally, the repressor motif requires factors encoded by *TCA1* and *MCA1* to control *petA* translation [125–127].

This CES function of MCA1p provides an example of a PPR protein with translational regulatory function [128]. Many PPR and OPR proteins have defined biochemical functions in gene expression within chloroplasts and mitochondria and are required for translation of the mRNA of a specific chloroplast gene [17,19]. However, only *MCA1* has been shown to have a regulatory function, as opposed to a function that is required for translation to occur, but does not modulate it in response to changing requirements for the polypeptide product, to our knowledge [17,19]. Therefore, the regulatory function of MCA1p in CES supports the hypothesis that PPR proteins actually regulate translation in chloroplasts and mitochondria.

Evidence of CES has been reported in the biogenesis of the cytochrome b6/f complex and the Rubisco holoenzyme complex in tobacco and maize, respectively [129–132]. In addition, in spinach chloroplasts, the synthesis and co-translational membrane insertion of the PSII subunit D1 requires the pre-existence of its assembly partner D2 [87,133–135], a feature of CES regulation in the biogenesis of PSII of Chlamydomonas [112,119]. Chloroplast ATP synthase biogenesis in maize probably does not involve the CES regulation described in Chlamydomonas, based on results of profiling the ribosome-bound mRNAs [136]. Evidence of highly conserved autoregulatory feedback repression in *rbcL* translation has been proposed (Section 5.2) [137]. Otherwise, additional work is required to determine the extent of CES conservation in photosynthetic organisms; cyanobacteria, algae, and plants and possibly in the biogenesis of integral membrane complexes in general.

5. Translational regulation for chloroplast homeostasis

Chloroplast homeostasis involves translational regulation. This section reviews two examples; the regulation of *psbA* translation for the repair of photodamaged PSII complexes and the repression of *rbcL* translation during oxidative stress.

5.1. Translation of the psbA mRNA to replace D1 subunit damaged by light

The *psbA* mRNA is the most actively translated mRNA under high light stress conditions and its translation is stimulated by light over a broad range of intensities in mature chloroplasts [18,138]. This is due to the fact that light exposure damages PSII, resulting in a vicious cycle of loss of PSII activity and reactive oxygen species production, in a complex stress condition called photoinhibition. Damage occurs preferentially to the oxygen evolving complex and the D1 subunit of the PSII reaction center. Translation of the *psbA* mRNA is specifically activated by light to provide new D1 subunit for the repair of photodamaged PSII complexes (Fig. 5). We have at least a basic understanding of the steps in this damage and repair cycle. Complex models describe mechanisms of photodamage [139]. Damaged PSII complexes are recognized and labeled by phosphorylation [140]. These complexes are translocated from appressed membranes in stacks of thylakoid vesicles, the grana, to the stroma-exposed membranes of "stromal thylakoids" and the margins. Damaged PSII complexes are then partially disassembled and the damaged D1 is degraded by proteolysis [141]. Protein factors act on the nascent D1 protein to ensure its stabilization, maturation, folding, and co-translational assembly into the PSII subcomplex [18,133–135,142–154]. REP27 is involved in the co-translational incorporation of D1 into PSII sub-complexes [155]. Depletion of the chloroplast-localized PDI6 in Arabidopsis enhances *psbA* translation and diminishes photoinhibition, suggesting roles in these processes (Section 4.6) [156]. Remaining unknown are the factors and mechanisms that selectively activate the translation of the *psbA* mRNA for PSII repair, despite the importance of this regulation for plant viability and its ubiquity across phyla with oxygenic photosynthesis.

The activation of *psbA* translation for PSII repair is distinct from roles in de novo PSII biogenesis involving CES regulation and the RB complex (Sections 4.8 and 4.6, respectively). The *psbA* 5′ UTR and 3′ UTR cannot confer high-light regulation to the translation of a reporter gene in vivo, while the translation of the same chimeric mRNA was induced over

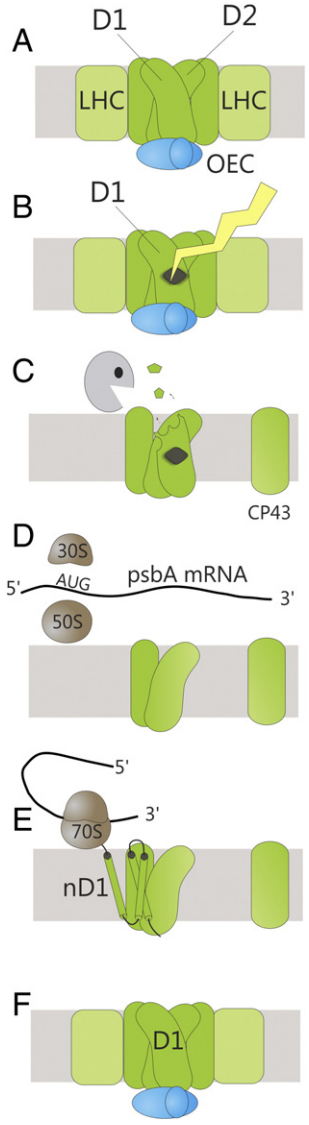

Fig. 5. Light activates translation of the *psbA* mRNA in the photosystem II damage and repair cycle. (A) A simplified illustration shows a functional photosystem II complex. This membrane is appressed against another thylakoid membrane in a granum; a stack of thylakoid vesicles (not shown). (B) Light induces damage to the D1 subunit (black spot). The damaged PSII complex then translocates to stroma-exposed membranes at the granal margins or the stromal thylakoids (not shown). (C) There, the CP43 subunit is removed and the damaged D1 subunit degraded by proteases; FtsH and DegP (gray) [164]. (D) Translation of the *psbA* mRNA is activated. (E) Assembly of the nascent D1 into the photosystem II subcomplex is co-translational and involves several known factors [18]. (F) The reassembled photosystem II complex is functional again. Abbreviations; photosystem II, PS II; oxygen evolving complex, OEC; Light harvesting complex II, LHCII; nascent D1, nD1.

10-fold by CES regulation [119]. By contrast, the *psbA* 5′ UTR does mediate the translational regulation by light for de novo PSII biogenesis (Sections 4.8 and 4.6). For example, moderate light exposure enhanced in vivo translation rates of reporter genes fused to the *psbA* 5′ UTR in Chlamydomonas and tobacco [38,39,157]. The *psbA* 5′ UTR contains the sequences that mediate RB complex binding and translational regulation by moderate light [158]. The studies of the RB complex in *psbA* translational regulation used moderate light conditions [47,65,85], which do not induce levels of preferential *psbA* translation for PSII repair [47,68]. These studies observed light-induced synthesis of chloroplast proteins in addition to D1, revealing a role in de novo complex biogenesis [47,65,85]. These included the Rubisco LSU, whose synthesis is repressed under the high light conditions that induce *psbA* translation for PSII repair (Section 5.2) [65,137]. Therefore, the moderate light conditions used in these studies activated *psbA* translation for de novo biogenesis of PSII, and not its repair. These are clearly two distinct modes of *psbA* translational regulation by light.

5.2. Translation of the rbcL mRNA is regulated by autoregulatory feedback repression in Chlamydomonas

Translation of the *rbcL* mRNA is repressed during high light stress [137,159–161]. This has been linked to an oxidative stress response, because it was induced under low light when ROS production was photosensitized by methyl viologen, and it was prevented by the antioxidant ascorbate at high light. Glutathione appears to be the redox sensor that mediates this response. Repression of *rbcL* translation is exerted, at least in part, during the entry to, or early in the elongation phase because the mRNA shifts from large to small polysomes and monosomes during oxidative stress condition ([161]).

The translation factor that mediates *rbcL* translational repression may be the *rbcL* product, LSU of Rubisco, because this protein binds RNA following its oxidation in vitro (Kd = 10 nm) [137,162]. RNA binding by the oxidized Rubisco large subunit showed no sequence specificity. This regulation of *rbcL* translation and the RNA-binding activity of LSU are conserved in at least two vascular plants and bacteria [137]. A model has been advanced in which RNA-binding activity by the large subunit is mediated by an RNA recognition motif in its N-terminal region that becomes exposed during oxidizing conditions due to partial unfolding, or when chaperones fail to bind this region on the nascent protein, e.g., when they are sequestered by the misfolded proteins that arise during oxidative stress [137,162]. A mutually compatible model proposes that the unassembled Rubisco large subunit represses *rbcL* translation to coordinate the synthesis of equimolar amounts of the large and small subunits for Rubisco assembly, via a CES mechanism [137] (see Section 4.8).

6. The utility of Chlamydomonas as a model organism for translational regulation in chloroplasts

Is Chlamydomonas research revealing general modes and mechanisms of translational regulation in chloroplasts? TAB2 homologues were identified in diverse photosynthetic organisms, including Arabidopsis (Section 2.1), and three cyanobacterial species [28]. Conservation at the biochemical level between Chlamydomonas TAB2 and Arabidopsis ATAB2 was demonstrated by the ability of Chlamydomonas *TAB2* to partially complement the mutant phenotypes of the Arabidopsis *atab2* mutant [27]. PPR and OPR translation factors have been found in Chlamydomonas and in vascular plants and the first regulatory role for one of them, MCA1p, was demonstrated in Chlamydomonas (Section 4.8). Autoregulation of *rbcL* translation was discovered in the Chlamydomonas chloroplast is conserved in vascular plants and cyanobacteria [137]. Of the many examples of CES found in Chlamydomonas, only the CES regulation in Rubisco holoenzyme biogenesis appears to be conserved in vascular plants, although this question remains to be fully explored. Finally, light regulation of *psbA* translation by the RB complex appears to not be conserved in Arabidopsis (Section 4.6). Therefore, some modes and mechanisms of translational regulation are conserved between Chlamydomonas and other photosynthetic phyla, while others are not.

7. Future perspectives

Many gaps remain in our understanding of translational regulation in chloroplasts. For example, nothing is known about how the *psbA* mRNA is specifically selected for translation to repair photodamaged PSII complexes, despite its importance to chloroplast biology and the productivity of agricultural plants. Regulatory functions identified for ATAB2 in Arabidopsis (Section 2) and TCA1p, MCA1p, NAC2, RBP40, and DLA2 in Chlamydomonas (Section 4) suggest that the many other

mRNA-specific translation factors have regulatory functions awaiting discovery. Little is known about the importance of translational control during chloroplast differentiation (Section 2). This may be difficult to study amidst the drastic increases in transcription brought about by the activation of the plastid-encoded-RNA polymerase and the resulting increases in chloroplast mRNA levels [5–8]. Further investigation of ATAB2 and TAB2 could elucidate translational control during this question (Section 2.1). Finally, the chloroplast controls nuclear gene expression via retrograde signaling [26]. By contrast, the signals that are known to control translation in the chloroplast arise within this organelle, e.g., unassembled CES-subunits (Section 4.8), biochemical light proxies (Section 4.4), and oxidized nascent RBCL (Section 5.2). It will be of interest to determine whether translation in chloroplasts is regulated by cross-talk with the nucleus or other intra-cellular compartments.

Transparency document

The Transparency document associated with this article can be found, in online version.

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References

[1] D. Leister, T. Kleine, Towards a comprehensive catalog of chloroplast proteins and their interactions, Cell Res. 18 (2008) 1081–1083.
[2] A.L. Manuell, J. Quispe, S.P. Mayfield, Structure of the chloroplast ribosome: novel domains for translation regulation, PLoS Biol. 5 (2007) e209.
[3] P. Lamesch, T.Z. Berardini, D. Li, D. Swarbreck, C. Wilks, R. Sasidharan, R. Muller, K. Dreher, D.L. Alexander, M. Garcia-Hernandez, A.S. Karthikeyan, C.H. Lee, W.D. Nelson, L. Ploetz, S. Singh, A. Wensel, E. Huala, The Arabidopsis Information Resource (TAIR): improved gene annotation and new tools, Nucleic Acids Res. 40 (2012) D1202–D1210.
[4] D.B. Stern, M.R. Hanson, A. Barkan, Genetics and genomics of chloroplast biogenesis: maize as a model system, Trends Plant Sci. 9 (2004) 293–301.
[5] C. Emanuel, A. Weihe, A. Graner, W.R. Hess, T. Börner, Chloroplast development affects expression of phage-type RNA polymerases in barley leaves, Plant J. 38 (2004) 460–472.
[6] R. Sharpe, A. Mahajan, E. Takacs, D. Stern, A.B. Cahoon, Developmental and cell type characterization of bundle sheath and mesophyll chloroplast transcript abundance in maize, Curr. Genet. 57 (2011) 89–102.
[7] A.B. Cahoon, E. Takacs, R. Sharpe, D. Stern, Nuclear, chloroplast, and mitochondrial transcript abundance along a maize leaf developmental gradient, Plant Mol. Biol. 66 (2008) 33–46.
[8] A.B. Cahoon, F.M. Harris, D.B. Stern, Analysis of developing maize plastids reveals two mRNA stability classes correlating with RNA polymerase type, EMBO Rep. 5 (2004) 801–806.
[9] R. Bock, Genetic engineering of the chloroplast: novel tools and new applications, Curr. Opin. Biotechnol. 26 (2014) 7–13.
[10] S.S. Merchant, S.E. Prochnik, O. Vallon, E.H. Harris, S.J. Karpowicz, G.B. Witman, A. Terry, A. Salamov, L.K. Fritz-Laylin, L. Marechal-Drouard, W.F. Marshall, L.H. Qu, D.R. Nelson, A.A. Sanderfoot, M.H. Spalding, V.V. Kapitonov, Q. Ren, P. Ferris, E. Lindquist, H. Shapiro, S.M. Lucas, J. Grimwood, J. Schmutz, P. Cardol, H. Cerutti, G. Chanfreau, C.L. Chen, V. Cognat, M.T. Croft, R. Dent, S. Dutcher, E. Fernandez, H. Fukuzawa, D. Gonzalez-Ballester, D. Gonzalez-Halphen, A. Hallmann, M. Hanikenne, M. Hippler, W. Inwood, K. Jabbari, M. Kalanon, R. Kuras, P.A. Lefebvre, S.D. Lemaire, A.V. Lobanov, M. Lohr, A. Manuell, I. Meier, L. Mets, M. Mittag, T. Mittelmeier, J.V. Moroney, J. Moseley, C. Napoli, A.M. Nedelcu, K. Niyogi, S.V. Novoselov, I.T. Paulsen, G. Pazour, S. Purton, J.P. Ral, D.M. Riano-Pachon, W. Riekhof, L. Rymarquis, M. Schroda, D. Stern, J. Umen, R. Willows, N. Wilson, S.L. Zimmer, J. Allmer, J. Balk, K. Bisova, C.J. Chen, M. Elias, K. Gendler, C. Hauser, M.R. Lamb, H. Ledford, J.C. Long, J. Minagawa, M.D. Page, J. Pan, W. Pootakham, S. Roje, A. Rose, E. Stahlberg, A.M. Terauchi, P. Yang, S. Ball, C. Bowler, C.L. Dieckmann, V.N. Gladyshev, P. Green, R. Jorgensen, S. Mayfield, B. Mueller-Roeber, S. Rajamani, R.T. Sayre, P. Brokstein, I. Dubchak, D. Goodstein, L. Hornick, Y.W. Huang, J. Jhaveri, Y. Luo, D. Martinez, W.C. Ngau, B. Otillar, A. Poliakov, A. Porter, L. Szajkowski, G. Werner, K. Zhou, I.V. Grigoriev, D.S. Rokhsar, A.R. Grossman, The Chlamydomonas genome reveals the evolution of key animal and plant functions, Science 318 (2007) 245–250.
[11] I.K. Blaby, C.E. Blaby-Haas, N. Tourasse, E.F. Hom, D. Lopez, M. Aksoy, A. Grossman, J. Umen, S. Dutcher, M. Porter, S. King, G.B. Witman, M. Stanke, E.H. Harris, D. Goodstein, J. Grimwood, J. Schmutz, O. Vallon, S.S. Merchant, S. Prochnik, The Chlamydomonas genome project: a decade on, Trends Plant Sci. 19 (2014) 672–680.
[12] M.A. Block, R. Douce, J. Joyard, N. Rolland, Chloroplast envelope membranes: a dynamic interface between plastids and the cytosol, Photosynth. Res. 92 (2007) 225–244.
[13] A. Rast, S. Heinz, J. Nickelsen, Biogenesis of thylakoid membranes, Biochim. Biophys. Acta 1847 (2015) 821–830.
[14] M. Sugiura, Plastid mRNA translation, in: P. Maliga (Ed.), Chloroplast Biotechnology, Humana Press 2014, pp. 73–91.
[15] J. Nickelsen, A.-V. Bohne, P. Westhoff, Chloroplast gene expression—translation, in: S.M. Theg, F.-A. Wollman (Eds.), Plastid Biology, Springer, New York 2014, pp. 49–78.
[16] W. Zerges, C. Hauser, Chapter 28—Protein synthesis in the chloroplast, in: E. Harris, D.B. Stern, G.B. Witman (Eds.), The Chlamydomonas Sourcebook, Second EditionElsevier 2009, pp. 967–1025.
[17] J.D. Rochaix, Redox regulation of thylakoid protein kinases and photosynthetic gene expression, Antioxid. Redox Signal. 18 (2013) 2184–2201.
[18] P. Mulo, I. Sakurai, E.M. Aro, Strategies for psbA gene expression in cyanobacteria, green algae and higher plants: from transcription to PSII repair, Biochim. Biophys. Acta 1817 (2012) 247–257.
[19] A. Barkan, I. Small, Pentatricopeptide repeat proteins in plants, Annu. Rev. Plant Biol. 65 (2014) 415–442.
[20] B.L. Weis, E. Schleiff, W. Zerges, Protein targeting to subcellular organelles via MRNA localization, Biochim. Biophys. Acta 1833 (2013) 260–273.
[21] J. Nickelsen, W. Zerges, Thylakoid biogenesis has joined the new era of bacterial cell biology, Front Plant Sci. 4 (2013) 458.
[22] A. Vitlin Gruber, S. Nisemblat, A. Azem, C. Weiss, The complexity of chloroplast chaperonins, Trends in Plant Science 18 (2013) 688–694.
[23] A. Nordhues, S.M. Miller, T. Mühlhaus, M. Schroda, Chapter two—New insights into the roles of molecular chaperones in Chlamydomonas and Volvox, in: W.J. Kwang (Ed.), International Review of Cell and Molecular BiologyAcademic Press 2010, pp. 75–113.
[24] A.M. Hotto, A. Germain, D.B. Stern, Plastid non-coding RNAs: emerging candidates for gene regulation, Trends Plant Sci. 17 (2012) 737–744.
[25] N. Tiller, R. Bock, The translational apparatus of plastids and its role in plant development, Mol. Plant 7 (2014) 1105–1120.
[26] P. Jarvis, E. Lopez-Juez, Biogenesis and homeostasis of chloroplasts and other plastids, Nat. Rev. Mol. Cell Biol. 14 (2013) 787–802.
[27] F. Barneche, V. Winter, M. Crevecoeur, J.D. Rochaix, ATAB2 is a novel factor in the signalling pathway of light-controlled synthesis of photosystem proteins, EMBO J. 25 (2006) 5907–5918.
[28] D. Dauvillee, O. Stampacchia, J. Girard-Bascou, J.D. Rochaix, Tab2 is a novel conserved RNA binding protein required for translation of the chloroplast psaB mRNA, EMBO J. 22 (2003) 6378–6388.
[29] M. Ploscher, V. Reisinger, L.A. Eichacker, Proteomic comparison of etioplast and chloroplast protein complexes, J. Proteome. 74 (2011) 1256–1265.
[30] T. Kleffmann, A. von Zychlinski, D. Russenberger, M. Hirsch-Hoffmann, P. Gehrig, W. Gruissem, S. Baginsky, Proteome dynamics during plastid differentiation in rice, Plant Physiol. 143 (2007) 912–923.
[31] J. Kim, J.E. Mullet, A mechanism for light-induced translation of the rbcL mRNA encoding the large subunit of ribulose-1,5-bisphosphate carboxylase in barley chloroplasts, Plant Cell Physiol. 44 (2003) 491–499.
[32] R.R. Klein, J.E. Mullet, Control of gene expression during higher plant chloroplast biogenesis. Protein synthesis and transcript levels of psbA, psaA-psaB, and rbcL in dark-grown and illuminated barley seedlings, J. Biol. Chem. 262 (1987) 4341–4348.
[33] R.R. Klein, J. Mullet, Regulation of Chloroplast-encoded Chlorophyll-binding protein translation during higher plant chloroplast biogenesis, J. Biol. Chem. 261 (1986) 11138–11145.
[34] J. Kim, L.A. Eichacker, W. Rudiger, J.E. Mullet, Chlorophyll regulates accumulation of the plastid-encoded chlorophyll proteins P700 and D1 by increasing apoprotein stability, Plant Physiol. 104 (1994) 907–916.
[35] R.R. Klein, H.S. Mason, J.E. Mullet, Light-regulated translation of chloroplast proteins. I. Transcripts of psaA-psaB, psbA, and rbcL are associated with polysomes in dark-grown and illuminated barley seedlings, J. Cell Biol. 106 (1988) 289–301.
[36] J. Kim, J.E. Mullet, Ribosome-binding sites on chloroplast rbcL and psbA mRNAs and light-induced initiation of D1 translation, Plant Mol. Biol. 25 (1994) 437–448.
[37] L. Eichacker, H. Paulsen, W. Rudiger, Synthesis of chlorophyll a regulates translation of chlorophyll a apoproteins P700, CP47, CP43 and D2 in barley etioplasts, Eur. J. Biochem. 205 (1992) 17–24.
[38] J.M. Staub, P. Maliga, Translation of psbA mRNA is regulated by light via the 5′-untranslated region in tobacco plastids, Plant J. 6 (1994) 547–553.
[39] J.M. Staub, P. Maliga, Accumulation of D1 polypeptide in tobacco plastids is regulated via the untranslated region of the psbA mRNA, EMBO J. 12 (1993) 601–606.
[40] L.A. Eichacker, J. Soll, P. Lauterbach, W. Rudiger, R.R. Klein, J.E. Mullet, In vitro synthesis of chlorophyll a in the dark triggers accumulation of chlorophyll a apoproteins in barley etioplasts, J. Biol. Chem. 265 (1990) 13566–13571.
[41] J.E. Boynton, N.W. Gillham, E.H. Harris, J.P. Hosler, A.M. Johnson, A.R. Jones, B.L. Randolph-Anderson, D. Robertson, T.M. Klein, K.B. Shark, et al., Chloroplast transformation in Chlamydomonas with high velocity microprojectiles, Science 240 (1988) 1534–1538.
[42] R.R. Klein, P.E. Gamble, J.E. Mullet, Light-dependent accumulation of radiolabeled plastid-encoded Chlorophyll a-apoproteins requires Chlorophyll a: I. Analysis of

Chlorophyll-deficient mutants and phytochrome involvement, Plant Physiol. 88 (1988) 1246–1256.
[43] E. López-Juez, E. Dillon, Z. Magyar, S. Khan, S. Hazeldine, S.M. de Jager, J.A.H. Murray, G.T.S. Beemster, L. Bögre, H. Shanahan, Distinct light-initiated gene expression and cell cycle programs in the shoot apex and cotyledons of Arabidopsis, Plant Cell Online 20 (2008) 947–968.
[44] I. Ohad, Biogenesis and modulation of membrane properties in greening *Chlamydomonas reinhardi*, y-1 cells, Methods Enzymol. 32 (Part) (1974) 865–871.
[45] I. Ohad, P. Siekevitz, G.E. Palade, Biogenesis of chloroplast membranes. II. Plastid differentiation during greening of a dark-grown algal mutant (*Chlamydomonas reinhardii*), J. Cell Biol. 35 (1967) 553–584.
[46] I. Ohad, P. Siekevitz, G.E. Palade, Biogenesis of chloroplast membranes. I. Plastid dedifferentiation in a dark-grown algal mutant (*Chlamydomonas reinhardii*), J. Cell Biol. 35 (1967) 521–552.
[47] P. Malnoe, S.P. Mayfield, J.D. Rochaix, Comparative analysis of the biogenesis of photosystem II in the wild-type and Y-1 mutant of *Chlamydomonas reinhardtii*, J. Cell Biol. 106 (1988) 609–616.
[48] C. Bouet, R. Schantz, G. Dubertret, B. Pineau, G. Ledoigt, Translational regulation of protein synthesis during light-induced chloroplast development in Euglena, Planta 167 (1986) 511–520.
[49] K. Okazaki, Y. Kabeya, S.Y. Miyagishima, The evolution of the regulatory mechanism of chloroplast division, Plant Signal. Behav. 5 (2010) 164–167.
[50] P. Klaff, W. Gruissem, Changes in chloroplast mRNA stability during leaf development, Plant Cell 3 (1991) 517–529.
[51] M. Kim, D.A. Christopher, J.E. Mullet, Direct evidence for selective modulation of psbA, rpoA, rbcL and 16S RNA stability during barley chloroplast development, Plant Mol. Biol. 22 (1993) 447–463.
[52] M.L. Salvador, U. Klein, L. Bogorad, Light-regulated and endogenous fluctuations of chloroplast transcript levels in Chlamydomonas. Regulation by transcription and RNA degradation, Plant J. 3 (1993) 213–219.
[53] J.P. Hosler, E.A. Wurtz, E.H. Harris, N.W. Gillham, J.E. Boynton, Relationship between gene dosage and gene-expression in the chloroplast of *Chlamydomonas reinhardtii*, Plant Physiol. 91 (1989) 648–655.
[54] S. Eberhard, D. Drapier, F.A. Wollman, Searching limiting steps in the expression of chloroplast-encoded proteins: relations between gene copy number, transcription, transcript abundance and translation rate in the chloroplast of *Chlamydomonas reinhardtii*, Plant J. 31 (2002) 149–160.
[55] A. Barkan, Expression of plastid genes: organelle-specific elaborations on a prokaryotic scaffold, Plant Physiol. 155 (2011) 1520–1532.
[56] T. Shikanai, S. Fujii, Function of PPR proteins in plastid gene expression, RNA Biol. 10 (2013) 1446–1456.
[57] A.D. Idoine, A. Boulouis, J. Rupprecht, R. Bock, The diurnal logic of the expression of the chloroplast genome in *Chlamydomonas reinhardtii*, PLoS One 9 (2014) e108760.
[58] D.L. Herrin, A.S. Michaels, A.L. Paul, Regulation of genes encoding the large subunit of ribulose-1,5-bisphosphate carboxylase and the photosystem II polypeptides D-1 and D-2 during the cell cycle of *Chlamydomonas reinhardtii*, J. Cell Biol. 103 (1986) 1837–1845.
[59] I. Edhofer, S.K. Muhlbauer, L.A. Eichacker, Light regulates the rate of translation elongation of chloroplast reaction center protein D1, Eur. J. Biochem. 257 (1998) 78–84.
[60] S.K. Muhlbauer, L.A. Eichacker, Light-dependent formation of the photosynthetic proton gradient regulates translation elongation in chloroplasts, J. Biol. Chem. 273 (1998) 20935–20940.
[61] A.K. Mattoo, H. Hoffman-Falk, J.B. Marder, M. Edelman, Regulation of protein metabolism: coupling of photosynthetic electron trasport to in vivo degradation of the rapidly metabolized 32-kilodalton protein in the chloroplast membranes, Proc. Natl. Acad. Sci. U. S. A. 81 (1984) 1380–1384.
[62] H. Fromm, M. Devic, R. Fluhr, M. Edelman, Control of psbA gene expression: in mature Spirodela chloroplasts light regulation fo 32-kd protein synthesis is independent of transcript level, EMBO J 4 (1985) 291–295.
[63] N.H. Chua, G. Blobel, P. Siekevitz, G.E. Palade, Periodic variations in the ratio of free to thylakoid-bound chloroplast ribosomes during the cell cycle of *Chlamydomonas reinhardtii*, J. Cell Biol. 71 (1976) 497–514.
[64] J. Lee, D. Herrin, Assessing the relative importance of light and the circadian clock in controlling chloroplast translation in *Chlamydomonas reinhardtii*, Photosynth. Res. 72 (2002) 295–306.
[65] T. Trebitsh, A. Levitan, A. Sofer, A. Danon, Translation of chloroplast psbA mRNA is modulated in the light by counteracting oxidizing and reducing activities, Mol. Cell. Biol. 20 (2000) 1116–1123.
[66] M.P. Timko, Pigment biosynthesis: chlorophylls, heme, and carotenoids, in: J.D. Rochaix, M. Goldschmidt-Clermont, S. Merchant (Eds.), Molecular Biology of Chlamydomonas: Chloroplasts and Mitochondria, Klewer Academic Publishers, Dordrecht, The Netherlands 1998, pp. 403–420.
[67] A.B. Cahoon, M.P. Timko, Yellow-in-the-dark mutants of Chlamydomonas lack the CHLL subunit of light-independent protochlorophyllide reductase, Plant Cell 12 (2000) 559–568.
[68] J. Uniacke, W. Zerges, Photosystem II assembly and repair are differentially localized in Chlamydomonas, Plant Cell 19 (2007) 3640–3654.
[69] J. Uniacke, W. Zerges, Chloroplast protein targeting involves localized translation in Chlamydomonas, Proc. Natl. Acad. Sci. U. S. A. 106 (2009) 1439–1444.
[70] A.V. Bohne, C. Schwarz, M. Schottkowski, M. Lidschreiber, M. Piotrowski, W. Zerges, J. Nickelsen, Reciprocal regulation of protein synthesis and carbon metabolism for thylakoid membrane biogenesis, PLoS Biol. 11 (2013) e1001482.
[71] M. Schottkowski, M. Peters, Y. Zhan, O. Rifai, Y. Zhang, W. Zerges, Biogenic membranes of the chloroplast in *Chlamydomonas reinhardtii*, Proc. Natl. Acad. Sci. U. S. A. 109 (2012) 19286–19291.
[72] W. Majeran, G. Friso, Y. Asakura, X. Qu, M. Huang, L. Ponnala, K.P. Watkins, A. Barkan, K.J. van Wijk, Nucleoid-enriched proteomes in developing plastids and chloroplasts from maize leaves: a new conceptual framework for nucleoid functions, Plant Physiol. 158 (2012) 156–189.
[73] M. Grote, M. Engelhard, P. Hegemann, Of ion pumps, sensors and channels—perspectives on microbial rhodopsins between science and history, Biochim. Biophys. Acta (BBA)-Bioenergetics 1837 (2014) 533–545.
[74] J.J. Casal, Photoreceptor signaling networks in plant responses to shade, Annu. Rev. Plant Biol. 64 (2013) 403–427.
[75] D.A. Christopher, P.H. Hoffer, DET1 represses a chloroplast blue light-responsive promoter in a developmental and tissue-specific manner in *Arabidopsis thaliana*, Plant J. 14 (1998) 1–11.
[76] D.A. Christopher, M. Kim, J.E. Mullet, A novel light-regulated promoter is conserved in cereal and dicot chloroplasts, Plant Cell 4 (1992) 785–798.
[77] T.B. Sexton, D.A. Christopher, J.E. Mullet, Light-induced switch in barley psbD-psbC promoter utilization: a novel mechanism regulating chloroplast gene expression, EMBO J 9 (1990) 4485–4494.
[78] K.E. Thum, M. Kim, D.A. Christopher, J.E. Mullet, Cryptochrome 1, cryptochrome 2, and phytochrome A co-activate the chloroplast psbD blue light-responsive promoter, Plant Cell 13 (2001) 2747–2760.
[79] J. Pfalz, M. Liebers, M. Hirth, B. Grubler, U. Holtzegel, Y. Schroter, L. Dietzel, T. Pfannschmidt, Environmental control of plant nuclear gene expression by chloroplast redox signals, Front Plant Sci. 3 (2012) 257.
[80] T. Pfannschmidt, C. Yang, The hidden function of photosynthesis: a sensing system for environmental conditions that regulates plant acclimation responses, Protoplasma 249 (Suppl. 2) (2012) S125–S136.
[81] C. Glasser, G. Haberer, I. Finkemeier, T. Pfannschmidt, T. Kleine, D. Leister, K.J. Dietz, R.E. Hausler, B. Grimm, K.F. Mayer, Meta-analysis of retrograde signaling in *Arabidopsis thaliana* reveals a core module of genes embedded in complex cellular signaling networks, Mol. Plant 7 (2014) 1167–1190.
[82] W. Zerges, Does complexity constrain organelle evolution? Trends Plant Sci. 7 (2002) 175–182.
[83] T. Pfannschmidt, A. Nilsson, A. Tullberg, G. Link, J.F. Allen, Direct transcriptional control of the chloroplast genes psbA and psaAB adjusts photosynthesis to light energy distribution in plants, IUBMB Life 48 (1999) 271–276.
[84] M.L. Salvador, U. Klein, The redox state regulates RNA degradation in the chloroplast of *Chlamydomonas reinhardtii*, Plant Physiol. 121 (1999) 1367–1374.
[85] T. Trebitsh, A. Danon, Translation of chloroplast psbA mRNA is regulated by signals initiated by both photosystems II and I, Proc. Natl. Acad. Sci. U. S. A. 98 (2001) 12289–12294.
[86] A. Danon, S.P. Mayfield, Light-regulated translation of chloroplast messenger RNAs through redox potential, Science 266 (1994) 1717–1719.
[87] L. Zhang, V. Paakkarinen, K.J. van Wijk, E.M. Aro, Biogenesis of the chloroplast-encoded D1 protein: regulation of translation elongation, insertion, and assembly into photosystem II, Plant Cell 12 (2000) 1769–1782.
[88] Y. Schroter, S. Steiner, K. Matthai, T. Pfannschmidt, Analysis of oligomeric protein complexes in the chloroplast sub-proteome of nucleic acid-binding proteins from mustard reveals potential redox regulators of plastid gene expression, Proteomics 10 (2010) 2191–2204.
[89] P.H. Quail, Phytochromes, Curr. Biol. 20 (2010) R504–R507.
[90] J. Li, G. Li, H. Wang, X. Wang Deng, Phytochrome Signaling Mechanisms, The Arabidopsis Book / American Society of Plant Biologists, 9 2011, p. e0148.
[91] A. Michaels, D.L. Herrin, Translational regulation of chloroplast gene expression during the *light–dark* cell cycle of Chlamydomonas: evidence for control by ATP/energy supply, Biochem. Biophys. Res. Commun. 170 (1990) 1082–1088.
[92] A. Danon, S.P. Mayfield, ADP-dependent phosphorylation regulates RNA-binding in vitro: implications in light-modulated translation, EMBO J. 13 (1994) 2227–2235.
[93] M. Taniguchi, H. Kuroda, K. Satoh, ATP-dependent protein synthesis in isolated pea chloroplasts. Evidence for accumulation of a translation intermediate of the D1 protein, FEBS Lett. 317 (1993) 57–61.
[94] W. Zerges, Translation in chloroplasts, Biochimie 82 (2000) 583–601.
[95] C. Schwarz, A.V. Bohne, F. Wang, F.J. Cejudo, J. Nickelsen, An intermolecular disulfide-based light switch for chloroplast psbD gene expression in *Chlamydomonas reinhardtii*, Plant J. 72 (2012) 378–389.
[96] D. Barnes, A. Cohen, R.K. Bruick, K. Kantardjieff, S. Fowler, E. Efuet, S.P. Mayfield, Identification and characterization of a novel RNA binding protein that associates with the 5′-untranslated region of the chloroplast psbA mRNA, Biochemistry 43 (2004) 8541–8550.
[97] C. Schwarz, I. Elles, J. Kortmann, M. Piotrowski, J. Nickelsen, Synthesis of the D2 protein of photosystem II in Chlamydomonas is controlled by a high molecular mass complex containing the RNA stabilization factor Nac2 and the translational activator RBP40, Plant Cell 19 (2007) 3627–3639.
[98] B. Klinkert, I. Elles, J. Nickelsen, Translation of chloroplast psbD mRNA in Chlamydomonas is controlled by a secondary RNA structure blocking the AUG start codon, Nucleic Acids Res. 34 (2006) 386–394.
[99] F. Ossenbuhl, J. Nickelsen, cis- and trans-Acting determinants for translation of psbD mRNA in *Chlamydomonas reinhardtii*, Mol. Cell. Biol. 20 (2000) 8134–8142.
[100] J. Nickelsen, M. Fleischmann, E. Boudreau, M. Rahire, J.D. Rochaix, Identification of cis-acting RNA leader elements required for chloroplast psbD gene expression in Chlamydomonas, Plant Cell 11 (1999) 957–970.
[101] A. Danon, S.P. Mayfield, Light regulated translational activators: identification of chloroplast gene specific mRNA binding proteins, EMBO J 10 (1991) 3993–4001.

[102] C.B. Yohn, A. Cohen, A. Danon, S.P. Mayfield, A poly(A) binding protein functions in the chloroplast as a message-specific translation factor, Proc. Natl. Acad. Sci. U. S. A. 95 (1998) 2238–2243.
[103] A. Manuell, M.V. Beligni, K. Yamaguchi, S.P. Mayfield, Regulation of chloroplast translation: interactions of RNA elements, RNA-binding proteins and the plastid ribosome, Biochem. Soc. Trans. 32 (2004) 601–605.
[104] J. Kim, S.P. Mayfield, Protein disulfide isomerase as a regulator of chloroplast translational activation, Science 278 (1997) 1954–1957.
[105] S.D. Lemaire, B. Guillon, P. Le Marechal, E. Keryer, M. Miginiac-Maslow, P. Decottignies, New thioredoxin targets in the unicellular photosynthetic eukaryote *Chlamydomonas reinhardtii*, Proc. Natl. Acad. Sci. U. S. A. 101 (2004) 7475–7480.
[106] C.L. Fong, A. Lentz, S.P. Mayfield, Disulfide bond formation between RNA binding domains is used to regulate mRNA binding activity of the chloroplast poly(A)-binding protein, J. Biol. Chem. 275 (2000) 8275–8278.
[107] T. Alergand, H. Peled-Zehavi, Y. Katz, A. Danon, The chloroplast protein disulfide isomerase RB60 reacts with a regulatory disulfide of the RNA-binding protein RB47, Plant Cell Physiol. 47 (2006) 540–548.
[108] G. Wittenberg, A. Levitan, T. Klein, I. Dangoor, N. Keren, A. Danon, Knockdown of the *Arabidopsis thaliana* chloroplast protein disulfide isomerase 6 results in reduced levels of photoinhibition and increased D1 synthesis in high light, Plant J. 78 (2014) 1003–1013.
[109] F. Ossenbuhl, K. Hartmann, J. Nickelsen, A chloroplast RNA binding protein from stromal thylakoid membranes specifically binds to the 5′ untranslated region of the psbA mRNA, Eur. J. Biochem. 269 (2002) 3912–3919.
[110] A. Tovar-Mendez, J.A. Miernyk, D.D. Randall, Regulation of pyruvate dehydrogenase complex activity in plant cells, Eur. J. Biochem. 270 (2003) 1043–1049.
[111] Y. Choquet, F.A. Wollman, The CES process, in: E.H. Harris, D.B. Stern, G.B. Witman (Eds.), The Chlamydomonas Sourcebook, Second EditionElsevier, Oxford 2009, pp. 1029–1066.
[112] C. de Vitry, J. Olive, D. Drapier, M. Recouvreur, F.A. Wollman, Posttranslational events leading to the assembly of photosystem II protein complex: a study using photosynthesis mutants from *Chlamydomonas reinhardtii*, J. Cell Biol. 109 (1989) 991–1006.
[113] J. Girard-Bascou, Y. Choquet, M. Schneider, M. Delosme, M. Dron, Characterization of a chloroplast mutation in the psaA2 gene of *Chlamydomonas reinhardtii*, Curr. Genet. 12 (1987) 489–495.
[114] R. Kuras, F.A. Wollman, The assembly of cytochrome b6/f complexes: an approach using genetic transformation of the green alga *Chlamydomonas reinhardtii*, EMBO J 13 (1994) 1019–1027.
[115] F. Morais, J. Barber, P.J. Nixon, The chloroplast-encoded alpha subunit of cytochrome b-559 is required for assembly of the photosystem two complex in both the light and the dark in *Chlamydomonas reinhardtii*, J. Biol. Chem. 273 (1998) 29315–29320.
[116] J.D. Rochaix, J. Erickson, Function and assembly of photosystem II: genetic and molecular analysis, Trends Biochem. Sci. 13 (1988) 56–59.
[117] O. Stampacchia, J. Girard-Bascou, J.L. Zanasco, W. Zerges, P. Bennoun, J.D. Rochaix, A nuclear-encoded function essential for translation of the chloroplast psaB mRNA in Chlamydomonas, Plant Cell 9 (1997) 773–782.
[118] K. Wostrikoff, J. Girard-Bascou, F.A. Wollman, Y. Choquet, Biogenesis of PSI involves a cascade of translational autoregulation in the chloroplast of Chlamydomonas, EMBO J. 23 (2004) 2696–2705.
[119] L. Minai, K. Wostrikoff, F.A. Wollman, Y. Choquet, Chloroplast biogenesis of photosystem II cores involves a series of assembly-controlled steps that regulate translation, Plant Cell 18 (2006) 159–175.
[120] D. Drapier, B. Rimbault, O. Vallon, F.A. Wollman, Y. Choquet, Intertwined translational regulations set uneven stoichiometry of chloroplast ATP synthase subunits, EMBO J. 26 (2007) 3581–3591.
[121] Y. Choquet, D.B. Stern, K. Wostrikoff, R. Kuras, J. Girard-Bascou, F.A. Wollman, Translation of cytochrome f is autoregulated through the 5′ untranslated region of petA mRNA in Chlamydomonas chloroplasts, Proc. Natl. Acad. Sci. U. S. A. 95 (1998) 4380–4385.
[122] R. Kuras, F.A. Wollman, P. Joliot, Conversion of cytochrome f to a soluble form in vivo in *Chlamydomonas reinhardtii*, Biochemistry 34 (1995) 7468–7475.
[123] Y. Choquet, F. Zito, K. Wostrikoff, F.A. Wollman, Cytochrome f translation in Chlamydomonas chloroplast is autoregulated by its carboxyl-terminal domain, Plant Cell 15 (2003) 1443–1454.
[124] K. Wostrikoff, Y. Choquet, F.A. Wollman, J. Girard-Bascou, TCA1, a single nuclear-encoded translational activator specific for petA mRNA in *Chlamydomonas reinhardtii* chloroplast, Genetics 159 (2001) 119–132.
[125] A. Boulouis, C. Raynaud, S. Bujaldon, A. Aznar, F.A. Wollman, Y. Choquet, The nucleus-encoded trans-acting factor MCA1 plays a critical role in the regulation of cytochrome f synthesis in Chlamydomonas chloroplasts, Plant cell 23 (2011) 333–349.
[126] E.M. del Campo, Post-Transcriptional Control of Chloroplast Gene Expression, Gene Regulation and Systems Biology 3 (2009) 31–47.
[127] C. Raynaud, C. Loiselay, K. Wostrikoff, R. Kuras, J. Girard-Bascou, F.A. Wollman, Y. Choquet, Evidence for regulatory function of nucleus-encoded factors on mRNA stabilization and translation in the chloroplast, Proc. Natl. Acad. Sci. U. S. A. 104 (2007) 9093–9098.
[128] C. Loiselay, N.J. Gumpel, J. Girard-Bascou, A.T. Watson, S. Purton, F.A. Wollman, Y. Choquet, Molecular identification and function of cis- and trans-acting determinants for petA transcript stability in *Chlamydomonas reinhardtii* chloroplasts, Mol. Cell. Biol. 28 (2008) 5529–5542.
[129] R.A. Monde, F. Zito, J. Olive, F.A. Wollman, D.B. Stern, Post-transcriptional defects in tobacco chloroplast mutants lacking the cytochrome b6/f complex, Plant J. 21 (2000) 61–72.
[130] K. Wostrikoff, D. Stern, Rubisco large-subunit translation is autoregulated in response to its assembly state in tobacco chloroplasts, Proc. Natl. Acad. Sci. U. S. A. 104 (2007) 6466–6471.
[131] S. Rodermel, J. Haley, C.Z. Jiang, C.H. Tsai, L. Bogorad, A mechanism for intergenomic integration: abundance of ribulose bisphosphate carboxylase small-subunit protein influences the translation of the large-subunit mRNA, Proc. Natl. Acad. Sci. U. S. A. 93 (1996) 3881–3885.
[132] K. Wostrikoff, A. Clark, S. Sato, T. Clemente, D. Stern, Ectopic expression of Rubisco subunits in maize mesophyll cells does not overcome barriers to cell type-specific accumulation, Plant Physiol. 160 (2012) 419–432.
[133] L. Zhang, V. Paakkarinen, K.J. van Wijk, E.M. Aro, Co-translational assembly of the D1 protein into photosystem II, J. Biol. Chem. 274 (1999) 16062–16067.
[134] K.J. van Wijk, S. Bingsmark, E.M. Aro, B. Andersson, In vitro synthesis and assembly of photosystem II core proteins. The D1 protein can be incorporated into photosystem II in isolated chloroplasts and thylakoids, J. Biol. Chem. 270 (1995) 25685–25695.
[135] K.J. van Wijk, B. Andersson, E.M. Aro, Kinetic resolution of the incorporation of the D1 protein into photosystem II and localization of assembly intermediates in thylakoid membranes of spinach chloroplasts, J. Biol. Chem. 271 (1996) 9627–9636.
[136] R. Zoschke, K.P. Watkins, A. Barkan, A rapid ribosome profiling method elucidates chloroplast ribosome behavior in vivo, Plant Cell 25 (2013) 2265–2275.
[137] I. Cohen, Y. Sapir, M. Shapira, A conserved mechanism controls translation of Rubisco large subunit in different photosynthetic organisms, Plant Physiol. 141 (2006) 1089–1097.
[138] N. Keren, H. Gong, I. Ohad, Oscillations of reaction center II-D1 protein degradation in vivo induced by repetitive light flashes. Correlation between the level of RCII-QB- and protein degradation in low light, J. Biol. Chem. 270 (1995) 806–814.
[139] I. Vass, Molecular mechanisms of photodamage in the Photosystem II complex, Biochim. Biophys. Acta (BBA)-Bioenergetics 1817 (2012) 209–217.
[140] S. Jarvi, M. Suorsa, E.M. Aro, PhotosystemII repair in plant chloroplasts—regulation, assisting proteins and shared components with photosystem II biogenesis, Biochim. Biophys. Acta 1847 (2015) 900–909.
[141] J. Nickelsen, B. Rengstl, Photosystem II assembly: from cyanobacteria to plants, Annu. Rev. Plant Biol. 64 (2013) 609–635.
[142] B. Walter, A. Hristou, M.M. Nowaczyk, D. Schunemann, In vitro reconstitution of cotranslational D1 insertion reveals a role of the cpSec/Alb3 translocase and Vipp1 in photosystem II biogenesis, Biochem J (2015).
[143] L. Zhang, V. Paakkarinen, M. Suorsa, E.M. Aro, A SecY homologue is involved in chloroplast-encoded D1 protein biogenesis, J. Biol. Chem. 276 (2001) 37809–37814.
[144] L. Zhang, E.-M. Aro, Synthesis, membrane insertion and assembly of the chloroplast-encoded D1 protein into photosystem II, FEBS Lett. 512 (2002) 13–18.
[145] L. Peng, J. Ma, W. Chi, J. Guo, S. Zhu, Q. Lu, C. Lu, L. Zhang, LOW PSII ACCUMULATION1 is involved in efficient assembly of photosystem II in *Arabidopsis thaliana*, Plant Cell 18 (2006) 955–969.
[146] U. Armbruster, J. Zuhlke, B. Rengstl, R. Kreller, E. Makarenko, T. Ruhle, D. Schunemann, P. Jahns, B. Weisshaar, J. Nickelsen, D. Leister, The Arabidopsis thylakoid protein PAM68 is required for efficient D1 biogenesis and photosystem II assembly, Plant Cell 22 (2010) 3439–3460.
[147] A. Fu, Z. He, H.S. Cho, A. Lima, B.B. Buchanan, S. Luan, A chloroplast cyclophilin functions in the assembly and maintenance of photosystem II in *Arabidopsis thaliana*, Proc. Natl. Acad. Sci. U. S. A. 104 (2007) 15947–15952.
[148] S. Sirpio, A. Khrouchtchova, Y. Allahverdiyeva, M. Hansson, R. Fristedt, A.V. Vener, H.V. Scheller, P.E. Jensen, A. Haldrup, E.M. Aro, AtCYP38 ensures early biogenesis, correct assembly and sustenance of photosystem II, Plant J. 55 (2008) 639–651.
[149] J. Komenda, J. Nickelsen, M. Tichy, O. Prasil, L.A. Eichacker, P.J. Nixon, The cyanobacterial homologue of HCF136/YCF48 is a component of an early photosystem II assembly complex and is important for both the efficient assembly and repair of photosystem II in Synechocystis sp. PCC 6803, J. Biol. Chem. 283 (2008) 22390–22399.
[150] H. Plucken, B. Muller, D. Grohmann, P. Westhoff, L.A. Eichacker, The HCF136 protein is essential for assembly of the photosystem II reaction center in *Arabidopsis thaliana*, FEBS Lett. 532 (2002) 85–90.
[151] M. Schroda, O. Vallon, F.A. Wollman, C.F. Beck, A chloroplast-targeted heat shock protein 70 (HSP70) contributes to the photoprotection and repair of photosystem II during and after photoinhibition, Plant Cell 11 (1999) 1165–1178.
[152] K. Yokthongwattana, B. Chrost, S. Behrman, C. Casper-Lindley, A. Melis, Photosystem II damage and repair cycle in the green alga *Dunaliella salina*: involvement of a chloroplast-localized HSP70, Plant Cell Physiol. 42 (2001) 1389–1397.
[153] K.J. van Wijk, M. Roobol-Boza, R. Kettunen, B. Andersson, E.M. Aro, Synthesis and assembly of the D1 protein into photosystem II: processing of the C-terminus and identification of the initial assembly partners and complexes during photosystem II repair, Biochemistry 36 (1997) 6178–6186.
[154] K.J. van Wijk, L. Eichacker, Light is required for efficient translation elongation and subsequent integration of the D1-protein into photosystem II, FEBS Lett. 388 (1996) 89–93.
[155] S. Park, P. Khamai, J.G. Garcia-Cerdan, A. Melis, REP27, a tetratricopeptide repeat nuclear-encoded and chloroplast-localized protein, functions in D1/32-kD reaction center protein turnover and photosystem II repair from photodamage, Plant Physiol. 143 (2007) 1547–1560.
[156] G. Wittenberg, A. Levitan, T. Klein, I. Dangoor, N. Keren, A. Danon, Knockdown of the *Arabidopsis thaliana* chloroplast protein disulfide isomerase 6 results in reduced levels of photoinhibition and increased D1 synthesis in high light, Plant J. 78 (2014) 1003–1013.
[157] S. Franklin, B. Ngo, E. Efuet, S. Mayfield, Development of a GFP reporter gene for *Chlamydomonas reinhardtii* chloroplast, Plant J. 30 (2002) 733–744.

[158] R.K. Bruick, S.P. Mayfield, Processing of the psbA 5′ untranslated region in *Chlamydomonas reinhardtii* depends upon factors mediating ribosome association, J. Cell Biol. 143 (1998) 1145–1153.
[159] M. Shapira, A. Lers, P.B. Heifetz, V. Irihimovitz, C.B. Osmond, N.W. Gillham, J.E. Boynton, Differential regulation of chloroplast gene expression in *Chlamydomonas reinhardtii* during photoacclimation: light stress transiently suppresses synthesis of the Rubisco LSU protein while enhancing synthesis of the PS II D1 protein, Plant Mol. Biol. 33 (1997) 1001–1011.
[160] V. Irihimovitch, M. Shapira, Glutathione redox potential modulated by reactive oxygen species regulates translation of Rubisco large subunit in the chloroplast, J. Biol. Chem. 275 (2000) 16289–16295.
[161] I. Cohen, J.A. Knopf, V. Irihimovitch, M. Shapira, A proposed mechanism for the inhibitory effects of oxidative stress on Rubisco assembly and its subunit expression, Plant Physiol. 137 (2005) 738–746.
[162] I. Yosef, V. Irihimovitch, J.A. Knopf, I. Cohen, I. Orr-Dahan, E. Nahum, C. Keasar, M. Shapira, RNA binding activity of the ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit from *Chlamydomonas reinhardtii*, J. Biol. Chem. 279 (2004) 10148–10156.
[163] Y. Yagi, T. Shiina, Recent advances in the study of chloroplast gene expression and its evolution, Front Plant Sci. 5 (2014) 61.
[164] P.J. Nixon, F. Michoux, J. Yu, M. Boehm, J. Komenda, Recent advances in understanding the assembly and repair of photosystem II, Ann. Bot. 106 (2010) 1–16.
[165] N.N. Deshpande, Y. Bao, D.L. Herrin, Evidence for light/redox-regulated splicing of psbA pre-RNAs in Chlamydomonas chloroplasts, RNA 3 (1997) 37–48.