

Cytokinins

Chemistry, Activity, and Function

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CRC Press

Boca Raton Ann Arbor London Tokyo

Library of Congress Cataloging-in-Publication Data

Cytokinins: chemistry, activity, and function / edited by David W. S. Mok and Machteld C. Mok

p. cm.

Includes bibliographical references and index.

ISBN 0-8493-6252-0

I. Cytokinins. I. Mok, David W. S. II. Mok, Machteld C.

QK898.C94C97 1994

581.19'27—dc20

93-6461

CIP

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International Standard Book Number 0-8493-6252-0

Library of Congress Card Number 93-6461

Printed in the United States of America 1 2 3 4 5 6 7 8 9 0

Printed on acid-free paper

Plastid Genes and Chloroplast Biogenesis

Ralf Reski

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I. PLASTIDS ARE A HETEROGENOUS ORGANELLE CLASS

Plastids are the DNA-containing organelles with the widest range of different forms and functions. Interconversion between different plastid types implies marked changes in their architecture and physiology. Furthermore, these changes go hand in hand with differentiation processes of cells and organs during plant development (reviewed by Herrmann et al.).¹ Energy, organic substances, and oxygen are provided by photosynthesis, and most of the photosynthetic products are formed in chloroplasts. They also catalyze key reactions in the reductive nitrogen and sulfur pathway, in lipid synthesis, and they synthesize important secondary metabolites. Specialized modifications are leukoplasts, amyloplasts, elaioplasts, and chromoplasts, which are characteristic for different tissues, exhibit marked structural differences, and lack chlorophyll. These organelle forms are involved in various fundamental biological processes, such as carbohydrate or lipid storage and plant propagation. During leaf senescence in angiosperms, chloroplast structures are degraded, temporally forming the last plastid type, gerontoplasts.² In vascular plants chloroplast biogenesis from less-differentiated organelle forms occurs: in vegetation tips the differentiation process starts from colorless proplastids. Angiosperms exhibit an additional pathway for chloroplast biogenesis: grown in darkness, proplastids differentiate to pale-yellow etioplasts with characteristic paracrystalline internal structures. Upon illumination, etioplasts develop into chloroplasts. In addition to light, in dicotyledonous angiosperms the biogenesis of chloroplasts is also regulated by intrinsic developmental signals that control leaf differentiation.³ However, in monocots the processes of primary leaf development and chloroplast development

are uncoupled.⁴ The common view is that in vascular plants only mesophyll cells house mature chloroplasts, indicating that cell-specific signals are also important for chloroplast biogenesis.⁵ Nevertheless, recent findings demonstrate active, but not fully differentiated, chloroplasts even in pith cells.⁶ Finally, the developmental stage of the chloroplast itself appears to regulate the expression of nuclear genes coding for plastid proteins.³

There are several established experimental systems to study chloroplast biogenesis and correlated cell and organ morphogenesis at the molecular level.

The light-controlled differentiation is studied during greening of etiolated seedlings. Morphogenetic changes occur within a few hours⁷ and are thus amenable to molecular analysis. Much work on chloroplast biogenesis in higher plants, particularly on the photocontrol of gene expression, has therefore been carried out with this etioplast/chloroplast transition.¹ However, this system is restricted to angiosperms, and plastid gene regulation during etioplast/chloroplast transition appears to be different from the one during regular proplastid/chloroplast transition.⁸

The *Arabidopsis thaliana det1* mutant develops as a light-grown plant even in darkness. The recessive nuclear mutation affects a variety of light-regulated traits, including leaf development, plastid morphology, and gene expression. Most probably, the wild-type *det1* gene product is a negative regulator in a signal transduction pathway that couples leaf and chloroplast development to light perception. This implies a constitutive expression of light-regulated genes in cell types where these genes are normally silent. In line with this model is the observation that cell cultures of this particular mutant become green even in the absence of cytokinins, conditions where normally no chloroplast biogenesis takes place.⁹

Leaves of monocots are widely used to study plastid differentiation processes. Cell division occurs only in a basal meristem, resulting in a gradient of cells, with increasing age, from the base to the tip.¹⁰ In a diurnal light regime, a continuous transition of proplastids to chloroplasts occurs in parallel to the basipetal increase in cell age.

In cereals the formation of plastid ribosomes is prevented by growth temperatures above 32°C.¹¹ The ribosome-deficient plastids resemble proplastids in size and structure. They do not differentiate into chloroplasts, although carotenoids are synthesized, and enzymes for chlorophyll biosynthesis are functioning, within these plastids.¹²⁻¹⁴ In contrast to treating plants with inhibitors of protein synthesis, the heat-induced deficiency of plastid ribosomes provides a system for studying interactions between plastids and the cytosol, with minimal risk of toxic side effects or damage by photodestruction (reviewed by Feierabend and Berberich¹⁵). Ribosome-deficient plastids can also be obtained from the barley nuclear mutant *albostrians*, with the advantage of ruling out side effects of elevated temperatures.¹⁶

II. PLASTIDS ARE SEMIAUTONOMOUS ORGANELLES

Plant cells are characterized by three different genomes that have their own machinery for gene expression: the prokaryotic ancestors of plastids and mitochondria lost their autonomy by losing most of their genes during the establishment of endosymbiosis.¹⁷ Some of these prokaryotic genes were transferred into the eukaryotic background of the nucleus. The problems arising for a coordinated expression of these genes, and the subsequent transport of their products into the ancestral organelle, are obvious and require the coevolution of three different genomes in one single cell.^{1,17} The eukaryon achieved its capability of photosynthesis by a process that started with the engulfment of autonomous prokaryotic cells, continued with the establishment of endosymbiosis between eukaryon and chloroplast, and culminated in the domestication of virile remnants (chloroplasts) to nongreen derivatives (proplastids, amyloplasts, gerontoplasts, chromoplasts, etc.) with specialized functions in higher plants. Thus, the phenomenon of plastid differentiation demonstrates the domestication of the prokaryon by the eukaryon and, finally, the evolutionary aspect of plant development.

The activity of genes involved in this differentiation of plastids has to be under temporal and spatial control. Furthermore, these genes have to respond to multiple extrinsic signals notifying

changes in the environment of the plant. Therefore, the role and importance of a specific signal, whether extrinsic or intrinsic, in the complex regulatory network around chloroplast biogenesis and accompanying cell and organ morphogenesis is likely to differ between the major plant groups.

Based on results from the *aurea* mutant^{18,19} and the *ghost* mutant²⁰ of tomato, the *albostrians* mutant²¹ and the *albina f17* mutant²² from barley, and carotenoid-deficient mutants in maize,²³ and from norflurazon treated plants,^{24,25} the *consensus* is now that the expression of some light-inducible nuclear genes is modulated by a factor generated by differentiated chloroplasts. This plastidic factor seems to be responsible for the expression of a certain set of nuclear genes: genes coding for proteins that are plastid constituents or that are, at least indirectly, involved in chloroplast biogenesis.²⁶⁻³¹ These observations reveal a common *trans*-acting factor modulating the expression of those nuclear genes that originally were coded by the prokaryotic DNA of the ancestors of chloroplasts. Nevertheless, the nature of the postulated plastidic factor is unknown.^{30,32}

A common view about gene regulation during light-induced chloroplast biogenesis is that it is transcriptional for nuclear genes, but translational or posttranslational for plastid genes.³³ Nevertheless, the situation seems to be more complex, as several plastid differentiation processes have been shown to be accompanied not only by changes in general transcriptional activity,³⁴ but also by changes in the relative transcription rates of individual genes, indicating the existence of gene-specific mechanisms for transcriptional regulation.¹ Examples are the development of proplastids to chloroplasts in *Hordeum* and *Sorghum*,^{8,35} light-dependent transformation of mature barley etioplasts to chloroplasts,³⁶ amyloplast formation in cultured tobacco cells,³⁷ and chromoplast formation in tomatoes.³⁸

Several mechanisms for changes in the transcriptional activity of plastid genes during plastid differentiation have been suggested; changes in the ptDNA copy number per cell can only confer to the nonspecific regulation of plastid genes and do not seem to play a vital role in chloroplast biogenesis.³⁹ Developmentally related changes in DNA methylation were observed in some studies,³⁸ but not in others.^{8,40} Likewise, variations in the conformation of the plastid DNA template, and differences in the three-dimensional structure of plastid nucleoids,⁴¹ have not been unequivocally proven yet. Differences in promoter strength and competition, changes in RNA polymerase to template ratios,³⁵ and different half-lives of mRNAs may influence transcription rates and cause accumulation rates that differ relative to each other as well.^{42,43} However, such

models are based on the hypothesis that all DNA circles in a given plastid are, to the same extent, physiologically active and that the *in vivo* situation is reflected by our *in vitro* data. In addition to these theories are two just emerging models for differential gene regulation.

The first model is that changes in the molecular composition of the transcriptional apparatus itself can cause differences in gene expression and the subsequent plastid differentiation processes. There are two possibilities: either these changes in gene expression can be caused by changes in the populations of several putative RNA-polymerases, or a varying specificity can be conferred, as in prokaryotes, by sigma factors associated with a core RNA-polymerase.

Plastid DNA encodes the *rpo* genes, with all polypeptides resembling the bacterial RNA-polymerase, and these genes are transcribed and translated.⁴⁴ Additionally, first evidence is available about sigma-like factors in the plastids of higher plants.⁴⁵⁻⁴⁷ Nevertheless, plastid extracts contain two fractions with RNA-polymerase activity, in all plants examined so far, whether alga or weed. These fractions differ from each other in biochemical terms (soluble vs. bound, molecular weight, composition) and were reported to differ in their preference to transcribe certain plastid genes, although these reports have given conflicting results.^{33,44,48-53} Whether the two fractions indeed contain different enzymes or just different states of one common core enzyme with various auxiliary proteins is still unknown.⁵⁴ However, in the last decade there have been hints for a nuclear-encoded plastidic RNA-polymerase.⁵⁵⁻⁵⁷ Utilizing barley with ribosome-deficient plastids, evidence was solidified for a plastidic RNA-polymerase translated on extraplastidic ribosomes.¹⁵ This nuclear-encoded enzyme seems to be constitutively active in proplastids, chloroplasts, and senescing plastids, whereas the soluble fraction, possibly encoded by the prokaryotic *rpo* genes, develops activity solely in differentiated chloroplasts,^{58,59} indicating a differential function of two different RNA-polymerases, at least in barley. Nevertheless, transcript levels of plastid genes coding proteins of the photosynthetic apparatus only accumulate during chloroplast biogenesis, pointing to the importance of posttranscriptional regulation.

The second model is that RNA-editing may be a mechanism involved in the differential regulation of gene expression. Editing was observed with kinetoplast RNA, mitochondrial, and nuclear genes.⁶⁰⁻⁶² All groups of plastid genes can be affected as well.⁶³⁻⁶⁵ The main function of RNA editing is the creation of an mRNA that can be translated into a

biologically active protein either by creating an initiator codon or by restoring codons for conserved amino acids. However, at the moment there are only first hints that differential mRNA editing really regulates gene expression. If so, quantitative Northern blots as well as *in vitro* transcription assays would not necessarily reflect the respective *in vivo* situation. According to our present knowledge, all editing processes in higher plants seem to bring down the peptide sequences to a *consensus* that is represented by the liverwort *Marchantia polymorpha*. This bryophyte is the first plant in which the total nucleotide sequence of ptDNA, as well as mtDNA, has been determined.^{66,67} Our analyses of mitochondrial and plastid genes of the moss *Phys-comitrella patens* reveal that moss and liverwort share significant gene homology different from higher plants.⁶⁸⁻⁷² Thus, RNA-editing of plastid genes might be a regulatory mechanism evolved during the "domestication of chloroplasts."

Analyzing plastid differentiation we find a complex informational network between at least two different genomes in a single cell across several membranes.^{1,73} Therefore, we have to dismiss the sedative simplification that each plant species reacts the same way as any other, neglecting the ongoing coevolution of these genomes.¹⁷ For example, the plastid genes of monocots and dicots diverged 100 to 200 million years ago.⁷⁴ Why should they use the same dialect in their communication with nuclear genes?

III. PLASTIDS ARE TARGETS FOR CYTOKININ ACTION

Since the pioneering work of Mothes,⁷⁵ plastids have seemingly been a primary target of cytokinin action; numerous papers reported on the hormone-stimulated synthesis of chloroplast components during etioplast/chloroplast transition in greening seedlings, cotyledons, or tissue cultures. In detached leaves and in cell culture, both depleted in endogenous cytokinin, exogenously applied hormone stimulates this transition in light and in darkness. In contrast, cytokinins do not influence structural or physiological plastid parameters in intact plants. Likewise, cytokinins retard senescence in detached leaves, including maintenance, or even promote the synthesis of plastid components, but have no effect on senescence retardation of albino barley leaves, or in N-deficient, chlorophyll-free detached leaves of tobacco (reviewed by Parthier⁷⁶).

Cytokinin-induced, as well as light-induced, chloroplast biogenesis is at the molecular level characterized by the accumulation of transcripts from plastid genes. A number of polyadenylated

transcripts exhibit enhanced steady-state levels in plants treated with naturally occurring cytokinins or with their nonphysiological substitutes kinetin or benzyladenine, as well. Interestingly, the hormone seems to act only on a certain set of nuclear genes: genes coding for proteins that are plastid constituents or that are at least indirectly involved in chloroplast biogenesis.^{31,77-80} These are the same eukaryotic remnants of prokaryotic ancestors that were suspected to be regulated by a yet-unknown plastidic factor. Nevertheless, this factor is triggering the expression of the *rbcS* and *cab* genes to a much higher extent than the expression of the gene coding chlorophyll synthetase.⁸¹ Furthermore, this factor seems not to interfere with light responsiveness of nuclear genes, at least in monocots.⁸²

It is still a controversy whether the enhancement of steady-state transcript levels of cytokinin-responsive genes is due to enhanced transcription rates or posttranscriptional events, although posttranscriptional regulation⁸³ is favored. Translational control by cytokinins has been described as polyribosome formation,⁸⁴ modification of the secondary structure of poly(A⁺)RNA, which leads to "unmasking" of the message,⁸⁵ phosphorylation of ribosomal proteins,⁸⁶ or regulation of tRNA activity.⁸⁷ Posttranslational control may be conferred by retarded protein degradation.⁸⁸ Stimulation of correct RNA editing might be another posttranscriptional mechanism modulated by cytokinin.

Already the early reports of Stetler and Laetsch⁸⁹ and Seyer et al.⁹⁰ describe a correlation between the two cellular processes promoted by cytokinin: the cell cycle and chloroplast biogenesis. In one case an inverse relationship between chloroplast differentiation and tissue growth was observed (either chloroplasts differentiated or cells divided); in the latter a restriction of cytokinin action on chloroplast biogenesis, to the cell growth phase, was found: cytokinin added during the stationary phase was inactive. A similar correlation was described by Suzuki et al.,⁹¹ who found preferential synthesis of plastid DNA prior to that of nuclear DNA, suggesting that ptDNA is synthesized and stored in large amounts to prepare for the following multiple cell divisions without organelle DNA synthesis. Thus, a communication between genome and plastome does exist, and cytokinin presumably interferes with it.

Repeatedly, a coaction of cytokinin and light, in plastid differentiation and multiplication, has been observed.⁷⁶ Even in molecular terms, a coaction of light and cytokinin is detectable.⁹²⁻⁹⁴ Molecular genetic analysis of the regulation of cytokinin-responsive nuclear genes is scarce, since, up to now, no gene expression has been known to be

triggered specifically by cytokinin. Thus, the vast amount of data on light-regulated genes⁹⁵ has to serve as a guideline for further characterizing the cytokinin stimulus on gene expression. In dicots, the expression of several "photogenes" (e.g., *rbcS*, *rbcL*) is seen only after exposure of the plants to light, leading to the idea that light is required for the expression of these genes. Leaf and chloroplast development also require exposure to light, again suggesting a control mechanism.⁴ In monocots the situation is quite different, as primary leaf development and chloroplast biogenesis are uncoupled. Nevertheless, leaf expansion and the expression of several "photogenes" still seem to be coupled; in contrast to dicots, they occur at near-light-grown levels, even in dark-grown plants.³⁴

The most extensively studied light-responsive genes are *rbcS* and *cab*. Expression of these genes coding for the small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (*rbcS*) and the chlorophyll a/b-binding proteins (*cab*), respectively, is regulated by light at the transcriptional level, by sets of *cis*-acting elements and *trans*-acting factors. Moreover, their expression is dependent on genome-plastome interaction as well as on cytokinin. The light signal is mediated via phytochrome, although the expression of many light-responsive genes is modulated by more than one wavelength, e.g., blue light. In fact, there is increasing evidence that blue light plays an important role in modulating plastid differentiation and the accompanying expression of plastome- as well as genome-coded genes for plastid polypeptides.⁹⁶⁻¹⁰⁰ A plastid promoter has been characterized that specifically responds to blue light: the light-responsive promoter (LRP) of the *psbD-psbC* operon.¹⁰¹ While genes such as *rbcL*, *atpB*, and 16 S rRNA are fully active in dark-grown barley, the LRP has evolved a light-regulated specificity unlike other chloroplast promoters. Interestingly, LRP is highly conserved in monocots, less in dicots, and was not found in liverwort chloroplast DNA, indicating differences in light-induced gene expression between the major plant groups. The same indication was given by analysis of the nuclear phytochrome gene of the moss *Ceratodon purpureus*. In contrast to all known phytochromes, the 3' terminus of *phyCer* codes for a putative polypeptide with striking homology to protein kinases.¹⁰² These results suggest that phytochrome in moss is a light-regulated protein kinase, revealing a simple transduction pathway for the light stimulus. Protein kinases are prime candidates for members of the signal transduction pathway for several stimuli in all kinds of plants; e.g., Kulaeva et al. proposed that cytokinin-binding proteins (CBPs) in barley may have protein kinase activity.¹⁰³

Both light-responsive genes *rbcS* and *cab* are not single-copy genes, but represent multigene families with members possessing individual responsiveness to light in an organ- and developmental-specific manner.¹⁰⁴⁻¹⁰⁸ An interaction between light responsiveness and an endogenous developmental program has also been proven for the expression of plastome-encoded genes.^{109,110} Furthermore, Eckes et al. described the organ-specific expression of three cDNA clones from potato, that are regulated by light and are correlated with chloroplast development.

Regulatory circuits are even more complex; in addition to being cytokinin modulated, developmentally programmed, and light responsive, an endogenous oscillator also controls the expression of the multigene families of *cab* and *rbcS*. Thus, mRNA levels of these genes exhibit distinct circadian rhythms,^{112,113} as do other light-responsive genes such as those coding for nitrate reductase and phosphoenolpyruvate carboxylase.^{114,115} Further extrinsic and intrinsic signals interfering with cytokinin action on chloroplast biogenesis and accompanying gene expression are temperature¹¹⁶ and auxin.¹¹⁷

Bearing these complex parameters in mind, it is small wonder that reports on the molecular genetic analysis of cytokinin action are scarce. However, cytokinins seem to interfere with, or modulate, the cooperation between the two genomes, but the molecular mechanisms of this regulatory circuit are far from being understood. Nevertheless, the use of mutants with altered response to external cytokinin as well as *ipt*-transformants^{118,119} should facilitate the molecular analysis of cytokinin action.

IV. THE MOLECULAR ANALYSIS OF CHLOROPLAST DIVISION

Since Schimper, 110 years ago, suggested the continuity of plastids,¹²⁰ studies on the number, orientation, and division of chloroplasts have been undertaken to trace the mechanisms that provide for their nearly equal distribution into daughter cells during cytokinesis.¹²¹ It is now generally assumed that the different plastid types can multiply by constriction division.¹²²⁻¹²⁴ Additionally, species- as well as organ-specific correlations between nuclear DNA content and plastid number per cell are well documented.¹²⁵ However, genes involved in plastid division have not been identified yet, although they have been known from prokaryotes for nearly 30 years.^{126,127} From inhibitor studies it was postulated that these genes are encoded by nuclear DNA in higher plants,¹²⁸ an indication supported by a nuclear mutant of *Arabidopsis thaliana*,

hampered in chloroplast division.¹²⁹ Obviously, these yet-unknown genes are members of the regulatory network around plastid differentiation, woven by nuclear and plastid genes.^{29,130,131}

The genome-plastome interaction in chloroplast multiplication can be seen in electron micrographs, as division appears to be a two-step process: (1) it is preceded by events within the plastid, such as the disintegration of starch grains and thylakoid membranes at the prospective constriction site, and is then followed by (2) the occurrence of a plastid dividing ring (PD ring) outside the plastid around this constriction. This cytoplasmic PD ring is composed of a bundle of actin-like filaments and can be found around dividing plastids of red, brown, and green algae, mosses and ferns (archegoniates), and gymnosperms. In angiosperms, the plastid dividing ring is a doublet that is composed of an outer ring and an inner ring. In any case plastid division occurs by contraction of the filament bundle (reviewed by Kuroiwa¹³²).

We have concentrated our studies on the mode of action of the physiological cytokinin *N*⁶-(Δ^2 -isopentenyl)adenine on differentiation of the haploid protonema of the moss *Physcomitrella patens*.¹³³ Special interest is directed at the mutant PC22, which is defective in chloroplast division, and thus the majority of cells possesses only one chloroplast per cell (Figures 1 and 2). Nevertheless, these macrochloroplasts have a normal internal fine structure (Figure 3). Under white-light conditions, they are severed during cell division by the enlarging cell plate, this being a, so far, unknown mechanism of plastid division. The defect of this particular mutant can be partially compensated for by exogenous cytokinin¹³⁴ and by blue-light treatment.³¹ Cytokinin-induced chloroplast division is accompanied by a transient accumulation of several plastid polypeptides and a dramatic increase in *rbcL* mRNA levels. Such molecular changes cannot be detected under blue-light conditions with already divided chloroplasts, indicating a coaction of cytokinin and light quality in chloroplast division at the molecular level.¹³⁵

Restriction Fragment Length Polymorphism (RFLP) analyses revealed methylation of a putative regulatory gene (*zfpA* gene¹³⁶) near the *rbcL* in chloroplast mutant PC22,¹³⁵ as a possible form of transcriptional control in plastid differentiation. We sequenced the 3' region of the wild-type *rbcL* and found a tRNA gene that was, so far, only known from the ptDNA of the liverwort *Marchantia*,⁶⁸ and an open reading frame (ORF) of 948 bp with homology to the *zfpA* from *Pisum*. The deduced polypeptide of this ORF contains a sequence (–Cys–X2–Cys–X15–Cys–X2–Cys–) that



Figure 14-1 Electron micrographs of a cross-section through one protonema cell of (a) the wild type of *Physcomitrella patens* and (b) the chloroplast mutant PC22 derived from it. Note the cup-shaped giant chloroplast in the mutant.

may fold to form a zinc-finger element.⁶⁹ These elements can interact with nucleic acids, thereby revealing a regulatory function of the respective polypeptide. However, the function of this protein is still unknown and is a subject of debate.^{137,138} Nevertheless, sequence comparison revealed that this protein contains two distinct domains: the

hydrophilic zinc-finger element and a hydrophobic C-terminal region.⁶⁹ Moreover, *zfpA* may be a marker gene for plastid evolution, as it is highly homologous within the archegoniates and dicots, respectively, but differs significantly between the two groups.¹³⁹ Furthermore, it is mutilated in the plastid DNA of monocots. In the moss we found

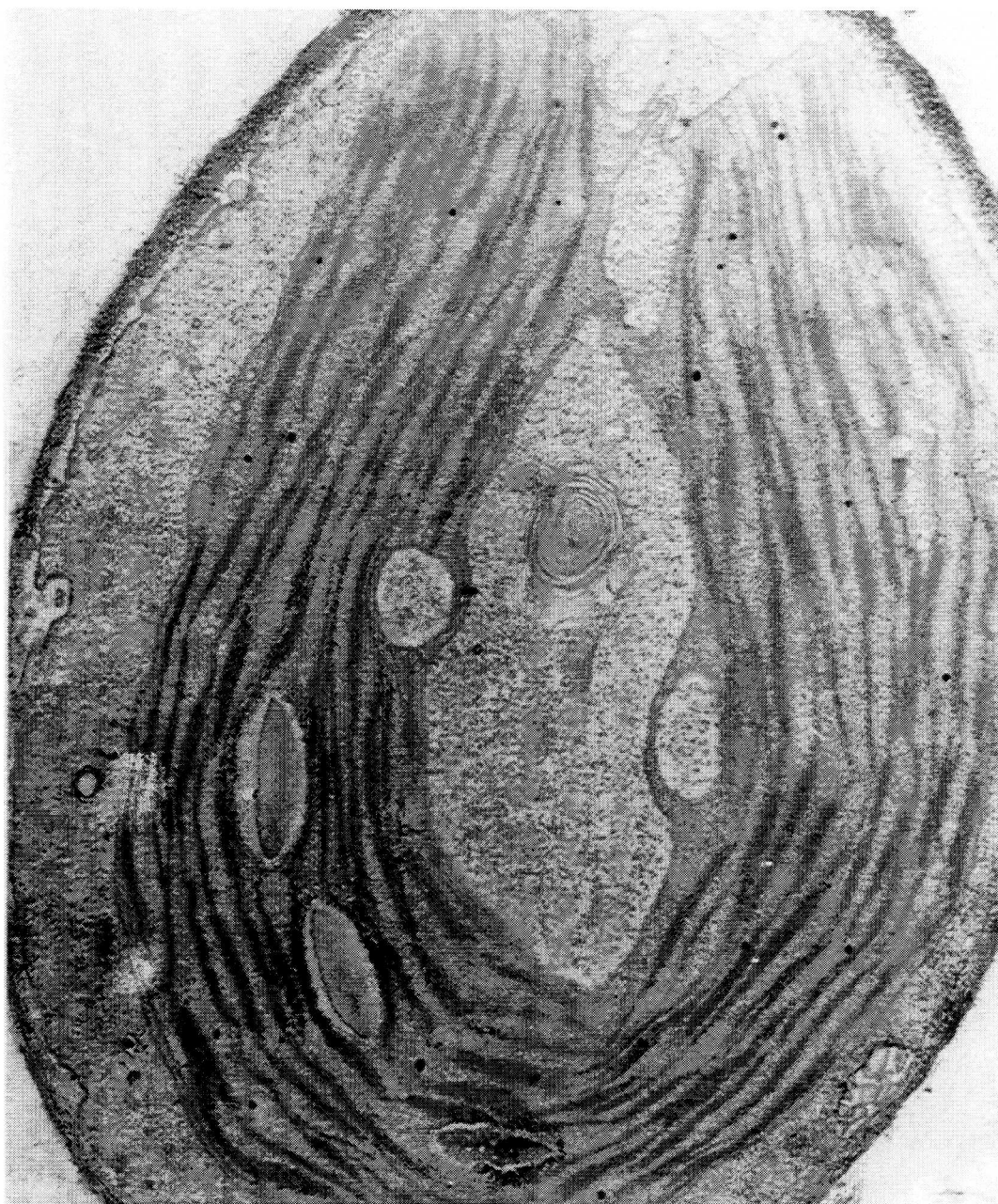


Figure 14-1 (continued).

prokaryotic promoter consensus sequences (-10, -35, Shine Dalgarno) as well as three TATA boxes that are known to be typical eukaryotic promoter sequences. Additionally, these elements are involved in the differential control of the *Sinapis alba* plastid *psbA* gene, depending on the state of plastid differentiation.¹⁴⁰ However, a multiplication of TATA boxes has not previously been reported for plastid promoters and reveals a complex

mechanism of transcriptional control. A gene-specific hybridization probe detected three transcripts of low abundance with apparent molecular weights larger than the gene. RNA accumulation patterns differed between wild-type and chloroplast mutants. Additionally, under the influence of cytokinin, the high-molecular-weight transcript of the mutant decreased in amount (Figure 4). Using riboprobes we ensured that these transcripts were

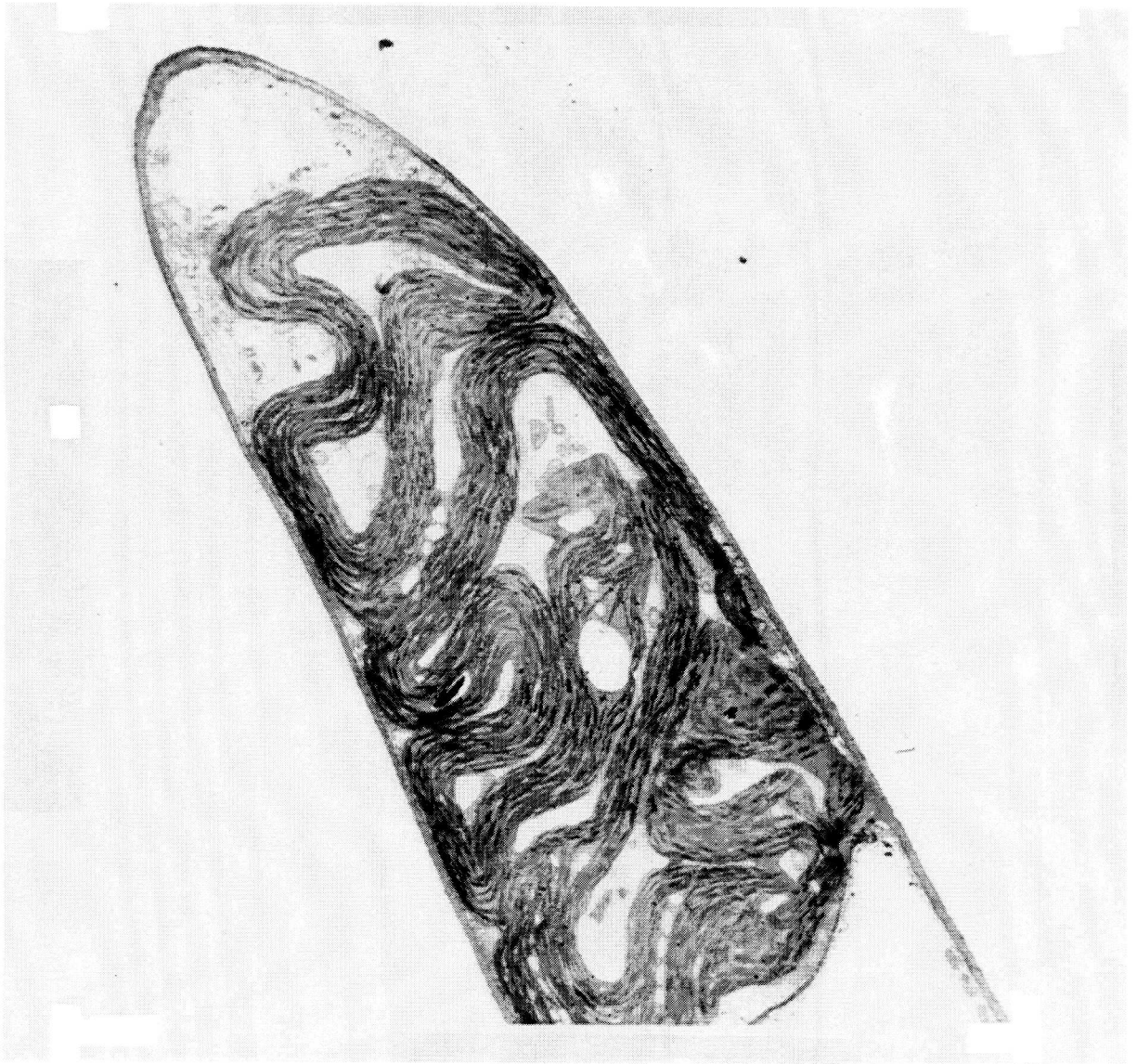


Figure 14-2 Electron micrograph of a longitudinal section through a PC22 protonema tip cell with one giant chloroplast.

encoded by the same ptDNA strand, thus being immature transcripts including *zfpA* sequences.

We performed Northern blots for several plastid genes with the *Physcomitrella* wild type, and two cytokinin-sensitive mutants derived from it (PC22 and P24), P24 not obviously being a chloroplast mutant. In every case we found an accumulation of immature plastid transcripts in both mutants (e.g., Figure 5). The amounts of high-molecular-weight transcripts were less in the wild type, as well as in mutant protonemata treated with cytokinin.¹⁴¹ Reports on qualitative changes in the RNA processing patterns of plastid genes are infrequent,

although most of them are organized in polycistronic transcription units, as in the ancestral bacterial operons.¹⁴²⁻¹⁴⁶ Evidence came from light-induced chloroplast development in mustard,¹⁰⁹ maize,¹⁴⁷ and barley.¹⁴⁸ Likewise, in an *Oenothera* plastome, mutant processing of plastid proteins, whether encoded by ptDNA or by nucDNA, was affected.¹⁴⁹ Thus, processing of mRNAs and proteins might be one way for cytokinins to modulate plastid gene expression posttranscriptionally.

Obviously, Western analyses will need to be employed to prove changes in *zfpA*-protein amounts upon cytokinin treatment of the moss mutants, in



Figure 14-3 Electron micrograph of a PC22 protonema cell showing a normal internal fine structure of the mutant chloroplast.

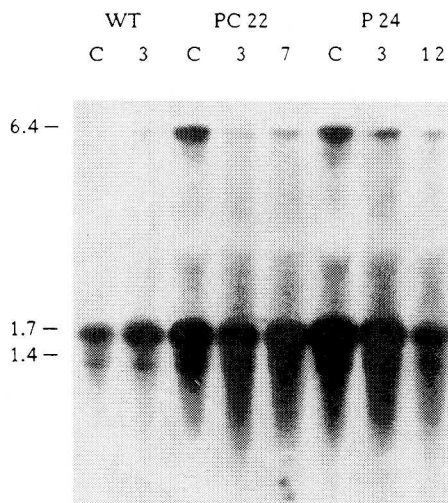
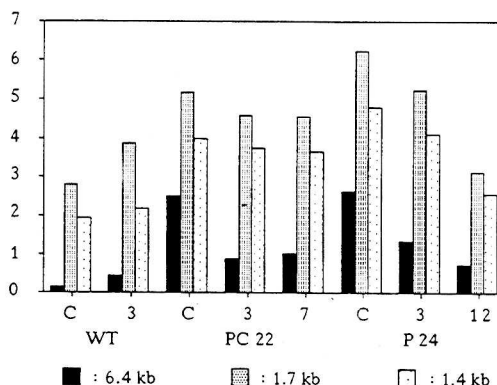
a: *zfpA*-transcriptsb: Quantification of *zfpA*-transcripts

Figure 14-4 Northern analysis of *Physcomitrella zfpA* transcripts. [WT: wild-type; PC22: cytokinin-sensitive chloroplast mutant; P24: cytokinin-sensitive mutant; C: protonemata grown 12 days without cytokinin; 3: protonemata after 9 days of culture with additional 3 days in cytokinin; 7: protonemata after 5 days of culture with additional 7 days in cytokinin; 12: protonemata after 12 days in cytokinin (compare to References 135 and 154).] (a:) Northern blot using a radioactive *zfpA*-specific gene probe. (b:) Densitometric quantification of the autoradiogram shown in (a). (Unit: pixel \times 1000. Transcript sizes are given in kilobases.)

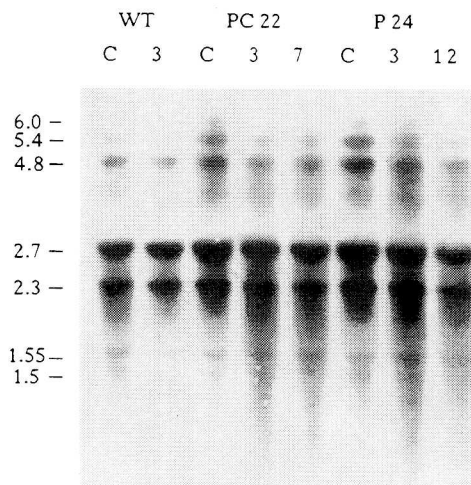
psbB-transcripts

Figure 14-5 Northern analysis of *Physcomitrella psbB* transcripts. [WT: wild-type; PC22: cytokinin-sensitive chloroplast mutant; P24: cytokinin-sensitive mutant; C: protonemata grown 12 days without cytokinin; 3: protonemata after 9 days of culture with additional 3 days in cytokinin; 7: protonemata after 5 days of culture with additional 7 days in cytokinin; 12: protonemata after 12 days in cytokinin (compare to References 135 and 154).] (Transcript sizes are given in kilobases.)

order to correlate them to the proposed enhancing effect on transcript processing. Furthermore, the postulated interaction of *zfpA* protein with nucleic acids has to be proven. However, we do not yet know if the mutation affecting plastid division in this particular moss mutant is located on nucDNA or on ptDNA.¹⁵⁰ Furthermore, most of the data on plastid gene regulation during chloroplast develop-

ment result from *in vitro* studies, and there is a need for plastid transformation systems, to study gene regulation *in vivo*. First reports on the successful transformation of the giant chloroplast of *Chlamydomonas*,¹⁵¹ as well as of higher-plant chloroplasts,^{152,153} demonstrate the feasibility of such an approach. The macrochloroplast of PC22 seems to be a prime candidate for chloroplast transformation

of multicellular plants, as it is amenable for micro-injection.¹³⁴ Thus, we will try to unravel the informational network around cytokinin-induced chloroplast division, with mutant curing experiments. Furthermore, we will attempt to transform moss mutants with *ipt* constructs, in order to manipulate endogenous cytokinin concentrations.

ACKNOWLEDGMENTS

Grants from the European Community, from the Deutsche Forschungsgemeinschaft, and from the city of Hamburg are gratefully acknowledged. Special thanks go to Prof. Dr. T. Börner and to Dr. K. Krupinska, who shared their unpublished results. I enjoyed stimulating discussions with Prof. Dr. W. O. Abel, Jon Falk, and the members of my group.

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