Current Genetics (1984) 8:543–549

Current Genetics

Nucleotide sequence of the clustered genes for apocytochrome *b6* and subunit 4 of the cytochrome *b/f* complex in the spinach plastid chromosome

Wolfgang Heinemeyer, Juliane Alt, and Reinhold G. Herrmann

Botanisches Institut der Universität, Universitätsstr. 1, D-4000 Düsseldorf 1, Federal Republic of Germany

Summary. A 2.4 kilobase-pair segment of the spinach plastid chromosome carrying the genes for apocytochrome *b6* and subunit 4 of the thylakoid membrane cytochrome *b/f* complex has been analysed by DNA sequencing and Northern blot analysis. The nucleotide sequence reveals two uninterrupted open reading frames of 211 and 139 triplets coding for two hydrophobic proteins of 23.7 kd (cytochrome *b6*) and 15.2 kd (subunit 4). The genes are located on the same strand and are separated from each other by 1018 untranslated base pairs. They map adjacent to the gene for the P_{680} chlorophyll *a* apoprotein of the photosystem II reaction center. The three genes appear to be under common transcriptional control and the transcripts post-transcriptionally modified. The deduced amino acid sequences of cytochrome *b6* and subunit 4 both exhibit significant homology with published sequences from mitochondrial *b* cytochromes (42 kd) suggesting that these functionally equivalent polypeptides in photosynthetic and respiratory electron transport chains arose monophyletically.

Key words: Plastid DNA – Cytochrome *b6* gene – Amino acid sequence – Hydropathy – Thylakoid membrane – Transcript modification – Evolution – Spinach

Introduction

The cytochrome *bf* complex of chloroplast thylakoid membranes and the cytochrome bc_1 complex on the inner mitochondrial membrane are functionally and structurally related multisubunit assemblies (Hauska et al. 1983). They act as proton-translocating plastoquinol-plastocyanin and ubiquinol-cytochrome *c* oxidoreductases in photosynthetic and oxidative respiratory electron transport chains, respectively. Both contain *c*- and *b*-type cytochromes and high potential iron-sulfur centers. The mitochondrial complex in addition has several low molecular weight core polypeptides (Capaldi 1982).

Current analysis of the molecular organization and complex biogenesis of energy transducing membranes proceeds mainly along two paths: (i) DNA sequence analysis directed towards the derivation of the primary and secondary structures of the membrane proteins, as well as identification of segments involved in the biogenesis of nuclear and organelle-coded components, and (ii) spectral and functional identification of individual components. Among the four proteins constituting the spinach *bf* complex only one, the Rieske FeS protein (19 kd) is encoded by nuclear DNA. The other three, cytochromes *f* (34 kd) and *b6* (23 kd), and a 17 kd protein (subunit 4) of unknown function originate in the plastome (Alt et al. 1983). By contrast, in mitochondria only a single component of the bc_1 complex, cytochrome *b* (ca. 42 kd), is derived from an organelle gene (e.g., Nobrega and Tzagoloff 1980).

The genes for the cytochromes *f, b6* and subunit 4 have been localized in the large single-copy segment on the plastid chromosomes of spinach, *Oenothera* and tobacco (Alt et al. 1983; Herrmann et al. 1983a). Although they are encoded by the same strand, they are not all part of one operon. Only the genes for the latter two proteins map close to one another and appear to be under common transcriptional control. We have sequenced the entire DNA region containing these genes including flanking and intercistronic regions, allowing us to compare these sequences to those of their mitochondrial equivalents. The organization of the three genes displays features that have not previously been demonstrated to occur in plastid chromosomes. In this paper we report

Offprint requests to: R. G. Herrmann

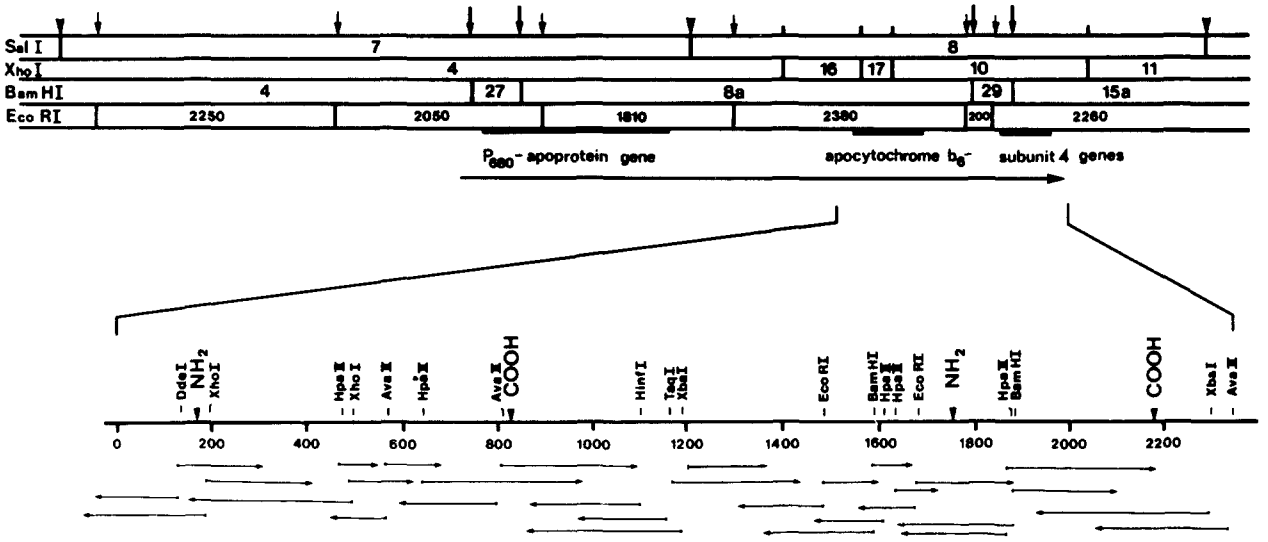

Fig. 1. Restriction map of the spinach plastidDNA segment encoding the genes for cytochrome *b6*, subunit 4, and P_{680} chlorophyll *a* apoprotein, and summary of the extent and direction of individual sequence determinations (*small arrows*). The map was drawn to scale with use of data described in Alt et al. (1983); Westhoff et al. (1983); Morris and Herrmann (1984) and in this paper. Restriction sites for the various enzymes (left) are designated as previously described (Herrmann et al. 1983). The fragments are designated in decreasing size (SalI, XhoI, BamHI) or given in bp (EcoRI). The small, closely spaced BamHI-fragments have been renumbered (cf. Alt et al. 1983; Westhoff et al. 1983). The direction of transcription is marked by an *arrow*

results for cytochrome *b6* and subunit 4; the evaluation of the structural consequence of the protein sequence has been the subject of a separate paper (Widger et al. 1984). Information on the gene for apocytochrome *f* which is located some 12 kbp away and transcribed into separate RNA species will be presented in the accompanying communication. Preliminary accounts of this work have been published (Heinemeyer 1983; Herrmann et al. 1983b, c).

Experimental procedures

The recombinant plasmid pWHsp208 carrying the 5.2 kbp primary fragment SalI-8 of spinach plastid DNA was used in these experiments. The fragment was cloned in the vector pBR322 and subcloned in pBR325 as previously described (Alt et al. 1983; Herrmann et al. 1980, 1983c). Restriction endonucleases were purchased from Boehringer (Mannheim; BamHI, BglI, EcoRI, HpaII, PvuI, SalI, TaqI) or New England Biolabs (Bad Schwalbach; AvaII, DdeI, HaeIII, HincII, HinfI, KpnI, RsaI, XbaI, XhoI). DNA digestions with restriction endonucleases and gel electrophoresis were performed as previously described (Herrmann and Whitfeld 1982). The 3' termini of the restriction fragments were labelled with (α^{32}P)-dXTP and Klenow fragment (Boehringer) filling-in the ends, after fragment purification by chromatography on Elutip columns (Schleicher and Schüll, Dassel). DNA was sequenced by the method developed by Maxam and Gilbert (1980) as outlined in Morris and Herrmann (1984).

Results and discussion

The location and transcription polarity of the genes for cytochrome *b6* (23 kd), subunit 4 (17 kd) and the P_{680} chlorophyll *a* apoprotein of the photosystem II reaction center ("51 kd" protein) on a 7 kbp segment of the spinach chromosome, together with the relevant SalI, BamHI, EcoRI and XhoI sites is depicted in Fig. 1. The genes have been mapped by cell-free translation of appropriate recombinant DNAs carrying specific fragments of spinach plastid DNA or of chloroplast RNA fractions hybrid-selected with these fragments (Alt et al. 1983; Westhoff et al. 1983). Derivative clones, spanning the entire 7 kbp DNA segment, selected mRNA that directed the synthesis of all three polypeptides in vitro suggesting that these loci are active and form an operon-like transcriptional unit (Alt et al. 1983; Morris and Herrmann 1984). The genes for cytochrome *b6* and subunit 4 are completely contained within the 5.2 kbp fragment SalI-8 of spinach plastid DNA. Plasmid pWHsp208 containing this fragment directs the synthesis of both proteins in an *E. coli* S30 in vitro transcription-translation system (Alt et al. 1983). A more detailed restriction map for SalI-8 was constructed by the method of Smith and Birnstiel (1976), as well as by double and triple digestions, and was used to guide DNA sequence analysis as indicated in Fig. 1.

The sequence of the DNA segment encoding cytochrome *b6* and subunit 4 was determined using the procedure of Maxam and Gilbert (1980). Translation of this sequence disclosed the presence of only two reading frames large enough to code for both proteins. These reading frames of 211 and 139 codons are located on the same strand and are separated from each other by an untranslatable sequence of 1018 bp. No open reading

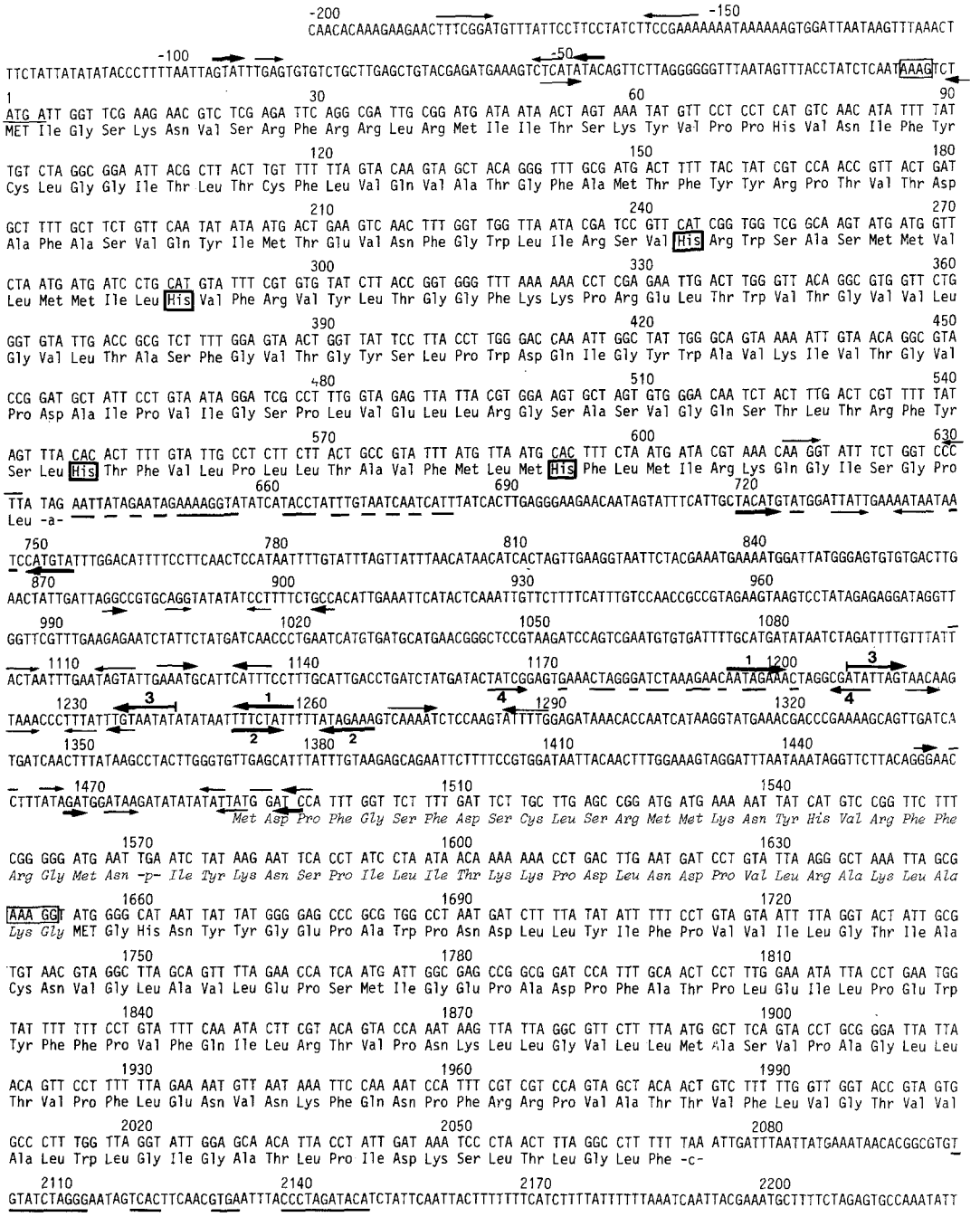

Fig. 2. Nucleotide sequence of the genes for cytochrome *b6* and subunit 4 as well as of their flanking and intercistronic regions. The sequence of the non-coding (mRNA-like) strand and the inferred amino acid sequences, commencing at the ATG codon at which translation is probably initiated, are shown. The positions of the sequence coding for proteins are presented in triplets, with the corresponding amino acid below. The discussed amino terminal extension of subunit 4 including an in-frame stop codon (nucleotide 1571) is marked by italic letter code. Possible ribosome binding and transcriptional termination sites are boxed and underlined, respectively. Conserved histidine residues in spans II and V (cf. Fig. 6) are boxed. Corresponding segments capable of forming secondary structure are marked by corresponding arrows; alternative possibilities are numbered 1–4

frame of comparable size was found in the segment of approximately 1400 nucleotides spanning the SalI-7/SalI-8 junction into the gene for the P_{680} chlorophyll *a* apoprotein (Morris and Herrmann 1984). These findings precisely located the gene for cytochrome *b6* (cf. Alt et al. 1983), established that there is a single gene per chromosome for this protein, and confirmed the position of the gene for subunit 4. In accord with hybrid selection data, all three genes are located on the same DNA strand. The interval of 2424 nucleotides starting

	T		C		A		G		
T	Phe	13	Ser	4	Tyr	8	Cys	2	T
	Phe	1	Ser	2	Tyr	1	Cys	0	C
	Leu	8	Ser	0	Stop	0	Stop	0	A
	Leu	6	Ser	4	Stop	1	Trp	5	G
C	Leu	4	Pro	7	His	3	Arg	5	T
	Leu	0	Pro	1	His	2	Arg	0	C
	Leu	3	Pro	1	Gln	5	Arg	3	A
	Leu	2	Pro	1	Gln	0	Arg	2	G
A	Ile	6	Thr	11	Asn	0	Ser	5	T
	Ile	1	Thr	3	Asn	3	Ser	0	C
	Ile	7	Thr	3	Lys	5	Arg	1	A
	Met	11	Thr	1	Lys	1	Arg	1	G
G	Val	7	Ala	5	Asp	2	Gly	7	T
	Val	3	Ala	1	Asp	1	Gly	4	C
	Val	12	Ala	2	Glu	2	Gly	5	A
	Val	3	Ala	2	Glu	1	Gly	2	G

a

	T		C		A		G		
T	Phe	9	Ser	0	Tyr	4	Cys	1	T
	Phe	1	Ser	1	Tyr	0	Cys	0	C
	Leu	14	Ser	2	Stop	1	Stop	0	A
	Leu	2	Ser	0	Stop	0	Trp	3	G
C	Leu	5	Pro	8	His	1	Arg	3	T
	Leu	0	Pro	1	His	0	Arg	0	C
	Leu	1	Pro	5	Gln	2	Arg	0	A
	Leu	0	Pro	1	Gln	0	Arg	0	G
A	Ile	6	Thr	4	Asn	6	Ser	0	T
	Ile	0	Thr	1	Asn	1	Ser	0	C
	Ile	2	Thr	4	Lys	2	Arg	0	A
	Met	3	Thr	0	Lys	1	Arg	0	G
G	Val	5	Ala	2	Asp	3	Gly	3	T
	Val	1	Ala	1	Asp	0	Gly	4	C
	Val	8	Ala	3	Glu	4	Gly	2	A
	Val	1	Ala	4	Glu	2	Gly	2	G

b

Fig. 3. Codon usage for the genes for cytochrome *b6* (a) and subunit 4 (b)

164 kp prior to an DdeI site and ending at an AvaII site is shown by Fig. 2; the predicted coding regions are written as triplets and translated.

The amino acid sequence of the 211 residue protein, inferred from the DNA sequence and beginning at the first in-frame methionine, gives a polypeptide chain of 23.7 kd, which matches the molecular weight of 23,000 of cytochrome *b6* determined from its electrophoretic mobility in SDS-polyacrylamide gels (Hurt and Hauska 1981; Alt et al. 1983). The sequence shares a 31–38% homology with residues 50–209 of mitochondrial *b* cytochromes from five different sources (Widger et al. 1984). The derived protein includes four invariant histidine residues (Fig. 2) that probably act as binding sites for two protohemes (Widger et al. 1984; Saraste 1984; see below). This establishes unequivocally that this DNA region codes for cytochrome *b6*.

The second open reading frame in the sequence (nucleotides 1655 to 2074) is identified as the gene for subunit 4 on the basis of cell-free translation (Alt et al. 1983) and amino acid sequence. The gene has the same polarity as cytochrome *b6* but is in a different reading frame. The position of the N-terminal ATG codon (position 1655) for this gene was initially ambiguous. The determined sequence preceding the indicated initiation point contains a potential protein-coding segment for 54 amino acids with four methionine residues but includes an in-frame TGA stop codon at position 1571 (Fig. 2). In order to eliminate the possibility of sequencing and cloning artifacts this segment was analysed from two independently selected pWHsp208 clones, as well as from authentic spinach plastid DNA, using five individual sequence reactions starting from different restriction sites in different orientations. As the TGA triplet was found in each instance, we conclude that the coding region for subunit 4 begins at the indicated methionine and that the molecular weight of the primary translation product is 15.2 kd. This assignment is further substantiated by hydropathy analysis (see below). If translation were to commence at the first methionine indicated (position 1490), the predicted molecular weight would be much greater than the 17 kd reported as that for the authentic protein and in vitro translation products of spinach chloroplast RNA and plastid DNA (Hurt and Hauska 1981; Alt et al. 1983).

The codon usage for both proteins obeys the general code and is tabulated separately for the two proteins in Fig. 3. Only 5 of the 61 possible codons are not used. There is a 70 and 80% preference for A and T at the third (and first) position for cytochrome *b6* and subunit 4, respectively. Of the 18 triplets not used in subunit 4, 14 include C or G in the third codon position. Biased codon usage has been noted for several plastome-coded genes (e.g., Zurawski et al. 1981; Howe et al. 1982) and is probably a consequence of the relatively low CG contents of plastid DNAs (37 mole-%).

The motifs AAAG (*b6*) and AAAGG (subunit 4) preceding the respective initiation codons (Fig. 2) may operate as ribosomal binding sites (Shine and Dalgarno 1974) as they correspond to conserved sequences of 16S plastid rRNA in maize (Schwarz and Kössel 1980), tobacco (Tohdoh and Sugiura 1982) and prokaryotes (Shine and Dalgarno 1974). The protein-coding regions terminate at TAG amber (*b6*) and TAA ochre (subunit 4) codons immediately following leucine and phenylalanine codon numbers 211 and 139, respectively. It is unlikely that the small open reading frame (1490–1570) is expressed because it is not preceeded by a typical ribosomal binding site.

The transcriptional organization of this DNA segment is complex. More than half a dozen RNA species have been identified by a Northern blot survey (Fig. 4; Morris and Herrmann 1984). These include a large colinear transcript of approximately 6 kb spanning the three

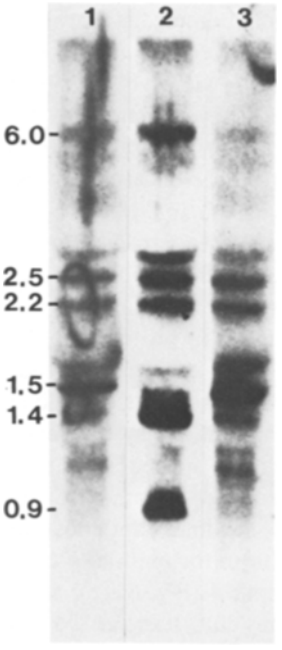

Fig. 4. Autoradiogram of blot hybridization analysis of total cellular RNA from spinach with segments from the spinach plastid chromosome. Denatured (McMaster and Carmichael 1977) RNA (5 μg per blot) was separated by electrophoresis on a 1.3% agarose slab gel and transferred to nitrocellulose sheets. The hybridization probes were (1) a 427 bp HpaII-HaeIII fragment (residues 453-880), (2) a 207 bp HaeIII-XbaI fragment (residues 881-1088), and (3) a 305 bp XbaI-EcoRI fragment (residues 1098–1394). The probes were labelled by nick-translation (Rigby et al. 1977). RNA sizes are given in kb (left)

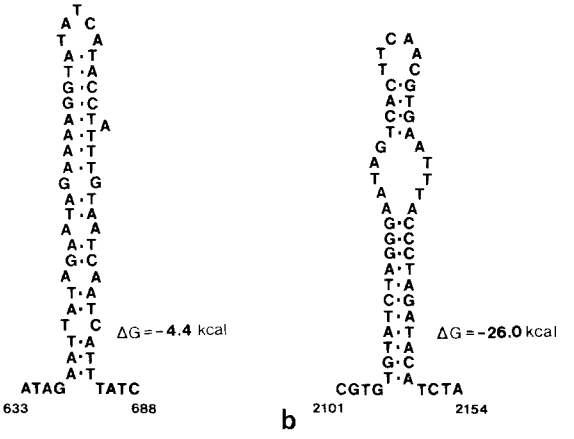

Fig. 5. Possible stem and loop structures at the 3′ ends of the spinach cytochrome *b6* (a) and subunit 4 (b) genes. Numbering of nucleotides corresponds to that in Fig. 2. The free energies of formation, ΔG, were calculated according to Tinoco et al. (1973)

protein-coding regions and components of 2.5 kb for cytochrome *b6 plus* subunit 4 (Alt et al. 1983) and of 2.1 kb for the P_{680} chlorophyll *a* apoprotein alone (Morris and Herrmann 1984). Remarkably, RNA species in the range of 2.4–4 kb are also detected hybridising with protein-coding segments from all three genes (Morris and Herrmann 1984) as well as discrete species of 1.4 and 0.9 kb appearing with a 207 bp HaeIII-XbaI segment from within the 1018 bp nontranslated intercistronic spacer (Fig. 4, track 2). The patterns obtained with RNA from etiolated or illuminated material are almost indistinguishable. On the other hand, Western blot analysis (Towbin et al. 1979) shows that only cytochrome *b6* and subunit 4 are stably made in the dark; no trace of the P_{680} chlorophyll *a* apoprotein is detectable under the chosen growth conditions (Westhoff, Alt and Herrmann, unpublished). Apparently the genes for proteins belonging to different membrane complexes can be under common transcriptional control but are not necessarily co-produced. These results indicate post-transcriptional processing, the existence of various transcription initiation and termination points, or both, and suggest strongly that post-transcriptional, translational, or post-translational control constitutes an essential element in the biogenesis of the thylakoid membrane (Morris and Herrmann 1984). Bearing in mind that the three genes are more than 5 kbp apart, the existence of the last of the above mentioned RNA species might indicate that RNA processing in plastids includes *inter*cistronic splicing (Morris and Herrmann 1984).

The stem-loop structures following the translational termination codons at positions 637–684 (*b6*; Fig. 5a) and 2105–2150 (subunit 4; Fig. 5b) and extensive secondary structure within the intercistronic spacer (Fig. 2) may, therefore, function in transcriptional termination, RNA processing or attenuation analogous to those involved in corresponding processes in prokaryotic genes (Rosenberg and Kramer 1977; Rosenberg and Court 1979; Yanofsky 1981; Altmann et al. 1982). At first glance, the spacer sequence elements which can form single and multiple stem-loop structure do not exhibit the typical consensus motifs of group I and II introns described for fungal mitochondrial RNA (Michel and Dujon 1983; Langford et al. 1984). The remarkably low free enthalpy (Tinoco et al. 1973) of the stem-loop stuctures distal to the cytochrome *b6* gene (ΔG = −4.4 kcal) or within the untranslated spacer when compared to the structure following the gene for subunits 4 (ΔG = −26 kcal; Fig. 5a, b) may reflect a basic difference in the roles these elements may play in the flux of genetic information. Only the latter may function in transcriptional termination analogous to those involved in termination of prokaryotic genes (Rosenberg and Court 1979). This organization may also explain why typical −10 and −35 consensus regions resembling prokaryotic transcription start sites that are generally located upstream of other plastid genes are not found in the vicinity of the two genes. The transcriptional organization outlined here deserves further study.

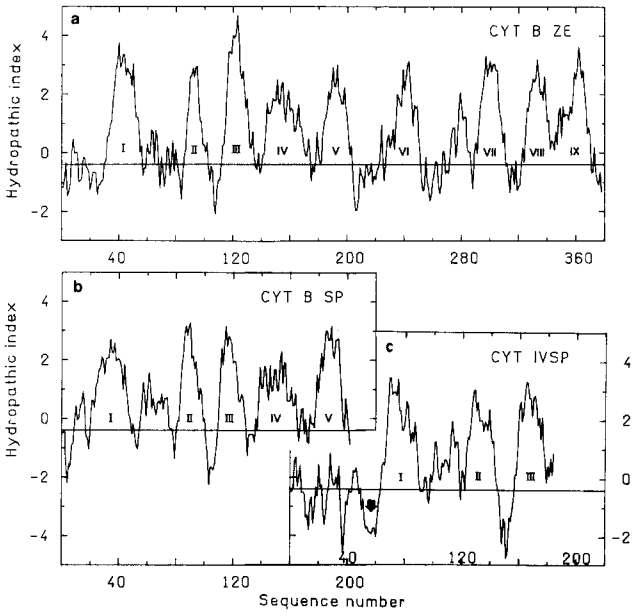

Fig. 6. Calculated (Kyte and Doolittle 1982) hydropathy profile of cytochrome *b6* (b) subunit 4 (c) from spinach and cytochrome *b* from maize mitochondria (a; by courtesy of Prof. Leaver). The curves represent the averaged hydrophobicity values of a nonopeptide composed of amino acid residue i − 4 to i + 4 plotted against i, where i represents the amino acid number. They are drawn to place corresponding membrane spanning segments at equivalent positions. Roman numbers indicate the proposed membrane-spanning segments (cf. Saraste 1984; Widger et al. 1984). Designation of amino acids is as in Fig. 2. The 5′ terminal segment in front of the subunit 4 gene including the translational opal stop codon (position 1571) is marked by an *arrow* (c)

The amino acid sequences of cytochrome *b6* and subunit 4 were analysed by computer for secondary structure (Kyte and Doolittle 1982). As would be expected in a membrane protein, there is a high proportion of hydrophobic amino acid residues. When the free energy of transfer of each amino acid residue from a helix in water to a helix in a non-polar solvent lacking hydrogen-bonding capacity is integrated, patterns of interspersed hydrophilic and hydrophobic regions emerge. The hydropathy profile, shown in Fig. 6, exhibits five and three hydrophobic regions of about 20 amino acid residues each for *b6* and subunit 4, respectively, that probably traverse the membrane. These segments are generally flanked by single or pairs of basic amino acids that could fix the spans by interaction with the negative surface charges of the lipid bilayer. Since the number of spanning segments is not even, the N- and C-terminal ends of the proteins must be on opposite sides of the membrane.

The comparison of the deduced amino acid sequences for both chloroplast proteins with those published for mitochondrial *b* cytochromes discloses the striking fact that both cytochrome *b6* and subunit 4 exhibit significant homology (ca. 40 and 30%, respectively) with N- and C-terminal parts of the highly homolgous *b*-proteins from such diverse organisms as *Saccharomyces, Neurospora,* human, bovine and mouse (Widger et al. 1984). Homology or cross-correlation is even greater in the hydropathy profiles of cytochrome *b6* (70–90%, Fig. 6). Conservation includes the four conserved histidine residues at positions 82 and 96 (span II) and 183 and 197 (span V) that could bind two hemes per cytochrome molecule (Fig. 2; Widger et al. 1984), and an acidic amino acid residue in span IV, aspartic acid, in *b6* at positon 152, that might be involved in proton pumping across the membrane (Hauska et al. 1983). The greater conservation of cytochrome *b6* may reflect its functional role in the catalytic reaction. Subunit 4 may only exert structural and regulatory functions, and constraints on its sequence may be less demanding. Alignment of the sequences in such a way as to maximize homology indicates that the last span in the mitochondrial *b* cytochromes that is lacking in subunit 4 (Fig. 6a, c), and a deletion of 5–6 amino acid residues between *b6* and subunit 4, could account for most of the molecular weight difference observed between the mitochondrial (42 kd) and the sum of the weights of the plastid proteins (39 kd; Widger et al. 1984). The sequence of 54 amino acid residues preceding the indicated initiative methionine codon in the gene for subunit 4 (see above) is higly hydrophilic and must be untranslated as no structural conservation is observed in this segment. These data support strongly that *b* cytochromes in photosynthetic and respiratory electron transport chains have arisen *monophyletically.* The gross divergence has either resulted by fusion of genes for two ancestor proteins in mitochondria, or by insertion of an untranslatable segment into a single ancestor gene in plastid chromosomes.

Acknowledgements. The authors are most grateful to Prof. B. Hallick and Prof. W. Cramer for their help in the preparation of this manuscript, and to Prof. Ch. Leaver for providing the sequence for corn mitochondrial cytochrome *b* before publication. They acknowledge the expert technical assistance of Ms. Barbara Schiller and Ms. Gabriele Schewe. The work was supported by a grant from the Stiftung Volkswagenwerk and by Forschungsmittel des Landes Nordrhein/Westfalen.

References

Alt J, Westhoff P, Sears BB, Nelson N, Hurt E, Hauska G, Herrmann RG (1983) EMBO J 2:979–986

Altmann S, Guervier-Takada C, Frankfort HM, Robertson HD (1982) In: Linn SM, Roberts JR (eds) Nucleases. Cold Spring Harbor, New York, pp 243–274

Capaldi RA (1982) Biochim Biophys Acta 694:291–306

Hauska G, Hurt E, Gabellini N, Lockau W (1983) Biochim Biophys Acta 726:97–133

Heinemeyer W (1983) Diplomarbeit, Univ Düsseldorf

Herrmann RG, Whitfeld PR (1982) In: Edelman M, Hallick R, Chua N-H (eds) Methods in chloroplast molecular biology. Elsevier, North-Holland Amsterdam, pp 451–468

Herrmann RG, Seyer P, Schedel R, Gordon K, Bisanz C, Winter P, Hildebrandt JW, Wlaschek M, Alt J, Driesel AJ, Sears BB (1980) In: Bücher Th, Sebald W, Weiss H (eds) Biological chemistry of organelle formation. Springer, Berlin Heidelberg New York, pp 97–112

Herrmann RG, Westhoff P, Alt J, Bisanz C, Heinemeyer W, Olesch B, Nelson N (1983a) In: Swaminathan MS, Chopra VL, Joshi BC, Sharma RP, Bansal HC (eds) Progr 15th Internatl. Congr Genetics, pp 171–172

Herrmann RG, Westhoff P, Alt J, Bisanz C, Heinemeyer W, Olesch B, Nelson N (1983b) In: Progr 6th Internatl Congr on Photosynthesis, Brussels, vol 2, p 51

Herrmann RG, Westhoff P, Alt J, Winter P, Tittgen J, Bisanz C, Sears BB, Nelson N, Hurt E, Hauska G, Viebrock A, Sebald W (1983c) In: Cifferi O, Dure L III (eds) Structure and Function of Plant Genomes. Plenum Publ Corp, pp 143–154

Howe CJ, Auffret AD, Doherty A, Bowman CM, Dyer TA, Gray JC (1982) Proc Natl Acad Sci USA 79:6903–6907

Hurt E, Hauska G (1981) Eur J Biochem 117:591–599

Kyte J, Doolittle RF (1982) J Mol Biol 157:105–132

Langford CJ, Klinz FJ, Donath C, Gallwitz D (1984) Cell 36: 645–653

Maxam AM, Gilbert W (1980) In: Großman L, Moldave K (eds) Methods in enzymology, vol 65. Academic Press, New York, pp 499–560

McMaster GK, Carmichael GG (1977) Proc Natl Acad Sci USA 74:4835–4838

Michel F, Dujon B (1983) EMBO J 2:33–38

Morris J, Herrmann RG (1984) Nucleic Acids Res 12:2837–2850

Nobrega FG, Tzagoloff A (1980) J Biol Chem 255:9228–9837

Rigby PWJ, Dieckmann M, Rhodes C, Berg P (1977) J Mol Biol 113:237–251

Rosenberg M, Court D (1979) Ann Rev Genet 13:319–353

Rosenberg M, Kramer RA (1977) Proc Natl Acad Sci USA 74: 984–988

Saraste M (1984) FEBS Lett 166:367–372

Schwarz Z, Kössel H (1980) Nature 283:739–742

Shine J, Dalgarno L (1974) Proc Natl Acad Sci USA 71:1342–1346

Smith HO, Birnstiel ML (1976) Nucleic Acids Res 3:2387–2398

Tinoco J, Borer PN, Dengler B, Levine MD, Uhlenbeck OC, Crothers DM, Gralla J (1973) Nature (New Biology) 246:40–41

Tohdoh N, Sugiura M (1982) Gene 17:213–218

Towbin H, Staehelin T, Gordon J (1979) Proc Natl Acad Sci USA 76:4350–4354

Westhoff P, Alt J, Herrmann RG (1983) EMBO J 2:2229–2237

Widger WR, Cramer WA, Herrmann RG, Trebst A (1984) Proc Natl Acad Sci USA 81:674–678

Yanofsky C (1981) Nature 289:751–758

Zurawski G, Perrot B, Bottomley W, Whitfeld PR (1981) Nucleic Acids Res 9:3251–3270

Communicated by C. P. Hollenberg

Received June 7, 1984