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Transcription of succinate dehydrogenase subunit 4 (*sdh4*) gene in potato: detection of extensive RNA editing and co-transcription with cytochrome oxidase subunit III (*cox3*) gene

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Abstract The potato (*Solanum tuberosum* L.) mitochondrial *cox3/sdh4* gene cluster was previously identified by heterologous hybridization using a *Marchantia polymorpha* *sdh4* probe. In this work, this potato gene cluster was cloned, sequenced and its expression was evaluated. The gene sequence and gene locus organization were found to be similar to the corresponding gene cluster in other dicot species, where known. Northern hybridizations with potato and cauliflower (*Brassica oleraceae*) mtRNA and RT-PCR analyses using potato mtRNA indicated that *cox3* and *sdh4* are co-transcribed in both species, generating a complex transcription pattern, where several transcripts from 1.1 kb to 4.4 kb are found. The potato transcript from this cluster displayed 14 and 13 RNA-editing sites, in the *cox3* and *sdh4* genes respectively, which changed the codon identity to amino acids and created a *sdh4* partially edited stop codon. Forty-three cDNA clones were analyzed for editing process and revealed different partial-editing with no apparent sequential processing in the *sdh4* gene.

Keywords Mitochondrial DNA · Cytochrome oxidase subunit III · Succinate dehydrogenase subunit 4 · RNA editing · Potato

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Introduction

Analysis of the mitochondrial genome of different organisms has shown that they are greatly variable regarding gene organization, structure and expression. Interestingly, plant mitochondria possess the largest and most complex organellar genomes known. The sequencing of the angiosperm mitochondrial genome (Unsel et al. 1997; Kubo et al. 2000) has shown that they are further complicated by the presence of repeated sequences active in homologous recombination, which results in the simultaneous presence of molecules showing variable length and sequence organization. These repeated sequences allow intragenic recombinations leading to rearrangements (deletions, inversions, duplications), which might create pseudogenes and/or put genes together, which have been located in different genome regions during evolution.

The expression of plant mitochondrial genomes is achieved in a relatively complex way. Some of the characteristics of the mitochondrial transcription process which contribute to the transcription-complexity in plant mitochondria are the duplication of the transcribed region, the presence of multiple initiation and/or termination sites, the *cis*- and *trans*-splicing events involved in the processing of several genes, the RNA editing and the co-transcription of genes (for review, see Gray et al. 1992; Schuster and Brennicke 1994). Several plant mitochondrial genes are co-transcribed. Some of these polycistronic transcripts contain sequences coding for related products, such as ribosomal RNA (*rrn18/rrn5* in wheat; Falconet et al. 1984), ribosomal proteins (*rps13/rpl16* in maize; Hunt and Newton 1991) and ATPase subunits (*atpA/atp9* in maize; Covello and Gray 1991). However, co-transcribed genes involved in different metabolic pathways, such as *orf25/cox3* in rice (Liu et al. 1992) and *nad3/rps12* in wheat (Gualberto et al. 1988), are also found.

The coding capacity of the plant mitochondrial genome is approximately three times bigger than in other

organisms, although it encodes only a few percent of the genetic information needed for the biogenesis and correct function of the mitochondrial machinery. As an example, the *Arabidopsis thaliana* mitochondrial genome contains 57 genes (Unsold et al. 1997), coding for subunits of respiratory chain complexes, ribosomal proteins and at least 42 putative ORFs. However, although the coding capacity is similar in different angiosperm species, there is an intriguing diversity of gene complements, even among related species. It has been found that a given gene may be encoded in the mitochondrial DNA in one species but present in the nuclear genome of another (Brennicke et al. 1993). The gene coding for complex II subunit 4 (subunit of a mitochondrial membrane-bound complex) is an example of the genes showing diversity in genome location.

Gene coding for complex II subunits (succinate dehydrogenase) has been identified in bacterial and mitochondrial genomes from lower eukaryotes, such as algae and protists (Darlison and Guest 1984; Heizen et al. 1995; Leblanc et al. 1995; Burger et al. 1996). In other organisms, in general, complex II genes have been found in the nuclear genome (Morris et al. 1994; Au et al. 1995). However, in some plant species, such as *A. thaliana*, *Beta vulgaris*, *Lycopersicon esculentum*, *Marchantia polymorpha* and *Oenothera berteriana*, the gene coding for complex II subunit 4 (*sdh4* gene) was found in the mitochondrial genome (Oda et al. 1992; Giegé et al. 1998; Kubo et al. 2000; Adams et al. 2001).

This report describes the analysis of the *sdh4* gene from the potato mitochondrial genome, identified by heterologous hybridization with the homologous gene from *M. polymorpha*. The *sdh4* gene was found in a gene cluster that includes *cox3* and a partial *cox2* gene. The angiosperm conservation, sequence analysis, transcription and editing pattern of *cox3* and *sdh4* genes are described.

Materials and methods

Isolation and analysis of mitochondrial DNA and RNA

Mitochondrial DNA (mtDNA) was isolated from etiolated seedlings of *Coix lacryma-jobi* L. cv Adlay, maize (*Zea mays*, cv AGF352), pea (*Pisum sativum*, cv Mikado), soybean (*Glycine max*, cv IAC-5), potato tubers (*Solanum tuberosum*, cv Binje) and cauliflower inflorescence (*Brassica oleracea*, from a local market).

Purified mitochondria were prepared as described by Vedel and Quetier (1974): mtDNA was obtained after mitochondrial lysis and CsCl-ethidium bromide centrifugation. mtRNA was prepared as described by Stern and Newton (1986), treated with DNase I to remove the remaining DNA, then phenol extracted and precipitated. Standard procedures (Sambrook et al. 1989) were used for restriction enzyme digestions and agarose gel electrophoresis.

Southern and Northern hybridizations

Restriction-digested mtDNAs were transferred to Hybond-N filters (Amersham, UK) by standard procedures (Sambrook et al. 1989). DNA fragments used as probes were purified from gel-slices by electroelution and labeled by random hexamer priming. Heterologous hybridizations, using *M. polymorpha* mitochondrial *orf86a* as

a probe against *Bam*HI-digested mtDNA from different angiosperm species, were performed under low stringency conditions (Siqueira et al. 2001). Homologous hybridizations and washes were performed under stringent conditions (Sambrook et al. 1989). Isolated mtRNA (5.0 µg/lane) was treated and then the samples were fractionated on 1.2% agarose gel and blotted onto Hybond-N. Probe labeling, washes and the full procedures are described by Siqueira et al. (2001).

cDNA synthesis and PCR amplification (RT-PCR)

cDNAs were synthesized using reverse DNaseI-treated mtRNA as templates, as described by Dias et al. 2000; Siqueira et al. 2001). The amplified products were purified by agarose gel electrophoresis before cloning. A control for the cDNA synthesis was performed by replacing reverse transcriptase with water in the reaction mixtures and verifying through PCR that there was no amplification product from that template.

cDNA cloning and sequencing

Standard procedures were used in the preparation, isolation and analysis of recombinant clones of *Escherichia coli* (Sambrook et al. 1989). DNA restriction fragments of interest were cloned into pBluescript vectors (Stratagene, USA) and the cDNAs were cloned into the pGEM-T vector system I (Promega, USA). Nucleotide sequencing was performed by the dye terminator-cycle method on an ABI Prism 310 sequencer (Applied Biosystems, USA). Both strands of the cDNA and genomic clones were sequenced. The sequence data were analyzed using the Lasergene system (DNA Star, USA).

PCR amplification of *orf86a* from *M. polymorpha* mtDNA

Aliquots of 10–20 ng of *M. polymorpha* total DNA were mixed with 2.5 mM MgCl₂ on a buffer, supplied by the manufacturer, containing 0.1 mM of each dNTP, 10 pmol of appropriate primers and 2.5 units of *Taq* DNA polymerase (Gibco BRL) in a final reaction volume of 100 µl. The amplification conditions were as described by Siqueira et al. (2001). The products of amplification were cloned into the pGEM-T vector and sequenced to confirm their identity before using them as probes in heterologous hybridizations.

Oligonucleotides

For PCR amplification of the *sdh4* gene from total DNA of *M. polymorpha*, the primers used were: marpo 86a 5': 5'GAA ACC TTA GGG CAT TGG CTT CTT C3' and marpo 86a 3': 5'GAC TAT AAG GAG AGG GGA GAG ACG3'. For cDNA synthesis and RT-PCR amplification, the primers were: 1: 5'TCT ATC TAT TGG TGG GGA GGT3', 2: 5'AAT ACC CCT ATT CTC CCT TCA T3', 3: 5'ATG ATT GAA TCT CAG AGG CAT3', 4: 5'AAG CCC GGT TCT CTT TGT CTT3', 5: 5'CTA TTT GTC TCT ATC TAT TGG TG3', 6: 5'AAT AGT GGA GGG TGC TTG ATA ATA3', 7: 5'AGC TTT CCC ACT CCC TTT G3', 8: 5'CGA GAG ACA AGA AAA CAT C3', 9: 5'TAT GAG TTC GAT CCA TTA GGT TC3', 10: 5'CAT CTG ACC AAG GAG CAT3' and 11: 5'ACT GGC ATT TTG TAG ACG3'.

Results and discussion

Organization of the *sdh4* locus in potato mtDNA

In a previous study of transcribed sequences in the angiosperm mitochondrial genome homologous to *M. polymorpha* mitochondrial sequences, the *sdh4* locus

in a 1.8-kb *PvuII* potato mtDNA fragment (Siqueira et al. 2001) was identified. The *sdh4* gene was identified using the *M. polymorpha* mitochondrial *sdh4* gene as a probe in heterologous hybridizations against a filter containing angiosperm mtDNA (cauliflower, *Coix*, maize, pea, potato, soybean). The results showed a very strong hybridization signal in potato and cauliflower mtDNA and weaker intensities of the observed bands in the other species (data not shown). Cloning and sequencing of the 1.8-kb *PvuII* *sdh4* homologous potato mtDNA fragment indicated a 363-bp fragment showing 98% similarity with the *sdh4* sequence from *A. thaliana* (*orf95*; Giegé et al. 1998) and the presence of the *cox3* gene sequence immediately upstream from the *sdh4* gene. Similarly, in *Arabidopsis* and *Oenothera*, the *sdh4* sequence in potato overlaps 3' of the end of the *cox3* gene and shows two methionine codons, which could be used to initiate translation. The second ATG is located 23 codons downstream from the initial ATG and shares the TG nucleotides with the TGA stop codon of the *cox3* gene. Since the sequence of the *cox3* gene was interrupted by one of the terminal *PvuII* sites of the fragment, two *cox3* angiosperm consensus sequence-based primers (primers 3, 6) were used to amplify the missing portion of the *cox3* gene from potato mtDNA. The amplification product was cloned, sequenced and its sequence was added to the 5' terminus of the 1.8-kb *PvuII* fragment. Thirty-three base pairs downstream from the stop codon of the *sdh4* gene, 25 codons similar to the final portion of the *cox2* gene were found (GenBank accession number AF280607).

Conservation of the *cox3/sdh4* gene locus organization in different angiosperm species

The heterologous hybridization experiments performed using gene *sdh4* from *M. polymorpha* mtDNA as a probe, identified a homologous sequence in the mitochondrial genome of cauliflower, pea, potato and soybean (dicot species), but not in *Coix* and maize (monocot species; data not shown). In order to verify the organization of the *cox3/sdh4* locus found in potato, heterologous hybridizations were performed, employing the wheat *cox3* gene and potato *sdh4* gene (not including the *cox3*-overlapping region of the *sdh4* gene) as probes.

Results showed that the *M. polymorpha* *sdh4* and potato *sdh4* probes identified bands with identical length in dicot species, suggesting that they are the same fragments. The weak intensity signal obtained in pea and soybean hybridization employing a potato *sdh4* probe might be explained by a lesser similarity to the potato *sdh4* sequence. Effectively, the homologous soybean sequence present in the sequence database showed only the initial 58 nucleotides homologous to the potato *sdh4* gene, indicating the lack of most of this gene. *Coix* and maize mtDNA showed no homologous fragment for either probe. In this way, cauliflower, pea and soybean mitochondrial genomes have conserved the *sdh4*

sequence or, at least, a part of this sequence. Hybridizations with the wheat *cox3* gene as a probe revealed the same initially identified fragments by *cox3* and/or *sdh4* probes in the cauliflower, pea and soybean genomes (data not shown).

The *cox3* gene sequences from other plants published or found in the databases were evaluated in order to identify whether the *sdh4* gene was conserved downstream of this gene. The comparison indicated that there are sequences homologous to *sdh4* gene downstream of the *cox3* gene in most of those species. Even though the similarity to the mitochondrial *sdh4* sequence among different species remained high (96–98%), the functionality and length of this gene sequence conserved in the mitochondrial genome during evolution was different for each species. Hence, if the *sdh4* gene present in potato mitochondrial genome is considered a model for comparison with the others, the conservation of the *sdh4* gene might be classified in three categories.

1. Conserved coding sequence: in *Oenothera* (Giegé et al. 1998) and potato, the *sdh4* sequence has apparently been conserved in almost its totality, showing at least 100 amino acids homologous among themselves.
2. Coding sequence interrupted by stop codons: *A. thaliana* (Giegé et al. 1998), sugar beet (Kubo et al. 2000) and sunflower (*Helianthus annuus*, Quagliarillo et al. 1990) have conserved the *sdh4* sequence (sequences showing 95% similarity with potato *sdh4* gene), but mutations in the coding sequence produce stop codons interrupting the ORF in these species (Fig. 1).
3. Coding sequence interrupted by deletions: in broad bean (*Vicia faba*, Macfarlane et al. 1990), soybean (Grabau and Gengenbach 1989) and monocots, such as *Aegilops columnaris* (U46766), maize (McCarty et al. 1988), rice (*Oriza sativa*, Kaleikau et al. 1990) and wheat (*Triticum aestivum*, Gualberto et al. 1990a), the major portion of the *sdh4* gene sequence has been lost. A small sequence corresponding to approximately to 80 and 58 nucleotides of the *sdh4* gene was conserved in broad bean and soybean respectively, while sequences containing from 47 to 53 nucleotides were conserved in monocot species.

Hybridizations employing the *sdh4* gene as a probe against total and mitochondrial DNA from maize and sugar cane have indicated that there is probably no copy in the mtDNA of this gene (data not shown). The *Magnolia grandiflora* *cox3* 3' region (Perrota et al. 1996) does not extend far enough to allow any conclusion with regards to the presence of a complete *sdh4* gene. The available sequence indicates that its last 50 nucleotides (downstream from the *cox3* gene) are homologous to the *sdh4* gene. This great variation in the *sdh4* gene conservation among different species is unexpected, when compared with the high conservation of other respiratory chain genes. However, the magnitude of variation observed for gene *sdh4* seems to be similar to the variation of ribosomal protein genes in angiosperm mitochondrial

agrees with the angiosperm *sdh4* conservation analysis of Adams et al. (2001), which indicated several different events when *sdh4* was lost from the mitochondrial genome during the plant species evolution.

Transcription and RNA-editing analysis of the *cox3/sdh4* locus

Northern blot hybridization was carried out with total mtRNA from potato and cauliflower, using potato *cox3* and *sdh4* genes as probes (Fig. 2). The *cox3* probe revealed multiple transcripts in both species, ranging over 1.1–4.4 kb. Among these, the potato 4.4 kb transcript and the cauliflower 2.4 kb and 2.0 kb transcripts were also identified by the *sdh4* probe, strongly suggesting co-transcription of these two genes (Fig. 2).

To characterize the extent and sites of RNA editing in *cox3/sdh4* transcripts, cDNA covering the coding region was obtained by RT-PCR using a primer set, as indicated in Fig. 3. The 43 cDNAs revealed 14 C-to-U RNA editing events in *cox3* and 13 in the *sdh4* coding region. These 27 C-to-U editing sites resulted in 11 and 7 codon modifications in the *cox3* and *sdh4* genes, respectively, corresponding to 4.2% of the COX3 and 5.7% of the SDH4 amino acid sequences. Considering the length of both gene sequences, it is worth noting that *sdh4* has twice as many edited sites as *cox3*. However, 50% of the editing events in the *sdh4* gene are silent

mutations. A comparison of the *cox3* editing positions in *Solanum* and other angiosperms (Table 1) showed that ten sites have already been found in one of the four species analyzed. Thus, it appears that these positions have a common phylogenetic origin. Nine out of the ten common potato editing sites are found in *Magnolia* (Perrota et al. 1996) and wheat (Gualberto et al. 1990b), six in *A. thaliana* (Giegé and Brennicke 1999) and four in *Olea europaea* (Perrota et al. 1997). The fact that, comparatively, there are more editing sites in common between potato and wheat (Gualberto et al. 1990b), which is a monocot species, than among the other three dicot species, is intriguing. Editing at sequence positions 231, 267, 494 and 503 has been found only in potato. Two of the four species-specific editing sites (sequence positions 231, 267) are silent. The first silent editing site present in *Solanum* is only found in *Magnolia* (Perrota et al. 1996). The silent editing sites in *Arabidopsis* (Giegé and Brennicke 1999), *Olea* (Perrota et al. 1997) and wheat (Gualberto et al. 1990b) are also species-specific, thus illustrating that editing at silent sites is variable between different plant species. The same situation is observed for the *sdh4* silent editing sites in *Solanum* and *A. thaliana* (Giegé et al. 1998; Table 2).

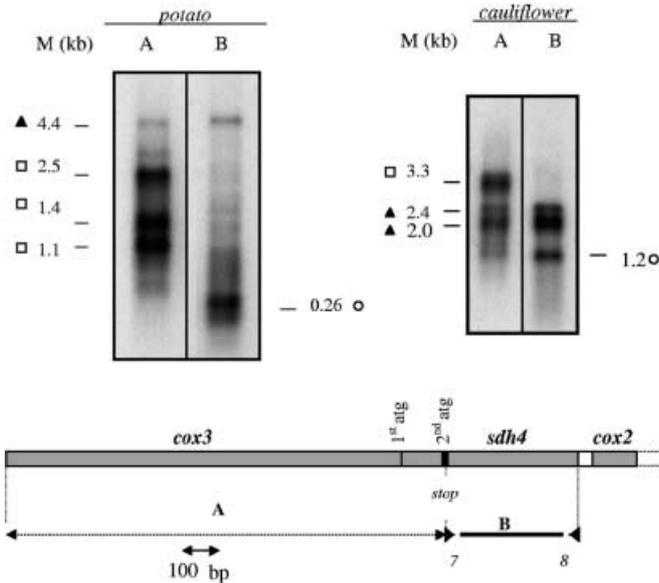


Fig. 2. RNA hybridizations of the *cox3* and *sdh4* transcripts in potato and cauliflower. Total mtRNAs (5 µg) were denatured and applied to each lane of a 1.2% agarose/formaldehyde gel, transferred to a Nylon membrane and hybridized with ³²P-labeled fragments. The probes used were *cox3* (A) and *sdh4* (B); and both are indicated by horizontal bars in the lower figure. M An RNA ladder (9.5–0.24 kb) was used to estimate molecular size. Solid triangles indicate transcripts identified by both probes, empty squares identify *cox3* transcripts and empty circles indicate specific *sdh4* transcripts

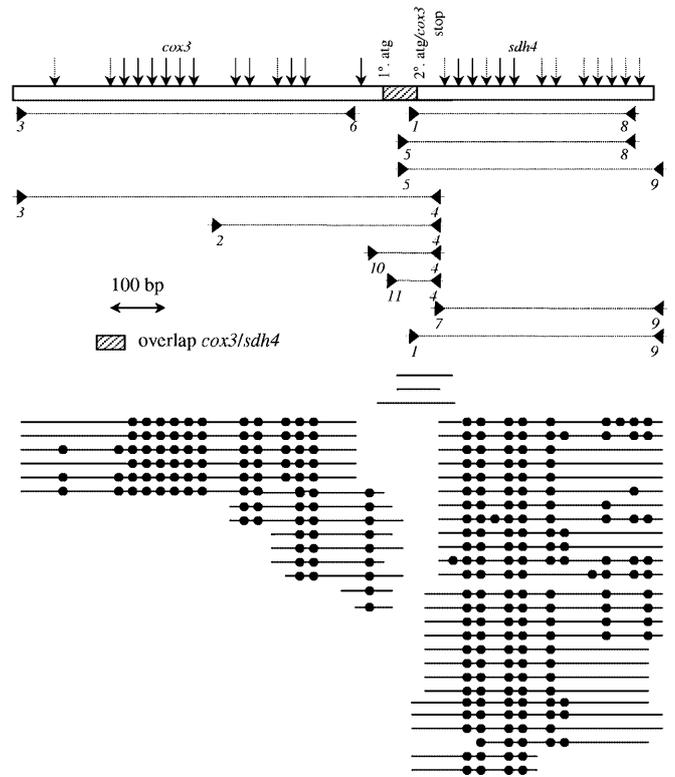


Fig. 3. *cox3*- and *sdh4*-editing sites found in 43 sequenced potato cDNA clones. The cDNA amplification strategy is indicated by arrows and dotted lines below the horizontal bar. Numbers below the arrows identify primer numbers. The dotted arrows above the horizontal bar indicate the partial-editing sites and the continuous arrows represent non-partial-editing sites. Horizontal bars with solid circles indicate sequenced cDNA clones with edited sites

Table 1. Number, sequence position and codon affected by RNA-editing in the *cox3* gene of potato, *Arabidopsis thaliana* (Giegé and Brennicke 1999), *Marchantia grandiflora* (Perrota et al. 1996), *Oenothera europaea* (Perrota et al. 1997) and wheat (Gualberto et al.

1990b). Codons in *bold* represent partial-editing sites. – Editing site absent, *C* editing site (C-to-U editing), *NS* number of non-silent editing sites, *S* number of silent editing sites, *sil* silent editing site, *Total* total number of editing sites by species

Potato			<i>A. thaliana</i>			<i>M. grandiflora</i>			<i>O. europaea</i>			Wheat				
Affected codon	Base number	Changed amino acid	Affected codon	Base number	Changed amino acid	Affected codon	Base number	Changed amino acid	Affected codon	Base number	Changed amino acid	Affected codon	Base number	Changed amino acid		
CTC	69	L→sil	–	–	–	CTC	69	L→sil	–	–	–	–	–	–		
–	–	–	CCA	112	P→S	CCA	112	P→S	–	–	–	–	–	–		
GTC	231	V→sil	–	–	–	–	–	–	–	–	–	–	–	–		
CCT	245	P→L	CCT	245	P→L	CCT	245	P→L	CCT	245	P→L	CCT	245	P→L		
TCT	257	S→F	TCT	257	S→F	TCT	257	S→F	–	–	–	TCT	257	S→F		
–	–	–	–	–	–	CCG	263	P→L	–	–	–	–	–	–		
TTC	267	F→sil	–	–	–	–	–	–	–	–	–	–	–	–		
CTT	289	L→F	–	–	–	CTT	289	L→F	–	–	–	CTT	289	L→F		
–	–	–	–	–	–	CTT	298	L→F	–	–	–	–	–	–		
–	–	–	–	–	–	CGG	304	R→W	CGG	304	R→W	–	–	–		
TCT	311	S→F	TCT	311	S→F	TCT	311	S→F	TCT	311	S→F	TCT	311	S→F		
TCT	314	S→F	TCT	314	S→F	TCT	314	S→F	TCT	314	S→F	TCT	314	S→F		
–	–	–	–	–	–	CGG	388	R→W	–	–	–	–	–	–		
CCT	413	P→L	CCT	413	P→L	CCT	413	P→L	–	–	–	CCT	413	P→L		
–	–	–	–	–	–	CCC	419	P→L	CCC	419	P→L	–	–	–		
CCT	422	P→L	CCT	422	P→L	CCT	422	P→L	–	–	–	CCT	422	P→L		
GCT	494	A→V	–	–	–	–	–	–	–	–	–	–	–	–		
GCT	503	A→V	–	–	–	–	–	–	–	–	–	–	–	–		
TCA	512	S→L	–	–	–	TCA	512	S→L	–	–	–	TCA	512	S→L		
–	–	–	–	–	–	TCC	527	S→F	–	–	–	TCC	527	S→L		
–	–	–	–	–	–	–	–	–	–	–	–	ACT^a	531	T→sil		
TCC	566	S→F	–	–	–	TCC	566	S→F	TCC	566/567	S→F/–	TCC	566	S→F		
–	–	–	–	–	–	TCC	602	S→F	–	–	–	–	–	–		
–	–	–	TTC	603	F→sil	–	–	–	–	–	–	–	–	–		
–	–	–	–	–	–	TCA	605	S→L	–	–	–	–	–	–		
–	–	–	–	–	–	TCG	653	S→L	TCG	653	S→L	–	–	–		
–	–	–	–	–	–	CGG	754	R→W	CGG	754	R→W	CGG	754	R→W		
–	–	–	–	–	–	CCA	764	P→L	CCA	764	P→L	CCA	764	P→L		
Total = 14, S = 3, NS = 11				Total = 8, S = 1, NS = 7				Total = 22, S = 1, NS = 21				Total = 10, S = 1, NS = 9				Total = 13, S = 1, NS = 12

^a U-to-C editing

Editing in the potato *sdh4* gene is extensive, involving 13 C-to-U nucleotide transitions. Seven editing events alter the significance of the codon; and three of these events also occur in *A. thaliana* (Giegé et al. 1998). Six out of the seven codon alterations improve the similarity between the potato and *Marchantia* (Oda et al. 1992) SDH4 protein. The editing site at sequence position 280 (Fig. 1), which originates a stop codon, is noteworthy. This editing occurs two amino acids before the stop codon present in the *A. thaliana sdh4* mitochondrial sequence (Giegé et al. 1998), although it does not occur in tomato (Adams et al. 2001), the phylogenetically nearest species to potato. There are five other editing sites identified after the edited stop codon in potato. The silent editing events correspond to almost 50% of the editing in the *Solanum sdh4* gene. This fact indicates that silent editing is remarkably important in the editing process of this gene. Seven editing sites present in the potato *sdh4* gene are common with sites found in *A. thaliana* (Giegé et al. 1998), *Podophyllum* (Adams et al. 2001) and tomato (Table 2). As expected, all editing sites existing in the tomato *sdh4* gene (Adams et al. 2001) are present in potato; and *Euphorbia* (Adams et al. 2001) does not share any *sdh4*-editing site with potato (Table 2).

Partial editing in potato *cox3/sdh4* gene cluster

Sequence analysis of 43 cDNA clones revealed partially edited clones for both genes. The number of partially edited sites and the extent of editing differed between the *cox3* and *sdh4* genes. Three and eight partially edited sites, respectively, were found in *cox3* and *sdh4* genes; and, in both genes, 50% of them are silent. This finding suggests that *cox3*-editing sites are edited before *sdh4*-editing sites. Considering the number and importance of these partial-editing events in the alteration of the coding sequence, one may suggest that they might represent a transition state of either losing or gaining new editing sites.

Considering the eight partial-editing sites in *sdh4*, four are silent alterations, three change the codon specificity and one originates a stop codon. It is important to note that, in the gene sequence after the editing site originating at the stop codon (sequence position 211, Table 2), all preceding edits are partially and differentially processed at a low frequency. Thus, the editing pattern for this gene portion is totally different from the 5' gene region, suggesting that, in the *sdh4* gene, there is a polarity in the editing process

Table 2. Number, sequence position and codon affected by RNA-editing in the *sdh4* gene of potato, *A. thaliana* (Giegé et al. 1998), tomato (Adams et al. 2001), *Podophyllum* (Adams et al. 2001) and *Euphorbia* (Adams et al. 2001). Codons in bold represent partial

editing sites. – Editing site absent, *C* editing site (C-to-U editing), *NS* number of non-silent editing sites, *S* number of silent editing sites, *sil* silent editing site, *Total* total number of editing sites by species

Potato			<i>A. thaliana</i>			Tomato			<i>Podophyllum</i>			<i>Euphorbia</i>		
Affected codon	Base number	Changed amino acid	Affected codon	Base number	Changed amino acid	Affected codon	Base number	Changed amino acid	Affected codon	Base number	Changed amino acid	Affected codon	Base number	Changed amino acid
–	–	–	–	–	–	–	–	–	ATC	15	I→sil	–	–	–
–	–	–	ACC	53	T→I	–	–	–	–	–	–	–	–	–
TTC	63	F→sil	–	–	–	–	–	–	–	–	–	–	–	–
TTC	84	F→sil	–	–	–	TTC	84	F→sil	TTC	84	F→sil	–	–	–
–	–	–	–	–	–	–	–	–	CCA	85/86	P→S/ S→L	–	–	–
CCA	86	P→L	CCA	86	P→L	CCA	86	P→L	–	–	–	–	–	–
ATC	102	I→sil	–	–	–	–	–	–	ATC	102	I→sil	–	–	–
–	–	–	–	–	–	–	–	–	–	–	–	ACA	104	T→I
TCC	123	S→sil	–	–	–	TCC	123	S→sil	–	–	–	–	–	–
CCA	134	P→L	CCA	134	P→L	CCA	134	P→L	–	–	–	–	–	–
–	–	–	ATC	171	I→sil	–	–	–	–	–	–	–	–	–
CAT	190	H→Y	CAT	190	H→Y	CAT	190	H→Y	–	–	–	–	–	–
CGA	211	R→ ^a	–	–	–	–	–	–	–	–	–	–	–	–
TTC	243	F→sil	–	–	–	–	–	–	–	–	–	–	–	–
CTT	244	L→F	–	–	–	–	–	–	–	–	–	–	–	–
CTC	277/279	L→F/sil	–	–	–	–	–	–	–	–	–	–	–	–
–	–	–	–	–	–	CTC	279	L→sil	–	–	–	–	–	–
TCT	284	S→F	–	–	–	TCT	284	S→F	–	–	–	–	–	–
Total = 13, S = 6, NS = 7			Total = 5, S = 1, NS = 4			Total = 7, S = 3, NS = 4			Total = 5, S = 3, NS = 2			Total = 1, S = 0, NS = 1		

^a Stop codon generated after editing

(Fig. 3). The edit resulting in a stop codon was found to be processed in only 30% of the sequenced cDNA clones. Four partial *sdh4* editing sites were found processed only once in 26 sequenced cDNA. In spite of the low processing frequency of these sites, they seem to be real editing sites and not enzyme or sequencing errors, as no other base change was found in the 43 analyzed cDNAs. In order to reduce the possibility of reproducing an eventual reverse transcriptase and/or polymerase error in most clones, the cDNA clones were obtained from different cDNA synthesis reactions and amplifications. Furthermore, the possibility of obtaining four enzyme/sequencing errors in C-to-U transitions for the same gene is extremely low. The causes for this differential editing remain unclear and it is suggested that incompletely edited pre-RNAs reflect intermediates in the editing process (Mulligan et al. 1999). Analyzed as a whole, the *sdh4* gene partial-editing results suggest that there might be translation of incompletely edited mtRNA. This appears to be possible for the *sdh4* gene translation, especially due to the presence of a partially edited stop codon.

Taken together, the editing results for the potato *sdh4* gene and Southern and Northern hybridization results using the *sdh4* sequence as a probe against total and mtDNA and mtRNA from cauliflower and potato suggest that the *sdh4* gene is probably functional in the mitochondria of both these species.

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References

- Adams KL, Rosenblueth M, Qiu Y-L, Palmer JD (2001) Multiple losses and transfers to the nucleus of two mitochondrial succinate dehydrogenase genes during angiosperm evolution. *Genetics* 158:1289–1300
- Au HC, Ream-Robinson D, Bellew LA, Broomfield PL, Saghbini M, Scheffler IE (1995) Structural organization of the gene encoding the human iron-sulfur subunit of succinate dehydrogenase. *Gene* 159:249–253
- Brennicke A, Grohmann L, Hiesel R, Knoop V, Schuster W (1993) The mitochondrial genome on its way to the nucleus: different stages of gene transfer in higher plants. *FEBS Lett* 325:140–145
- Burger G, Lang BF, Reith M, Gray MW (1996) Genes encoding the same three subunits of the respiratory complex II are present in the mitochondrial DNA of two phylogenetically distant eukaryotes. *Proc Natl Acad Sci USA* 93:2328–2332
- Covello PS, Gray MW (1991) Sequence-analysis of wheat mitochondrial transcripts capped in vitro: definitive identification of transcription initiation sites. *Curr Genet* 20:245–251
- Darlison MG, Guest JR (1984) Nucleotide sequence encoding the iron-sulfur protein subunit of the succinate dehydrogenase of the *Escherichia coli*. *Biochem J* 223:507–517
- Dias SMG, Siqueira SF, Lejeune B, Souza AP (2000) Identification and characterization of the *trnS/pseudo-tRNA/nad3/rps12* gene

- cluster from *Coix lacryma-jobi* L.: organization, transcription and RNA editing. *Plant Sci* 158:97–105
- Falconet D, Lejeune B, Quétier F, Gray MW (1984) Evidence for homologous recombination between repeated sequences containing 18 S and 5 S ribosomal RNA genes in wheat mitochondrial DNA *EMBO J* 3:297–302
- Giegé P, Brennicke A (1999) RNA editing in *Arabidopsis* mitochondria effects 441 C to U changes in ORFs. *Proc Natl Acad Sci USA* 96:15324–15329
- Giegé P, Knoop V, Brennicke A (1998) Complex II subunit 4 (*sdh4*) homologous sequences in plant mitochondrial genomes. *Curr Genet* 34:313–317
- Grabau EA, Gengenbach BG (1989) Cytochrome oxidase subunit III gene from soybean mitochondria. *Plant Mol Biol* 13:595–597
- Gray MW, Hanic-Joyce PJ, Covello PS (1992) Transcription, processing and editing in plant mitochondria. *Annu Rev Plant Physiol Plant Mol Biol* 43:145–175
- Gualberto JM, Wintz H, Weil JH, Grienberger JM (1988) The genes coding for subunit 3 of NADH-dehydrogenase and for ribosomal protein S12 are present in the wheat and maize mitochondrial genomes and are co-transcribed. *Mol Gen Genet* 215:118–127
- Gualberto JM, Domon C, Weil J-H, Grienberger J-M (1990a) Structure and transcription of the gene coding for subunit 3 of cytochrome oxidase in wheat mitochondria. *Curr Genet* 17:41–47
- Gualberto JM, Weil J-H, Grienberger J-M (1990b) Editing of the wheat *coxIII* transcript: evidence for twelve C to U and one U to C conversions and for sequence similarities around editing sites. *Nucleic Acids Res* 18:3771
- Heizen RA, Mo YY, Robertson SJ, Mallavia LP (1995) Characterisation of the succinate dehydrogenase-encoding gene cluster (*sdh*) from the Rickettsia *Coxiella burnetti*. *Gene* 155:27–34
- Hunt MD, Newton KJ (1991) The NC3 mutation-genetic-evidence for the expression of ribosomal-protein genes in *Zea mays* mitochondria. *EMBO J* 10:1045–1052
- Kaleikau EK, André CP, Walbot V (1990) Sequence of the rice mitochondrial gene for cytochrome oxidase subunit 3. *Nucleic Acids Res* 18:371
- Kubo T, Nishizawa S, Sugawara A, Itchoda N, Estiati A, Mikami T (2000) The complete nucleotide sequence of the mitochondrial genome of sugar beet (*Beta vulgaris* L.) reveals a novel gene for tRNA^{Cys} (GCA). *Nucleic Acids Res* 28:2571–2576
- Leblanc C, Boyen C, Richard O, Bonnard G, Grienberger JM, Kloareg B (1995) Complete sequence of mitochondrial DNA of the rhodophyte *Chondrus crispus* (Gigartinales). Gene content and genome organization. *J Mol Biol* 250:484–495
- Liu AW, Narayanan KK, André CP, Kaleikau EW, Walbot V (1992) Co-transcription of *orf25* and *coxIII* in rice mitochondria. *Curr Genet* 21:507–513
- Macfarlane JL, Wahleithner JA, Wolstenholme DR (1990) A gene for cytochrome c oxidase subunit III (COXIII) in broad bean mitochondrial DNA: structural features and sequence evolution. *Curr Genet* 17:33–40
- McCarty DM, Hehman GL, Hauswirth WW (1988) Nucleotide sequence of the *Zea mays* mitochondrial cytochrome oxidase subunit III gene. *Nucleic Acids Res* 16:9873
- Morris AA, Farnsworth L, Ackrell BA, Turnbull DM, Birch-Machin MA (1994) The cDNA sequence of the flavo-protein subunit of human heart succinate dehydrogenase. *Biochem Biophys Acta* 1185:125–128
- Mulligan RM, Williams MA, Shanahan MT (1999) RNA editing site recognition in higher plant mitochondria. *J Hered* 90:338–344
- Nugent JM, Palmer JD (1991) RNA-mediated transfer of the gene *coxII* from the mitochondrion to the nucleus during flowering plant evolution. *Cell* 66:473–481
- Oda K, Yamato K, Ohta E, Nakamura Y, Takemura M, Nozato N, Akashi K, Kanegae T, Ogura Y, Kohchi T, Ohyama K (1992) Gene organization deduced from the complete sequence of liverwort *Marchantia polymorpha* mitochondrial DNA: a primitive form of plant mitochondrial genome. *J Mol Biol* 223:1–7
- Palmer JD, Adams KL, Cho Y, Parkinson CL, Qiu Y-L, Song K (2000) Dynamic evolution of plant mitochondrial genomes: mobile genes and introns and highly variable mutation rates. *Proc Natl Acad Sci USA* 97:6960–6966
- Perrota G, Malek O, Heiser V, Brennicke A, Grohmann L, Quagliariello C (1996) RNA editing in the *cox3* mRNA of *Magnolia* is more extensive than in other dicot or monocot plants. *Biochem Biophys Acta* 1307:254–258
- Perrota G, Cavallotti A, Quagliariello C (1997) Reduced requirement for RNA editing in the mitochondrial *cox3* transcript of *Olea europaea* L. *Curr Genet* 31:185–189
- Quagliariello C, Saiardi A, Gallerani R (1990) The cytochrome oxidase subunit-III gene in sunflower is cotranscribed with an open reading frame conserved in higher plants. *Curr Genet* 18:355–363
- Sambrook J, Fritsch EF, Maniatis T (1989) *Molecular cloning: a laboratory manual*, 2nd edn. Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.
- Schuster W, Brennicke A (1994) The plant mitochondrial genome: physical structure, information content, RNA editing, and gene migration to the nucleus. *Annu Rev Plant Physiol Plant Mol Biol* 45:61–78
- Siqueira SF, Dias SMG, Lejeune B, Souza AP (2001) *Marchantia polymorpha* mitochondrial *orf* identifies transcribed sequence in angiosperm mitochondrial genome. *Biochem Biophys Acta* 1520:202–211
- Stern DB, Newton KJ (1986) Isolation of plant mitochondrial RNA. *Methods Enzymol* 118:488–496
- Unsel M, Marienfeld JR, Brandt P, Brennicke A (1997) The mitochondrial genome of *Arabidopsis thaliana* contains 57 genes in 366,924 nucleotides. *Nat Genet* 15:57–61
- Vedel F, Quétier F (1974) Physico-chemical characterization of mitochondrial DNA from potato tubers. *Biochem Biophys Acta* 340:374–387