Research Article

Title: Evolutionary aspects of a unique internal mitochondrial targeting signal in nuclear-migrated rps19 of sugar beet (Beta vulgaris)

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Abstract

The endosymbiotic theory postulates that many genes migrated from endosymbionts to the nuclear genomes of their hosts. Some migrated genes lack presequences directing proteins to mitochondria, and their mitochondrial targeting signals appear to be inscribed in the core coding regions as internal targeting signals (ITFs). ITFs may have evolved after sequence transfer to nuclei or ITFs may have pre-existed before sequence transfer. Here, we report the molecular cloning of a sugar beet gene for ribosomal protein S19 (Rps19; the first letter is capitalized when the gene is a nuclear gene). We show that sugar beet Rps19 (BvRps19) is an ITS-type gene. Based on amino-acid sequence comparison, dicotyledonous rps19s (the first letter is lower-cased when the gene is a mitochondrial gene), such as tobacco rps19 (Ntrps19), resemble an ancestral form of BvRps19. We investigated whether differences in amino-acid sequences between BvRps19 and Ntrps19 were involved in ITS evolution. Analyses of the intracellular localization of chimaeric GFP-fusion proteins that were transiently expressed in Welsh onion cells showed that Ntrps19-gfp was not localized in mitochondria. When several BvRps19-type amino acid substitutions, none of which was seen in any other angiosperm rps19, were introduced into Ntrps19-gfp, the modified Ntrps19-gfp became localized in mitochondria, supporting the notion that an ITS in BvRps19 evolved following sequence transfer to nuclei. Not all of these substitutions were seen in other ITS-type Rps19s, suggesting that the ITSs of Rps19 are diverse.

Keywords: plant mitochondria, gene migration, ribosomal protein, mitochondrial targeting, mitochondrial gene

Abbreviations: rps10, gene for ribosomal protein S10 (mitochondrion encoded); Rps10, gene for ribosomal protein S10 (nucleus encoded); ORF, open reading frame; mRNA, messenger RNA, cDNA, DNA complementary to RNA; MTS, mitochondrial targeting
signal; ITS, internal targeting signal; rps19, gene for ribosomal protein S19 (mitochondrial encoded); Rps19, gene for ribosomal protein S19 (nuclear encoded); GFP, green fluorescent protein; RFP, red fluorescent protein; RPS10, ribosomal protein S10; RPS19, ribosomal protein S19; RT-PCR, reverse transcription-polymerase chain reaction; 5' RACE, 5' rapid amplification of cDNA ends; 3' RACE, 3' rapid amplification of cDNA ends; DAPI, 4'-6-diamidino-2-phenylindole; BvRps19, Beta vulgaris Rps19; UTR, untranslated region; Ntrps19, Nicotiana tabacum rps19; Cox2, gene for cytochrome oxidase subunit II (nuclear encoded); NLS, nuclear localization signal; TOM, translocase of outer mitochondrial membrane.

1. Introduction

Mitochondria were once free-living organisms resembling α-proteobacteria but became cellular organelles after the completion of endosymbiosis with ancestral eukaryotes (Scheffler, 1999). Mitochondrial genomes, therefore, can be considered as relatives of the initial endosymbionts (Timmis et al., 2004); however, genetic information encoded by the current mitochondrial genomes is insufficient to support life as independent organisms because a number of genes have been lost from the mitochondrial genomes (Gray, 1999; Gray et al., 2004). Genes of bacterial origin have been found in nuclear genomes, and the gene products are imported into mitochondria (e.g. Duchene et al., 2005), indicating that some, but not all, of the lost genes have migrated to nuclear genomes during the course of eukaryotic evolution.

Although the gene repertoire of animal mitochondrial genomes is rather constant, which suggests that gene migration events ceased long ago evolutionarily, the gene repertoire of angiosperm mitochondria is varied (reviewed in Kubo and Newton 2008 and Kubo et al. 2011). This variation has been a starting point for exploring gene migration events; for example, loss of ribosomal protein S10 gene (rps10) from
mitochondria occurred in at least 26 lineages during angiosperm evolution, and each of these events was possibly complemented by independent gene migration (Adams et al., 2000). Together with many other instances (Kadowaki et al., 1996; Adams and Palmer, 2003), angiosperms are considered to be one of the best models for the study of gene migration.

Angiosperm mitochondrial genes per se appear to function improperly when situated in nuclei (Covello and Gray, 1992). One of the reasons for this problem is that their open reading frames (ORFs) have some cytidine residues that are post-transcriptionally converted to uridine within mRNA, a phenomenon called RNA editing (Takenaka et al., 2008). Therefore, when mitochondrial genes were expressed in nuclei, the codons including editing sites would specify amino acids that are inappropriate for proper function. This issue cannot be ignored because developmental abnormalities occurred when unedited mitochondrial-gene products were engineered to target mitochondria in transgenic plants (Hernould et al., 1993). Gene migration was proposed to involve reverse transcription of edited mRNAs (Nugent and Palmer, 1991), which would provide pre-edited ORFs as cDNAs. However, accumulating evidence indicates that the major routes of organelle DNA transfer to nuclear DNA are mediated by DNA (Woischnik and Moraes, 2002; Shahmuradov et al., 2003; Kleine et al., 2009; Ueda and Kadowaki, 2012).

Another reason for improper gene function of nuclear-situated mitochondrial genes is associated with protein import into mitochondria. Because this process involves a mitochondrial targeting signal (MTS), a sequence in the preprotein that is both necessary and sufficient to direct the protein to mitochondria (Neupert, 1997), gene organization of migrated genes has been inspected to find targeting signals. The migrated genes identified to date have been classified into two classes (for review, see Adams and Palmer, 2003). The first class includes genes with an N-terminal presequence that functions as an MTS. The presequence is cleaved upon import into
mitochondria (Neupert, 1997). Since no such presequence is encoded in mitochondrial-resident genes, migrated genes must have acquired presequences after transfer to nuclei. The origin of presequences associated with migrated genes has been proposed to be either duplicated copies of pre-existing mitochondrial targeting genes or unknown DNA sequences (Kadowaki et al., 1996; Adams et al., 2000; Liu et al., 2009). The second class of migrated genes includes genes lacking presequences. In Arabidopsis thaliana and rice (Oryza sativa), about one-fourth of the nuclear genes coding for mitochondrial ribosomal proteins lack presequences (Bonen and Calixte, 2006). The MTS of presequence-less genes appears to be inscribed in the core coding regions as internal targeting signals (ITSs) (Neupert, 1997).

An ITS-type Rps10 (hereafter, the first letter of the gene symbol is shown in upper case when the gene is encoded by nuclear genomes, whereas those shown in lower case are genes encoded by mitochondria) was identified in maize (Zea mays) (Murcha et al., 2005). On the other hand, in vitro translation products of soybean (Glycine max) rps10, a mitochondrion-resident gene, are not imported into isolated mitochondria (Murcha et al., 2005). After introducing some amino-acid substitutions into soybean rps10 with reference to maize Rps10, the modified soybean RPS10 protein was successfully imported into isolated mitochondria in vitro (Murcha et al., 2005), suggesting that the ITS in maize Rps10 had evolved after the transfer of the non-importable rps10 sequence to the nuclear genome.

The mitochondrial gene coding for ribosomal protein S19 (rps19) is an interesting example of gene migration because at least 39 independent migrations have occurred during angiosperm evolution (Adams et al., 2002) and both presequence-type and ITS-type Rps19s have been found (Sanchez et al., 1996; Adams et al., 2002; Liu et al., 2009). The evolution of the ITS in Rps19 is open to dispute. ITSs are hypothesized to have pre-existed in ancestral mitochondrion-resident rps19 as latent ITSs. A latent ITS was found from rice by the following experiment: rice rps19 was tagged with green
fluorescent protein (GFP) gene, and the fusion gene was expressed in nuclei, but the expressed protein localized to mitochondria (Ueda et al., 2008). An ITS-type Rps19 was found from melon (Cucumis melo) and orange (Citrus sinensis) (Liu et al., 2009), but no further analysis was conducted. The questions we wanted to address in this study are whether the latent ITS is preserved in other angiosperm rps19, and, if so, whether there are any evolutionary relationships between the latent ITS and the ITS in Rps19.

We have determined the entire nucleotide sequence of the sugar beet mitochondrial genome, and found that rps19 had been lost (Kubo, 2000). A close look at the data presented by Adams et al. (2002) indicated that loss of the mitochondrion-resident rps19 from sugar beet (Caryophyllales) occurred independently from those of melon (Cucurbitales) and orange (Sapindales) (see also Fig. 1), but it was unknown whether loss of rps19 from sugar beet mitochondria was complemented by a nuclear-migrated copy. We hypothesized that if a nuclear-migrated copy existed in the sugar beet nuclear genome, sugar beet Rps19 could be a good example for investigating the evolutionary mechanism for gene migration. Here, we show that sugar beet Rps19 belongs to a class of ITS-type genes and likely evolved a unique ITS after its ancestral rps19 sequence was transferred to the nuclear genome.

2. Material and methods

2.1 Plant materials

A sugar beet line TK–81mm–O (Kubo et al., 2000) and a tobacco (Nicotiana tabacum) cultivar SR-1 were used in this study. Petunias (Petunia x hybrida) were purchased from a local market.

2.2 Nucleic acid isolation
Total cellular DNA was isolated from green leaves according to the procedure of Doyle and Doyle (1990). DNA samples were purified by centrifugation in a CsCl-continuous density gradient, if necessary. Total RNA was isolated from green leaves by using an RNeasy Plant Mini Kit (Qiagen, Valencia, CA). Isolated RNA samples were further purified by incubation with RNase-free DNase I (Takara Bio, Ohtsu, Japan) according to the manufacturer’s instructions.

2.3 DNA gel blot analysis

Total cellular DNA was digested with restriction endonucleases purchased from Takara Bio and electrophoresed in a 1% agarose gel. Separated DNA fragments were blotted onto a Hybond N+ membrane (GE Healthcare UK, Amersham Place, England). DNA fragments of interest were labeled with alkaline phosphatases using AlkPhos Direct DNA labeling system (GE Healthcare UK). Hybridization was done according to the instruction manual. Signal bands were detected by the exposure to X-ray films.

2.4 Molecular cloning

Preparation of the TK–81mm–O-genomic library used in this study was described in Matsuhira et al. (2007). About 1 x 10^6 recombinant phages were transferred onto Hybond N membrane (GE Healthcare UK) according to the instruction manual. Plaque hybridization was carried out using the same procedure as that used for DNA gel blot analysis. DNA fragments of interest were subcloned into the pBluescript SK+ vector (Stratagene, La Jolla, CA, U.S.A.). Nucleotide sequences were determined using a Li-COR4200L automated DNA sequencer (Li-COR, Lincoln, NE, U.S.A) or an ABI3130 genetic analyzer (Applied Biosystems, Foster City, CA, U.S.A.). Sequence
analysis was conducted using GENETYX (GENETYX CORPORATION, Tokyo, Japan) or Sequencher (Hitachi Software Engineering, Tokyo, Japan). BLAST searches were conducted at the NCBI website (http://blast.ncbi.nlm.nih.gov/Blast.cgi). Sequence alignment was carried out using CLUSTALW (http://clustalw.ddbj.nig.ac.jp/top-j.html) and modified manually. Subcellular localization was predicted using Predotar (http://urgi.versailles.inra.fr/predotar/predotar.html) and Wolf PSORT (http://wolfpsort.org/). The nucleotide sequences obtained in this study were deposited in DDBJ/EMBL/GenBank under accession numbers AB751612, AB751613 and AB752306.

2.5 Reverse transcription-polymerase chain reaction

Reverse transcription (RT) was performed using Superscript III (Invitrogen, Carlsbad, CA, U.S.A.) according to the instruction manual. The subsequent PCR reaction was carried out using BlendTaq (Toyobo Life Science, Osaka, Japan). See also Table S1.

2.6 5′- and 3′-rapid amplification of cDNA ends

Both of the cDNA ends were PCR amplified using a GeneRacer Kit with Super Script III RT (Invitrogen, Carlsbad, CA) according to the instruction manual. See also Table S1.

2.7 Construction of chimaeric green fluorescent protein genes and transient assays

Procedures for PCR amplification to obtain DNA fragments that were to be fused with the 5′ to GFP genes are summarized in Table S1 and Fig. S1. Constructed DNA
fragments were inserted into the pTH2 vector (Chiu et al., 1996), in which GFP gene expression is driven by the Cauliflower-Mosaic Virus 35S promoter. Sequence integrity was verified by nucleotide sequencing. The resultant plasmid was introduced into the epidermal cells of Welsh onion sheathes using an IDERA GIE-III particle delivery system (Frontier Science, Ishikari, Japan). Mitochondria were marked by red fluorescent protein (RFP) fluorescence which was expressed by the co-introduced pMt-R plasmid (Arimura and Tsutsumi, 2002), encoding RFP fused with the N-terminal region of F1-ATPase δ-subunit. Nuclei were marked by RFP with nuclear localization signal of SV40 large T-antigen (van der Krol and Chua, 1991) that was expressed from pNc-R plasmid, which was made by modifying pMt-R (see Table S1). Fluorescent signals were observed with a Nikon E600 fluorescence microscope (Nikon, Tokyo, Japan). The images were captured, pseudo-colored and merged using Photoshop (Adobe, San Jose, CA, USA).

3. Results and Discussion

3.1 Molecular cloning of sugar beet Rps19

A nuclear-transferred Rps19 sequence in sugar beet was detected by DNA gel blot analysis. The probe was a mitochondrion-resident rps19 sequence that was PCR amplified from petunia total cellular DNA using a pair of primers (see Table S1). The amplicon was labeled and hybridized to a blot containing sugar-beet total cellular DNA. Three bands, a 7.7-kbp BamHI fragment, a 6.2-kbp EcoRI fragment and a 2.6-kbp HindIII fragment, were detected on the blot (Fig. 2A). We cloned the 2.6-kbp HindIII fragment and found that the fragment contained an ORF showing high homology to plant mitochondrial rps19 (see Supporting Information-1).

The 5′ and 3′ termini of mRNA containing the rps19-like ORF were investigated by
5′ rapid amplification of cDNA ends (5′-RACE) and 3′-RACE, respectively. Assembly of cDNA sequences revealed a continuous sequence of 809 bp, apart from the poly (A) tail (Fig. S2). In this cDNA sequence, an in-frame termination codon was found upstream of the *rps19*-like ORF. Hereafter, we designated this *rps19*-like ORF as *BvRps19* (after *B. vulgaris Rps19*). The lengths of the 5′ untranslated region (UTR) and the 3′ UTR were 271 and 260 bp, respectively.

Whereas the nucleotide sequence of the 3′ UTR matched the 2596-bp genomic sequence, the -271 to -19 sequence of the 5′ UTR was missing, suggesting the interruption of the 5′ UTR by one or more intron(s) in the sugar-beet genome. PCR amplification of sugar-beet total cellular DNA with a pair of primers (see Table S1), corresponding to the 5′ terminus of the cDNA and internal to *BvRps19*, respectively, generated a 2.8-kbp DNA fragment that was larger than that expected from the cDNA sequence. The nucleotide sequence of the 2.8-kbp fragment had an overlapping region with the 2596-bp genomic sequence, and, by assembling the 2.8-kbp sequence and the 2596-bp genomic sequence, a continuous sequence of 3825-bp was revealed (Fig. S2). Comparison of the cDNA- and the genomic sequences revealed that an intron of 2586 bp intervened between the first exon (253 bp) and the second exon (556 bp) (Fig. 2B). The presence of an intron in the 5′ UTR is atypical of angiosperm mitochondrial genes (Kubo and Newton, 2008).

Transcripts of *BvRps19* were detected from flower bud-, leaf- and root total RNA by RT-PCR (Fig. 2C).

3.2 *BvRps19* lacks an N-terminal presequence

We compared the amino acid sequence of *BvRps19* with those of several plant *rps19* and *Rps19* deduced proteins, the latter of which include presequence-type (soybean, maize, cotton, and *A. thaliana*) and ITS-type (orange and melon) proteins
(Fig. 3). As a result, it became clear that *BvRps19* belongs to the ITS-type *Rps19* class. Moreover, the amino-acid sequences of ITS-type *Rps19* and *rps19* are highly homologous to each other, but rather diverse from those of presequence-type *Rps19*. This tendency is conspicuous in the first 10 amino acids in the sequences as shown in Fig. 2.

3.3 *Intracellular localization is different between BvRPS19-GFP and tobacco RPS19-GFP*

Although it is impossible to know the nucleotide sequence of an ancestral mitochondrial copy of *BvRps19*, it seems likely that the ancestral copy was very similar to the present dicotyledonous *rps19*, given that migration of *BvRps19* may have occurred after the divergence of the Caryophyllales lineage (see Fig. 2 of Adams et al. 2002; see Fig. 1 of this study). Additionally, amino-acid sequences of dicotyledonous *rps19* are highly conserved (Fig. 3). Therefore, it is reasonable to consider one of the dicotyledonous *rps19* genes as a model of the ancestral *Bvrps19* gene. We chose tobacco *rps19* (DDBJ/EMBL/GenBank ID: BA000042) for further study.

Tobacco *rps19* (*Nt*rps19, after *N. tabacum rps19*) was PCR amplified from leaf cDNA with a pair of primers (see Table S1). Comparing the cDNA sequence with the PCR-amplified genomic sequence, we found five cytidine-to-uridine RNA editing sites, of which three altered the amino acid specificity of the codons (Fig. S3). These edits increased the homology between BvRPS19 and NtRPS19, suggesting the possibility that the migration of *BvRps19* may have involved reverse transcription of mitochondrial mRNA.

We next examined whether *BvRps19* encoded a mitochondrial protein and whether a latent ITS existed in *Nt*rps19. First, the intracellular localization of BvRPS19 and NtRPS19 was predicted *in silico* by two programs. WolfPsort predicted the nuclear
localization of BvRPS19 (score = 7.0) and NtRPS19 (5.0). Predotar's prediction was ‘possibly mitochondrial (0.46)’ and ‘mitochondrial (0.72)’ for BvRPS19 and NtRPS19, respectively.

The intracellular localization of BvRPS19 was tested by expressing a GFP-tagged chimaeric gene. The entire \textit{BvRps19} was fused 5' to the GFP gene to make a \textit{BvRps19-GFP} fusion gene (#1 in Fig. 4; residue 92 [arginine] was replaced with proline to introduce a restriction site). The fusion gene was delivered into epidermal cells of Welsh onion sheath by particle bombardment. Cells expressing the fusion gene were observed by fluorescence microscopy. As a result, green fluorescent signals were localized to small intracellular particles that clearly matched with the red fluorescent signals of MTP-RFP expressed from the co-introduced plasmid pMt-R (Fig. 4A2 and Fig. 4A3).

The entire \textit{Ntrps19} ORF was fused 5' to the GFP gene (#2 in Fig. 4; residue 94 [lysine] was replaced with threonine to introduce a restriction site) and expressed in Welsh onion sheath epidermal cells. The green signals obtained from NtRPS19-GFP co-localized with red signals from nuclear localizing RFP (#2 in Fig. 4). Our GFP-fusion assay failed to find any signs of a latent ITS from \textit{Ntrps19}.

3.4 Modified NtRPS19-GFP localized to mitochondria

Comparing NtRPS19 with BvRPS19, several amino acid substitutions are present, although the two sequences are very similar (Fig. 3). We next examined whether these substitutions are involved in the differential localization between NtRPS19-GFP and BvRPS19-GFP. The fluorescence localization results of a series of GFP-fusion proteins are shown in Fig. 4.

We first focused our analysis on the N-terminal region of BvRPS19 because the translation products of fusion gene #3 (see Fig. 4; the first 37 amino acid residues of
BvRPS19 were fused to GFP) localized to mitochondria. In the first 37 amino acid residues, the differences between BvRPS19 and NtRPS19 are P2S, I6L, and a diverged region (19th-29th residues), whereas the other residues are identical (Fig. 3). We introduced all these changes into NtRPS19-GFP (#4 in Fig. 4); however, the modified NtRPS19-GFP localized in nuclei. As mentioned by Neupert (1997), overall conformation of a preprotein can influence mitochondrial import due to changes in signal accessibility. It was possible that the conformation of NtRPS19 might be associated with the failure in mitochondrial localization. This notion was supported by our data showing that deletion of K90-to-K94 from #4 resulted in mitochondrial localization of the modified fusion protein (#5 in Fig. 4).

Conversely, #6 (Fig. 4), a fusion protein where K90-to-K94 was deleted but otherwise the same as #2, was nuclearly localized. This result indicates that the K90-to-K94 deletion is insufficient for mitochondrial localization of NtRPS19-GFP, perhaps due to the lack of an ITS in NtRPS19.

Of the three differences in the N-terminal 37 amino acid residues (P2S, I6L, and a diverged region [19th-29th residues]), some of these differences may have functional significance and others may be silent polymorphisms. To identify the functionally significant differences, each of the three regions in #5 was reversed compared to that of NtRPS19. Reversion of the 19th-29th residues had no effect on the localization pattern (#7); however, #8 (P2S substitution alone) fusion protein localized in nuclei as well as in mitochondria (Fig. 4). This localization pattern was distinct from that of #1. Also, #9 (I6L substitution alone) fusion protein was localized to nuclei (Fig. 4). We concluded that both P2S and I6L are functionally significant for the N-terminal segment of BvRPS19 to be imported into mitochondria.

Consistent with the result of the localization assay using #4 fusion protein, the introduction of both P2S and I6L to #2 did not alter the localization pattern (#10 in Fig. 4), indicating that an additional change is necessary. We noticed that, whereas the
C-terminal ~14 amino acid residues of \( rps19 \) deduced proteins were fairly conserved, those of presequence-type and ITS-type \( Rps19 \) diverged from \( rps19 \) (Fig. 3). In addition to this finding, whereas D44-C45-S46 is conserved among \( rps19 \) deduced proteins, this amino-acid sequence is not seen in presequence-type and ITS-type \( Rps19 \)s. We tested whether changes in these regions were associated with the mitochondrial localization of BvRPS19. The 81st to 94th residues of #10 were substituted with the corresponding region of BvRPS19 (81st to 92nd residues, see Fig. 3). The resultant fusion gene was termed #11, and its translation products exhibited nuclear, as well as mitochondrial, localizations (Fig. 4). Then, three additional substitutions, D44G, C45S, and S46A, were introduced (#12). Translation products of fusion gene #12 localized to mitochondria (Fig. 4). On the other hand, #13 fusion protein, in which the second and sixth residues were reversed to proline and isoleucine, respectively, was not specifically localized (Fig. 4).

4. Conclusion

\( BvRps19 \) is an ITS-type migrated gene. Assuming that \( Ntrps19 \) represents an ancestral form of \( BvRps19 \), involvement of latent ITS in \( BvRps19 \) migration seems unlikely. Rather, \( BvRps19 \) migration is associated with sequence alterations in four regions (2nd, 6th, 44th-to-46th, and 81st-to-94th residues). These changes are not seen in any dicotyledonous \( rps19 \) deduced proteins identified so far, suggesting that these alterations occurred after sequence transfer to the nuclear genome. It is very likely that these alterations contain some functionally silent polymorphisms. Further analyses for specifying the significant substitutions are infeasible for us because it would require tests of at least additional 32768 fusion proteins \( (2^{15}, \text{for single and combinations of 13 substitutions}) \).

Compared to the study of maize \( Rps10 \) and soybean \( rps10 \) (Murcha et al. 2005), in
which changes in the N-terminal 20 residues were sufficient for importing soybean rps10 protein, the alterations associated with BvRps19 protein importability were scattered throughout the entire protein. One of the reasons for this difference may be associated with the adopted methodology, i.e. in vitro assay (rps10) and GFP-fusion assay (this study), as pointed out by Logan (2009).

The two regions, the 44th-to-46th and 81st-to-94th residues, are also altered in other nuclear-migrated Rps19s. Therefore, it is possible that alterations in the 44th-to-46th and 81st-to-94th residues may be involved in some other Rps19 migration events. We hypothesize that any alterations in these regions are forbidden in mitochondria because of an unknown constraint that no longer works in nuclei. In the soybean Cox2 gene product, successful migration involves a reduction in the hydrophobicity of the transmembrane region (Daley et al., 2002). However, the hydrophobicity of BvRPS19, melon RPS19 and orange RPS19 was not necessarily reduced compared to that of Ntrps19 (Fig. S4). Therefore, functional aspects of these alterations are unclear. Considering the nuclear localization of NtRPS19-GFP, the C-terminus of rps19 may function as a nuclear localization signal (NLS) due to the lysine and arginine string that resembles a NLS, but it remains unknown why no mitochondrial targeting happened for a chimaeric protein consisting of the N-terminus of BvRPS19 and the C-terminus of NtRPS19, such as #4 (Fig. 4). Recently, a transcription factor ATFS-1, which has both a MTS and a NLS, was reported to be normally imported into mitochondria but localized to nuclei when mitochondrial import efficiency was reduced (Nargund et al. 2012). Therefore, alterations in the C-terminal region might be associated with mitochondrial import efficiency.

The function of P2S and I6L in Bvrps19 remains obscure. It is unlikely that these substitutions generated a motif that has been defined as a receptor for TOM complex (TOM20) binding, θXX00, where θ is any hydrophobic amino acid and X is an aliphatic amino acid with a preference for those with a long side chain (Murcha et al.,
2005). Melon- and orange *Rps19* have P2S and I6L, respectively (Fig. 3), suggesting that these substitutions also involved in other migration events; however, neither of the two *Rps19* has both substitutions simultaneously. Instead, each of the two *rps19* has unique amino-acid substitutions compared to the dicotyledonous *rps19*, such as R3P and S10G (melon), and L17A (orange). This result led us to infer that the ITS of *Rps19* may be diverse, although further analyses will be necessary to describe fully ITS evolution in dicot *Rps19*s.

Supplementary materials related to this article can be found at the journal online.

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**References**


**Figure legends**

**Fig. 1** Phylogenetic relationship and presence/absence of \textit{rps19} and \textit{Rps19} in nine plants. Nuclear (Nuc.) \textit{Rps19} status is abbreviated as P (presence of presequence type), \(\psi\) (pseudo gene), I (presence of ITS type) and ? (unknown). Mitochondrial (Mit.) \textit{rps19} status is abbreviated as - (absence), +/-ITS (presence with latent ITS), -? (probably absence), - (absence), +?/? (probably presence but latent ITS unknown), +/- (presence with no latent ITS). The phylogenetic tree was adopted from the Angiosperm Phylogeny Website (http://www.mobot.org/mobot/research/apweb/welcome.html), but the length of the branches are not correlated with phylogenetic distances. Data from: maize, Adams et al. (2002), DDBJ/GenBank/EMBL accession number EE292591 and AY506529; rice, Ueda et al. (2008) and our unpublished result; soybean, Adams et al. (2002); melon, Adams et al. (2002), Liu et al. (2009), JF412792 and JF412800; orange, Adams et al. (2002) and Liu et al. (2009); cotton, Adams et al. (2002); \textit{Arabidopsis}, Sanchez et al. (1996), and Y08501; tobacco, Adams et al. (2002) and BA000042; sugar beet, BA000009 and this study.

**Fig. 2** Organization and expression of sugar beet \textit{rps19} genes. Panel A  DNA gel blot analysis of total cellular DNA (5\(\mu\)g) from sugar beet cv. TK–81mm–O probed with petunia \textit{rps19}. Restriction endonucleases used in this experiment are \textit{BamHI} (B), \textit{EcoRI} (E), and \textit{HindIII} (H). Size markers are shown on the left (kb). Panel B  Schematic organization of sugar beet \textit{Rps19}. The arrow indicates transcriptional direction. Open- and filled boxes show the UTR and coding region, respectively. An intron interrupts the 5' UTR (depicted by a dotted line). The scale bar is shown in kbp. Panel C  RT-PCR analysis of \textit{BvRps19} and the sugar beet \textit{Actin} gene, as a control. Sizes of the PCR products are shown on the left. Total RNAs from flower buds (1), leaves (2), and roots (3) were subjected to reverse transcription with (+) or without (–) reverse transcriptase.
Fig. 3 Alignment of deduced amino acid sequences of RPS19s. Thirteen RPS19 deduced protein sequences were aligned. Residues highlighted in Black indicate amino-acid residues conserved in 7 or more sequences. Positions of amino acid residues that are associated with the ITS evolution of *BvRps19* are highlighted in blue. Nucleus-resident copies and mitochondrion-resident copies are indicated by nc and mt, respectively. Amino acid sequences of mitochondrial RPS19s were deduced from their cDNA sequences. Presequences are not shown, but the lengths of the presequences are shown in parentheses. Sources of sequences are: sugar beet (Bv), this study; tobacco (Nt), DDBJ/GenBank/EMBL accession number BA000042 and this study; grapevine (Vv), RNA editing database (REDIdb) (http://biologia.unical.it/py_script/search.html) accession number EDI_000000871; *Magnolia x soulangeana* (Ms), REDIdb accession number EDI_000000722; rice (Os), REDIdb accession number EDI_000000941; *Cycas revoluta* (Cr), REDIdb accession number EDI_000000253; *Ginkgo biloba* (Gb), REDIdb accession number EDI_000000929; orange (Cs), DDBJ/GenBank/EMBL accession numbers CV718812 and CX071875; melon (Cm), DDBJ/GenBank/EMBL accession number AM727919; soybean (Gm), DDBJ/GenBank/EMBL accession numbers EV279429 and EH260323; maize (Zm), DDBJ/GenBank/EMBL accession number EE292591; cotton (*Gossypium raimondii*), DDBJ/GenBank/EMBL accession number CO082119; *Arabidopsis thaliana* (At), DDBJ/GenBank/EMBL accession number AY049255.

Fig. 4 Summary of localization analyses. A schematic diagram of proteins that were fused with GFP is shown (#1 to #13). Localization of the fusion proteins are abbreviated as: Mt, mitochondria; Nc, nuclei; Mt/Nc, mitochondria and nuclei; nc, no specific localization. The coding region of *Nirps19* is indicated by orange rectangles. Amino acid substitutions in *BvRps19* are depicted as blue vertical lines. Numbers above the rectangles indicate positions of amino acid residues. The locations of P2S and I6L are...
emphatically shown. A1 to O3 are fluorescence images of epidermal cells of Welsh onion sheathes: expressing #1 (A1), and pMt-R (A2); expressing #2 (B1), and pNc-R (B2); expressing #3 (C1), and pMt-R (C2); expressing #4 (D1), and pNc-R (D2); expressing #6 (F1), and pNc-R (F2); expressing #7 (G1), and pMt-R (G2); expressing #8 (H1), and pMt-R (H2); expressing #8 (I1), and pNc-R (I2); expressing #9 (J1), and pNc-R (J2); expressing #10 (K1), and pNc-R (K2); expressing #11 (L1), and pMt-R (L2); expressing #11 (M1), and pNc-R (M2); expressing #12 (N1), and pMt-R (N2); expressing #13 (O1), and pMt-R (O2). Images with a suffix of 3 are merged images of those-with suffixes 1 and 2 having the same prefix.
Zea (maize)  | Nuc. | Mit.  
---|---|---
Oryza (rice) | ψ | +/- ITS
Glycine (soybean) | P | +/- P
Cucumis (melon) | I | -
Citrus (orange) | I | -?
Gossypium (cotton) | P | +/- P
Arabidopsis | P | -
Nicotiana (tobacco) | ? | +/- ITS
Beta (beet) | I | -
1. Sugar beet

#1: Mt

#2: Nc

P2S: L6L 19-29

#3: Mt

#4: Nc

#5: Mt

- Tobacco

A1, A2, A3

B1, B2, B3

C1, C2, C3

D1, D2, D3

E1, E2, E3
Generation of DNA fragments for hybridization probe

<table>
<thead>
<tr>
<th>Probe Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total cellular DNA of petunia</td>
<td>PCR amplified using P1 (5'-AGTGGCAGGATCCCATATG-3') and P2 (5'-GGCTCAATAATTTTGTC-3') primers.</td>
</tr>
<tr>
<td>5' RACE</td>
<td>One microgram of total cellular RNA from leaves were dephosphorylated and reverse transcibed with GeneRacer oligo dT Primer (supplied with GeneRacer III R T Module) as the manufacturer’s instruction. The resultant cDNA was PCR amplified using primers P3 (5'-GAGGCCCTTTTCCTCCCTTTG-3') and GeneRacer 5' Primer (supplied by the manufacturer).</td>
</tr>
<tr>
<td>3' RACE</td>
<td>The cDNA mentioned above was PCR amplified using primers P4 (5'-AGTCGAGACCCACGACTTCTC-3') and GeneRacer 3' Primer (supplied by the manufacturer).</td>
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Amplification of intrinsic sequence

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<th>PCR</th>
<th>Description</th>
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<tr>
<td>Tobacco genomic rps19 amplification</td>
<td>Total cellular DNA of tobacco was PCR amplified using P9 and P10.</td>
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Construction of fusion gene #1

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<th>Description</th>
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<tr>
<td>Primer</td>
<td>ACGTCGACAATTCCGAGAATATCAGAGAGAGAAAGGTAATGGTGCGCTCTCC-3'</td>
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Construction of fusion gene #2

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Construction of fusion gene #3

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<td>Primer</td>
<td>5'-TCAACCAGAAAACCCCTTTTTTTTTTTTTTCT-3'</td>
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Construction of fusion gene #4

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<tr>
<td>Primer</td>
<td>P20 (5'-CCAACGAATTCTGGCAAGATAGA-3')</td>
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Construction of fusion gene #5

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<td>Primer</td>
<td>5'-ACCATGGTTTTCCCCCTTTTTTCTTCC-3'</td>
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Construction of fusion gene #6

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<tbody>
<tr>
<td>Primer</td>
<td>P1 (5'-ATGCCACGACGATCCATATG-3')</td>
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</tbody>
</table>
C

Sugar beet Rps19

P11 \rightarrow PCR \leftarrow P18

SalI \quad NcoI

Sali \quad Ncoli

CaMV35S \quad \textbf{GFP}

pTH2

D

Tobacco rps19

P9 \rightarrow PCR \leftarrow P19

SalI \quad NcoI \quad PstI

pBluescript SK+
H

CaMV35S → 1

P23

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<th>NcoI</th>
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pTH2 → GFP

PCR → p#6

CaMV35S → 89

GFP

P21

I

CaMV35S → 1

P24

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pTH2 → GFP

PCR → p#6

CaMV35S → 89

GFP

P21

CaMV35S → I6L

p#9
Site directed mutagenesis via PCR
Fig. S1  Schematic illustration of plasmid construction. CaMV35S indicates 35S promoter region of Cauliflower Mosaic Virus. Primers are shown by horizontal arrows. Colors of the gene-coding regions are the same as in Fig. 4. Restriction sites are shown when necessary. See Table S1 for details. A to M corresponds to the procedures for construction of #1 to #13, respectively.
Fig. S2  Nucleotide sequence of sugar beet Rps19 locus. The open reading frame was translated into amino acid residues (shown in one letter symbols below the nucleotide sequence). Untranslated regions are shown by dashed underlines. Donor- (5'-GT-3') and acceptor sites (5'-AG-3') of the intron are boxed. An in-frame stop codon is indicated by red-colored letters.

3001  TTTACAATGGAAAGTCATTCGTTCGCTGTAAGATCACTGAATCAAAAGTTGGTCACAAAT  3060  Y N G K S F V R C K I T E S K V G H K F

3061  TTGGAGAGTTTGCTTTCACACGGAAAAGAAGGCCTCACAAATTAGATGTTGAAGAAAA  3120  G E F A F T R K R R P H K L D G G K K K

3121  AGGGGGGTCGTTGAGCTCGGCTCAGCGGCTCTCATTACTGCTTTCGTTTATCAATTTT  3180  G G R *

3181  CTGGAGGGTACTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGCTTTGGC

Fig. S2  Nucleotide sequence of sugar beet Rps19 locus. The open reading frame was translated into amino acid residues (shown in one letter symbols below the nucleotide sequence). Untranslated regions are shown by dashed underlines. Donor- (5'-GT-3') and acceptor sites (5'-AG-3') of the intron are boxed. An in-frame stop codon is indicated by red-colored letters.
Fig. S3  Alignment of nucleotide sequences of sugar-beet Rps19 (Bv) and tobacco rps19 (Nt). Amino acid sequence of putative translation product of the tobacco rps19 is shown below. Primer sequences are shown by underlined font. RNA editing sites are shown by lower-case letters. Alteration of amino acid specificity by RNA editing is shown below the editing sites.
Kyte–Doolittle Hydropathy Plot

Hydropathy Score

Window Position

NtRPS19 (blue) vs. BvRPS19 (red)
Kyte-Doolittle Hydropathy Plot

NtRPS19 (blue) vs. melon RPS19 (red)
Kyte-Doolittle Hydropathy Plot

NtRPS19 (blue) vs. orange RPS19 (red)
Fig. S4  Comparison of Kyte-Doolittle hydropathy plots of NtRPS19 with three ITS-type RPS19 proteins, BvRPS19, melon RPS19 and orange RPS19. Plots were drawn at the web site (http://gcat.davidson.edu/DGBP/kd/kyte-doolittle.htm) with default parameters. The two images were merged using PowerPoint (Microsoft). Panels A, B, and C shows a comparison between NtRPS19 and BvRPS19, NtRPS19 and melon RPS19, and NtRPS19 and orange RPS19, respectively.
**Supporting information-1** Screening the genomic library and identifying the *rps19*-like ORF

To see the molecular organization of the region that had homology to petunia *rps19*, we screened a sugar-beet genomic library consisting of recombinant lambda phages. We obtained three positive clones that overlapped with each other and constituted a 14.5-kbp contig according to restriction mapping.

A 2.6-kbp *HindIII* fragment, which appeared to correspond to the 2.6-kbp *HindIII* band on the blot, was subcloned from one of the three recombinant phage DNAs into a plasmid vector, and was sequenced entirely. We obtained a 2596-bp sequence that contained an ORF encoding 92 amino acid-residue polypeptide showing high homology (62-75% identity) to land plant mitochondrial *rps19* (Fig. S2 and Fig. 3). No other homologous sequence was retrieved from DDBJ/EMBL/GenBank database by BLASTN and BLASTX.