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Genome Res. published online October 26, 2010
Access the most recent version at doi:10.1101/gr.111955.110

P<P Published online October 26, 2010 in advance of the print journal.

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Localized hypermutation and associated gene losses in legume chloroplast genomes

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Point mutations result from errors made during DNA replication or repair, so they are usually expected to be homogeneous across all regions of a genome. However, we have found a region of chloroplast DNA in plants related to sweetpea (*Lathyrus*) whose local point mutation rate is at least 20 times higher than elsewhere in the same molecule. There are very few precedents for such heterogeneity in any genome, and we suspect that the hypermutable region may be subject to an unusual process such as repeated DNA breakage and repair. The region is 1.5 kb long and coincides with a gene, *ycf4*, whose rate of evolution has increased dramatically. The product of *ycf4*, a photosystem I assembly protein, is more divergent within the single genus *Lathyrus* than between cyanobacteria and other angiosperms. Moreover, *ycf4* has been lost from the chloroplast genome in *Lathyrus odoratus* and separately in three other groups of legumes. Each of the four consecutive genes *ycf4–psaI–accD–rps16* has been lost in at least one member of the legume "inverted repeat loss" clade, despite the rarity of chloroplast gene losses in angiosperms. We established that *accD* has relocated to the nucleus in *Trifolium* species, but were unable to find nuclear copies of *ycf4* or *psaI* in *Lathyrus*. Our results suggest that, as well as accelerating sequence evolution, localized hypermutation has contributed to the phenomenon of gene loss or relocation to the nucleus.

[Supplemental material is available online at http://www.genome.org. The sequence data from this study have been submitted to GenBank (http://www.ncbi.nlm.nih.gov/Genbank/) under accession nos. HM029359–HM029371, HM048906–HM048910, and GO313838–GO322539.]

The genome organization and gene content of chloroplast DNA (cpDNA) are highly conserved among most flowering plant species (Palmer 1985; Sugiura 1992; Jansen et al. 2007). The chloroplast genome of the most recent common ancestor of all angiosperms contained 113 different genes (four rRNA genes, 30 tRNA genes, and 79 protein genes), and this content has been retained in many angiosperms (Kim and Lee 2004). Rates of synonymous nucleotide substitution in chloroplast genes are generally low (a few fold lower than plant nuclear genes) and relatively homogeneous within a genome except for a threefold difference in rate between the large inverted repeat (IR) and single-copy regions (Wolfe et al. 1987; Drouin et al. 2008). Lineage-specific variation in chloroplast synonymous rates has been documented (Gaut et al. 1993; Guo et al. 2007) but is relatively modest compared to the vast differences seen among some plant mitochondrial lineages (Palmer et al. 2000; Mower et al. 2007; Sloan et al. 2009).

Some angiosperm cpDNAs have fewer than the 79 canonical protein genes due to gene losses. Most notable here are parasitic plants such as *Cuscuta* and *Epifagus* that have lost some or all photosynthetic ability (Wolfe et al. 1992; Funk et al. 2007; McNeal et al. 2007). Chloroplast gene losses are rarer in photosynthetic species, because in many cases the gene cannot simply be discarded and must instead be either functionally transferred to the nuclear genome or functionally replaced by a nuclear gene ("gene substitution"). Successful gene transfers from the chloroplast to the nuclear genome during angiosperm evolution have been reported for *rpl22* in legumes (Gantt et al. 1991); for *infA* in several lineages, including almost all rosids (Millen et al. 2001); and for *rpl32* in two families of Malpighiales (Cusack and Wolfe 2007; Ueda et al. 2007). In addition, Ueda et al. (2008) identified gene substitution as the mechanism of loss of the *rps16* gene from cpDNA in *Medicago* and *Populus*. The loss of *rps16* from cpDNA is compensated by dual targeting (to chloroplasts as well as mitochondria) of mitochondrial ribosomal protein S16, which is encoded by a nuclear gene. Several other examples of losses of genes from cpDNA in photosynthetic angiosperms have been reported, and it is striking that the few species in which gene losses have occurred tend also to be those whose chloroplast genomes are highly rearranged relative to the ancestral angiosperm organization (Jansen et al. 2007). As with angiosperm mitochondrial genomes (Adams and Palmer 2003), most of the genes that have been lost from chloroplast genomes during recent evolution have coded for ribosomal proteins (Jansen et al. 2007). There have been no published reports of the loss of genes coding for components of photosystems I or II (*psa* and *psb* genes), the electron transfer chain (*pet* genes), or the chloroplast ATP synthase (*atp* genes) from cpDNA in any angiosperms except parasitic species (Wolfe et al. 1992; Funk et al. 2007; McNeal et al. 2007).

One group of angiosperms that is known to be relatively prone to cpDNA rearrangement and gene loss is the legume family

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Article published online before print. Article and publication date are at http://www.genome.org/cgi/doi/10.1101/gr.111955.110.

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(Fabaceae) (Palmer et al. 1988). The large IR that is otherwise almost universally present in chloroplast genomes is absent from one large clade of legumes (the IR loss clade, or IRLC) (Wojciechowski et al. 2004), some of which also show other rearrangements of gene order. Chloroplast genomes in the IRLC species are also notable for having significant amounts of repetitive DNA, something not usually seen in angiosperm cpDNA (Milligan et al. 1989; Saski et al. 2005; Cai et al. 2008). Five instances of gene loss from the IRLC chloroplast genomes have been discovered. As well as the aforementioned gene transfers of *rpl22* and *infA* and substitution of *rps16* (Gantt et al. 1991; Millen et al. 2001; Ueda et al. 2008), it has been reported that that *accD* is completely absent from *Trifolium subterraneum* (subclover) cpDNA, and that *ycf4* in *Pisum sativum* (pea) is either absent or a pseudogene (Nagano et al. 1991a; Smith et al. 1991; Cai et al. 2008). Slot-blot hybridization experiments suggested that *ycf4* and *rps16* may have been lost independently multiple times in different lineages of legumes (Doyle et al. 1995).

In the course of this study, we reviewed all reported instances (in published papers or in GenBank annotations) of gene loss among the 103 complete angiosperm chloroplast genome sequences that are publicly available, and found that 27 different protein-coding genes have been lost in at least one lineage (Supplemental Table S1). We found that some reported gene losses are simply due to annotation errors; because of this, the numbers of losses we describe here are slightly different from those in Jansen et al. (2007). In particular, we noticed that the gene *ycf4*, which was originally not identified in the genome sequences of the legumes *Glycine max* (soybean; Saski et al. 2005), *T. subterraneum* (subclover; Cai et al. 2008), *Cicer arietinum* (chickpea), and *Medicago truncatula* (Jansen et al. 2008), is in fact present in the cpDNAs of all these species but is so divergent that it was not recognized by the DOGMA software (Wyman et al. 2004) used to annotate them. This discovery prompted us to investigate the rapid evolution of *ycf4* and its surrounding region in legumes.

Ycf4 is a thylakoid protein that has been shown to play a role in regulating photosystem I assembly in cyanobacteria (Wilde et al. 1995) and to be essential for photosystem I assembly in *Chlamydomonas* (Boudreau et al. 1997; Onishi and Takahashi 2009). Experiments in *Chlamydomonas* indicate that Ycf4 is the second of three scaffold proteins that act sequentially during the assembly process, with Ycf4's roles being to stabilize an intermediate subcomplex consisting of the PsaAB heterodimer and the three stromal subunits PsaCDE, and to add the PsaF subunit to this subcomplex (Ozawa et al. 2009). As well as the loss of *ycf4* in *P. sativum*, several other previous studies have indicated that the evolution of *ycf4* in legumes may be unusual. In soybean and *Lotus japonicus*, the Ycf4 protein, which is almost universally 184 or 185 amino acids long, has expanded to about 200 residues (Reverdatto et al. 1995; Kato et al. 2000). The gene also has a high rate of synonymous nucleotide substitution between the latter two species (Perry and Wolfe 2002). Phylogenetic trees for phaseoloid legumes constructed using *ycf4* were incongruent with trees constructed using seven other genes, due to accelerated evolution of codon positions 1 and 2 in *ycf4* (Stefanovic et al. 2009). In blot hybridizations to DNAs from 280 diverse angiosperms (as in Millen et al. 2001) using a *ycf4* probe from tobacco, we observed (SS and JDP, unpubl.) strong hybridization to all DNAs except those from the only Papillionoid legumes surveyed: *Medicago* (no signal from five species) and *Vigna* (considerably diminished signal). We show here that *ycf4* is situated in a local mutation hotspot, in *Lathyrus*, and possibly in other legume species, resulting in dramatic acceleration of sequence evolution in some species and evolutionary gene losses in others.

Results

Rapid evolution of *ycf4* in legumes

To investigate acceleration of the evolutionary rate of *ycf4* in legumes, we compared its nonsynonymous and synonymous nucleotide substitution rates in different angiosperm lineages to the rates observed in two other, widely sequenced chloroplast genes, *rbcL* and *matK*. This analysis included new *ycf4* sequence data from *Lathyrus* and other legumes, together with sequences from a previous phylogenetic study (GenBank [http://www.ncbi.nlm.nih.gov/Genbank/] accession nos. EU717431–EU717464; Stefanovic et al. 2009) and other database sequences. For each gene, we used a likelihood model to estimate the numbers of nonsynonymous (d_N) and synonymous (d_S) nucleotide substitutions that occurred on each branch of an angiosperm phylogenetic tree (see Methods). In the d_N trees, *ycf4* is seen to evolve much faster in most legumes than in other angiosperms (Fig. 1) but no similar acceleration is seen in legume *rbcL* or *matK*, which suggests that the acceleration is locus-specific, as well as lineage-specific. Within legumes, the first accelerated branch is the one leading to a large clade (Millettioids, Robinioids, and the IRLC; asterisk in Fig. 1), and the legumes that are outgroups to this branch do not show acceleration. This branch is also the first one on which the Ycf4 protein size expands above 200 amino acids (Fig. 1). Even faster periods of d_N evolution are seen in the genera *Desmodium* and *Lathyrus* relative to other legumes. *Ycf4* is a pseudogene in three of six *Desmodium* species we sequenced and in *Clitoria ternatea* (Supplemental Fig. S1C, left panel). In the d_S trees, some acceleration is seen in *ycf4* of legumes relative to other angiosperms, particularly in *Lathyrus*, but again no similar acceleration is seen in legume *rbcL* or *matK* (Fig. 1). The genus *Lathyrus* also shows by far the greatest increases in Ycf4 size, reaching 340 residues in *Lathyrus latifolius* and *Lathyrus cirrhosus*.

Remarkably, there is less amino acid sequence conservation between the Ycf4 proteins of two species within the genus *Lathyrus* (31% identity between *Lathyrus palustris* and *L. cirrhosus*), than between tobacco and the cyanobacterium *Synechocystis* (45% identity). Nevertheless, *ycf4* can be inferred to be functional in the four *Lathyrus* species in which it is intact (Fig. 2), for two reasons. First, even though the level of amino acid sequence conservation among *Lathyrus* species is very low, many of the sites in the C-terminal part of the protein (beginning at position 248 in Fig. 2) that are conserved among other land plants and cyanobacteria are also conserved in *Lathyrus*. Second, comparing *ycf4* sequences among *Lathyrus* species shows that they have lower levels of nonsynonymous than synonymous nucleotide substitutions ($d_N/d_S < 1$) (Table 1), which is a hallmark of sequences that are being constrained to code for proteins (Kimura 1977; Graur and Li 1999). We therefore infer that these long *ycf4* genes in *Lathyrus* species are biologically functional. However, the level of constraint on *Lathyrus ycf4* is lower than on other angiosperm *ycf4*s (e.g., d_N/d_S = 0.15 between tobacco and spinach *ycf4*, compared with d_N/d_S = 0.36–0.81 within the genus *Lathyrus*). Tests for positive (Darwinian) selection suggested that some *Desmodium* branches within the *ycf4* tree have undergone adaptive evolution, and in separate analyses, site-specific tests for positive selection were significant for some codons in *ycf4* when the whole legume tree was considered (data not shown). However, in view of the evidence that the whole region around *ycf4* has a high mutation rate (see below), and

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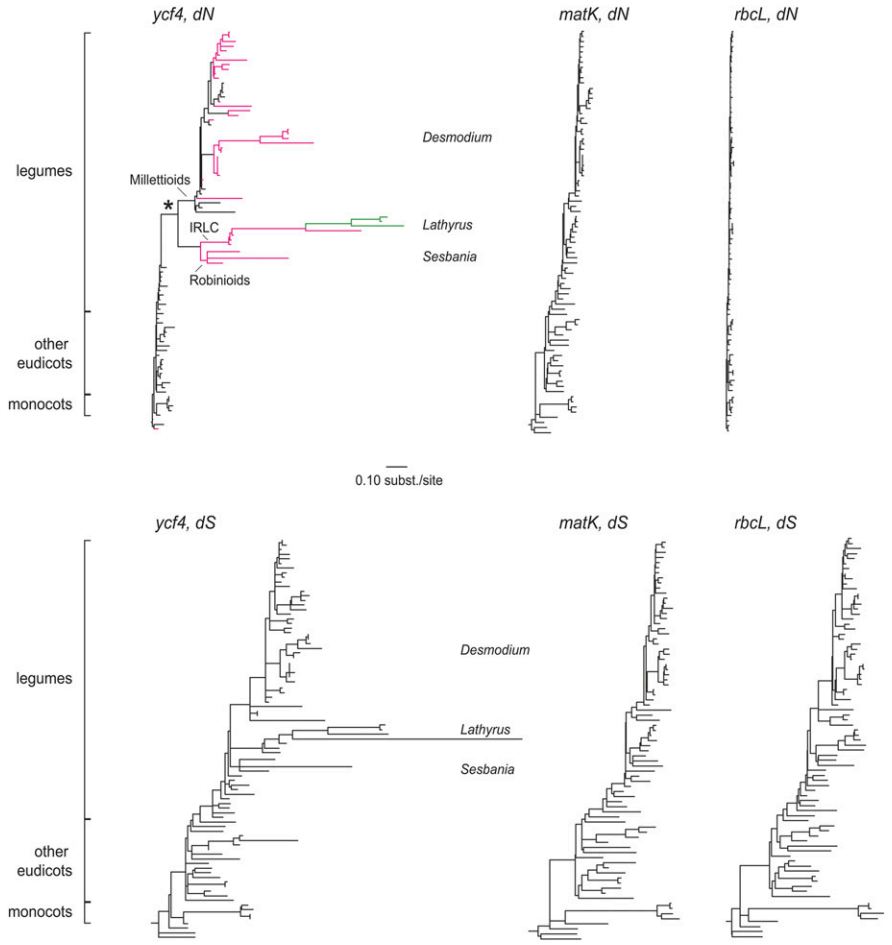


Figure 1. Synonymous and nonsynonymous divergence in angiosperm chloroplast *ycf4* sequences. Shown are d_N (*upper*) and d_S (*lower*) trees resulting from a codon-based likelihood analysis and a constrained topology, rooted using gymnosperm sequences (which are not included in the trees). All trees are drawn to the same scale. The species are in the same order from *top* to *bottom* in all trees, to the greatest extent possible, and are named in full in Supplemental Figure S1. Magenta branches in the d_N tree for *ycf4* indicate those on which the Ycf4 protein length is (or is inferred to have been) ≥200 amino acid residues; green branches indicate lengths ≥300 residues. The asterisk marks the branch (leading to Millettioids, Robinioids, and IRLC) in which rate acceleration is first seen. Trees for chloroplast *rbcL* and *matK* genes do not show comparable rate heterogeneity at either synonymous or nonsynonymous sites.

because we also found some d_N/d_S values greater than 1 within the genus *Lathyrus* for two genes flanking *ycf4* (*cemA* and *accD*) (Table 1), we suspect that the high d_N/d_S values are artifacts stemming from a combination of an increased mutation rate and lessened constraints on protein sequences, rather than being indicative of positive selection on multiple adjacent genes.

We may have slightly overestimated the divergence of *Lathyrus* Ycf4 proteins because we inferred protein sequences from chloroplast DNA sequences, whereas some chloroplast transcripts are known to undergo mRNA editing (Stern et al. 2010). Editing in angiosperms involves C → U changes and typically occurs at 30–40 sites per genome (Tsudzuki et al. 2001; Inada et al. 2004). However, even extensive C → U editing could only marginally reduce the divergence in *Lathyrus* Ycf4. For example, if we assume that every possible C → U editing event that could increase the similarity between *L. palustris* and *L. cirrhosus* Ycf4 proteins actually occurs, their sequence identity only increases from 31% to 32%. Furthermore, no sites in *ycf4* are known to undergo mRNA editing in other species (Tsudzuki et al. 2001; Chateigner-Boutin and Small 2007; and our analyses of EST data from *M. truncatula, Lotus japonicus*, and *G. max*).

Gene losses and repetitive DNA in the region around *ycf4* in legumes

We sequenced the region flanking the *ycf4* locus in five *Lathyrus* species, *P. sativum* (pea) and *Vicia faba* (broad bean) and compared it to the available data for other legumes (Fig. 3). This comparison reveals a history of multiple gene losses and gene length changes within a small region of cpDNA. We identified *ycf4* pseudogenes in both *P. sativum* and *Lathyrus odoratus* (sweetpea), which must be the result of two separate losses of the gene (Fig. 3). The small photosystem I gene *psaI*, normally found immediately upstream of *ycf4*, is missing from a clade of four *Lathyrus* species but is present in *L. palustris*. Also in this region of the genome, the ribosomal protein gene *rps16* was lost from cpDNA in the common ancestor of the IRLC clade (Doyle et al. 1995), and *accD*, coding for a subunit of acetyl-CoA carboxylase, is missing from *T. subterraneum* cpDNA, which has become rearranged in this region (Cai et al. 2008). Both *ycf4* and *accD* show extensive length variation among the legume species that retain them (Fig. 3).

The expansion of the *accD* open reading frame is partly explained by the presence of numerous tandemly repeated sequences in this region of legume cpDNA. As reported previously (Nagano et al. 1991a; Smith et al. 1991), and shown by a dot-matrix plot in Supplemental Figure S2A, *P. sativum accD* contains several in-frame internal repeats of up to 37 codons long. *L. sativus accD* has a similarly repetitive structure, but the sections of the gene that are repeated are different in the two species (Supplemental Fig. S2B,C). There are tandem repeats in the intergenic DNA between *accD* and *ycf4* in *L. latifolius* (Supplemental Fig. S2D), and a tandem repeat of 15 codons is located within the 5′ end of *L. sativus ycf4* (Supplemental Fig. S2B). All the repeats are species-specific, which suggests that these minisatellite-like sequences have a high turnover rate. However, some other species, such as *L. odoratus*, do not contain tandem repeats in this region, and the expanded size of *ycf4* in most *Lathyrus* species is not primarily due to the accumulation of repeats.

Sequences of the *P. sativum* and *L. sativus* chloroplast genomes

To establish whether the patterns of evolution seen around the *ycf4* locus are atypical of the rest of the genome, we sequenced the chloroplast genome of *L. sativus* (grasspea; 121,020 bp) and completed the genome sequence of *P. sativum* cpDNA (pea; 122,169 bp)

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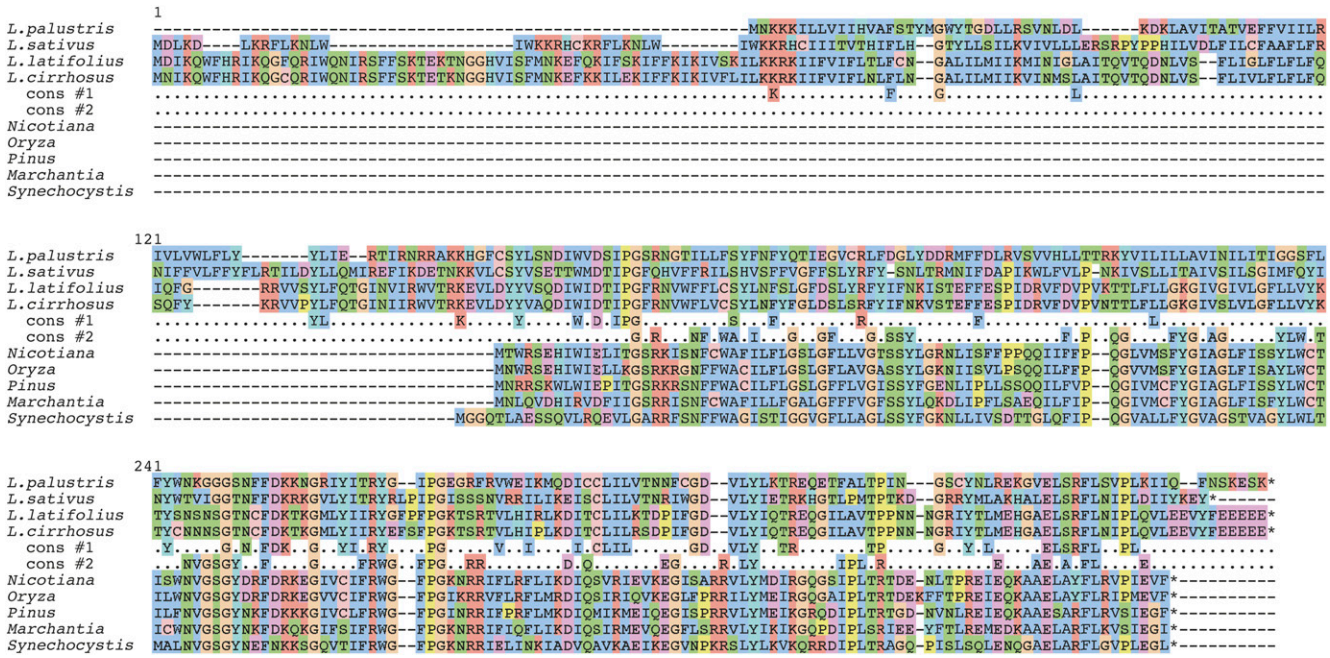


Figure 2. Alignments of Ycf4 protein sequences from four *Lathyrus* species, four diverse land plants, and the cyanobacterium *Synechocystis*. Cons #1 shows residues that are absolutely conserved among the four *Lathyrus* species. Cons #2 shows residues that are absolutely conserved among *Nicotiana tabacum*, *Oryza sativa*, *Pinus thunbergii*, *Marchantia polymorpha*, and *Synechocystis* species PCC 6803. The alignment was made using MUSCLE as implemented in SeaView (Gouy et al. 2010) with default coloring of conservative amino acid substitution groups.

(Supplemental Fig. S3). Both of these genomes lack the IR. They have rearrangements of gene order relative to the ancestral angiosperm order, as represented by tobacco, and also relative to each other. The gene order in *P. sativum* can be obtained from the tobacco order by eight inversion steps (Palmer et al. 1988), beginning with a 50-kb inversion that is shared by most legumes and that placed *rps16* beside *accD*. The first three inversions occurred before the separation of the lineages giving rise to *P. sativum* and *L. sativus*, after which there were five more inversions specific to *P. sativum*, and three more inversions specific to *L. sativus* (Supplemental Fig. S3). None of the inversions in *P. sativum* or *L. sativus* is shared with the highly rearranged cpDNA of *T. subterraneum* (Cai et al. 2008), other than the initial 50-kb inversion (Supplemental Fig. S3E).

The *L. sativus* genome sequence shows that it shares four gene losses that have already been reported in *P. sativum*: *infA*, *rps16*, *rpl22*, and *rpl23* (Gantt et al. 1991; Nagano et al. 1991a,b; Millen et al. 2001); whereas *L. sativus ycf4* is intact. The status of *rpl23* in *P. sativum* has been unclear because it contains a 190-bp

Table 1. Sequence divergence in cpDNA regions compared among *Lathyrus* species

		L. palustris vs. *L. latifolius*		*L. palustris* vs. *L. sativus*		*L. odoratus* vs. *L. latifolius*		*L. cirrhosus* vs. *L. latifolius*	
Sequence	**Sites[a]**	d_N/d_S	d_S ± SE (%)	d_N/d_S	d_S ± SE (%)	d_N/d_S	d_S ± SE (%)	d_N/d_S	d_S ± SE (%)
ycf4	109	0.362	152.2 ± 52.6	0.520	108.4 ± 23.7	NA	NA	0.805	4.8 ± 2.2
accD	112	0.677	7.1 ± 2.7	0.255	13.3 ± 3.7	1.399	2.3 ± 1.5	∞	0.0 ± 0.0
cemA	150	1.723	1.4 ± 1.0	2.971	1.4 ± 1.0	0.951	0.7 ± 0.7	∞	0.0 ± 0.0
rbcL	200	0.149	3.6 ± 1.4	0.130	2.0 ± 1.0	ND	ND	0.000	0.5 ± 0.5
matK	176	0.384	6.5 ± 2.0	0.550	5.4 ± 1.8	0.260	2.9 ± 1.3	ND	ND
Sequence	**Sites**	**Kimura's *K* ± SE (%)**		**Kimura's *K* ± SE (%)**		**Kimura's *K* ± SE (%)**		**Kimura's *K* ± SE (%)**	
rbcL-atpB spacer	747	3.9 ± 0.7		4.1 ± 0.8		ND		0.4 ± 0.2	
trnF-trnL spacer[b]	475	3.0 ± 0.8		3.7 ± 0.9		2.3 ± 0.7		ND	
trnS-trnG spacer[b]	616	2.7 ± 0.7		4.3 ± 0.8		2.5 ± 0.6		ND	

For protein-coding genes the synonymous divergence (d_S), its standard error (SE), and the nonsynonymous-to-synonymous ratio (d_N/d_S, also called ω) are shown. For intergenic regions, divergence (*K*) was calculated using Kimura's two-parameter method. NA, Not applicable (gene not present); ND, not determined.

[a]Average number of sites compared across the reported species pairs. The *ycf4*, *accD*, *cemA*, and *rbcL* comparisons are all not full-length. For *ycf4*, only the relatively conserved section between position 164 in Figure 2 and the C terminus was compared.

[b]Sequence data from Kenicer et al. (2005).

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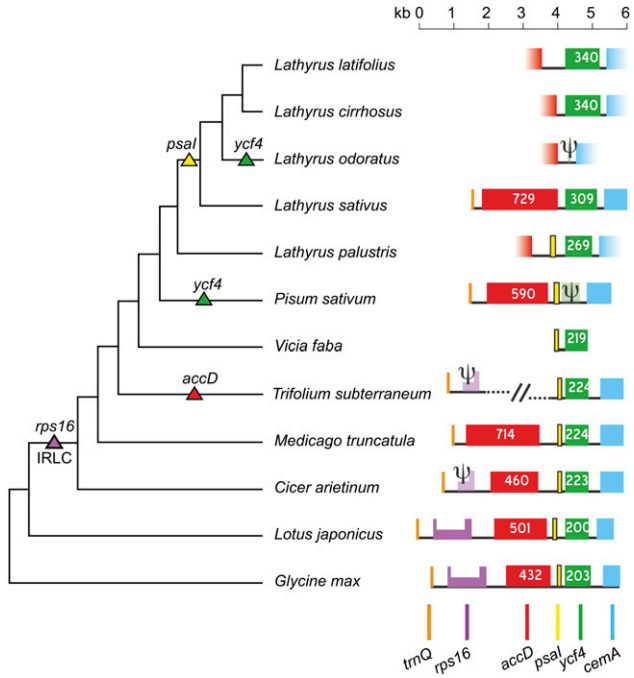


Figure 3. Gene organization around the *ycf4* locus in some legumes. Triangles indicate evolutionary losses of the indicated genes. Numbers indicate the numbers of codons in *accD* and *ycf4* genes. Psi symbols denote pseudogenes. All genes are transcribed from *left* to *right*. Fading colors denote genes that were not completely sequenced. The half-height region in *rps16* represents an intron. The slash marks indicate a genomic rearrangement in *T. subterraneum* (Cai et al. 2008). The topology of the phylogenetic tree (not drawn to scale) is from Asmussen and Liston (1998), Wojciechowski et al. (2004), and Kenicer et al. (2005).

frameshifting insert close to the normal 3′ end (Nagano et al. 1991b), but in *L. sativus* the same insert is present and more than half of *rpl23* is missing, so we infer that *rpl23* is a pseudogene in both species. In addition, these two species differ by the absence of *psaI* in *L. sativus*, and of *ycf4* in *P. sativum*. As well as the gene losses, *P. sativum* and *L. sativus* both lack two of the 21 introns normally found in angiosperm cpDNA—the first intron of *clpP*, and the *cis*-intron of *rps12*. These intron losses were reported previously as part of a survey that showed their occurrence at about the time of origin of the IRLC clade (Jansen et al. 2008).

Legume chloroplast genomes have long been thought to contain more repetitive sequences than other cpDNAs (e.g., Saski et al. 2005), and this is confirmed by dot-matrix analysis. Using a cutoff of 28 matching bases per 30-bp window, there are very few repeated sequences of this size in the tobacco and spinach chloroplast genomes other than the IR and some similarities among group II introns and among iso-accepting tRNA genes (Supplemental Fig. S4). However in *P. sativum*, *L. sativus*, and *Lotus japonicus* (as a representative IR-containing legume), it is striking that there are many tandem or near-tandem repeats (i.e., dots near the main diagonal in Supplemental Fig. S4), and the region around *ycf4* stands out as particularly repetitive.

Sites of gene loss coincide with a mutation hotspot

We measured synonymous divergence in each protein-coding gene between the *P. sativum* and *L. sativus* chloroplast genomes using d_S (black circle symbols in Fig. 4), calculated by the yn00 program (Yang 2007). For most loci, the divergence between these species is less than 0.1 substitutions per site (median $d_S = 0.055$ synonymous substitutions per site). Ycf4 cannot be included directly in this comparison because it is absent from *P. sativum* cpDNA, so instead, for *ycf4* in Figure 4 we have plotted the d_S value between *L. palustris* and *L. sativus*, which is 20-fold higher (1.084) than the median even though the comparison is over a shorter divergence time. We observed even higher d_S values in comparing *ycf4* between *L. palustris* and *L. cirrhosus* (1.481) or *L. latifolius* (1.522). Similarly, *psaI* is missing from *L. sativus* cpDNA so instead we compared *P. sativum psaI* to *L. palustris psaI* and found $d_S = 0.580$, which again is much higher than the genome average for *P. sativum* versus *L. sativus* (0.055). For *accD* we compared only the regions of the gene that could be reliably aligned between *P. sativum* and *L. sativus*, and obtained a d_S value (0.212) that is 3.8 times the genome average. This spike in local d_S values is matched by a local increase in divergence in the intergenic regions near the *ycf4* and *accD* loci (all compared between *P. sativum* and *L. sativus* using Kimura's *K*; open symbols in Fig. 4).

The very high level of synonymous substitution in *ycf4* made us question whether the mutational process at this locus might somehow be different than elsewhere in the genome. We investigated this possibility by sequencing regions of cpDNA from *L. latifolius* and *L. cirrhosus* (Fig. 3), two species that are evidently very closely related because there is only 1 nucleotide (nt) substitution between their *rbcL* genes, and only three substitutions in the *atpB-rbcL* intergenic spacer (Fig. 5). There are only two differences out of 1256 bp in the combined partial *accD* and *cemA* sequences obtained from these species, compared with 56 differences in the 1023-bp-long *ycf4* ($d_S = 0.048$, $d_N = 0.039$). Most strikingly, there are 19 differences (10% divergence) in the spacer between *accD* and *ycf4*. This spacer (from which *psaI* has been lost) is 238 bp in *L. cirrhosus*, most of which can be aligned to *L. latifolius*, but in *L. latifolius* the spacer has expanded to 648 bp due to the presence of multiple tandem repeat sequences comprising a 57-bp repeat unit (six complete and three partial copies) and a 67-bp repeat unit (two complete and one partial copy) (Supplemental Fig. S5). These results show that a region of ~1500 bp in these *Lathyrus* genomes, extending through the *accD-ycf4* spacer and most if not all of *ycf4* itself, is a hotspot with a mutation rate that is dramatically higher than in the rest of the genome. Despite this high mutation rate, the types of nucleotide substitution occurring in the *ycf4* region do not seem particularly biased, with an overall transition/transversion ratio of 0.9 (Fig. 5).

There also appears to be a smaller second peak of divergence values in the region around the genes *rpl14* and *rps8* (Fig. 4), which is the site from which *infA* was lost in an early ancestor of Fabales and Cucurbitales (Millen et al. 2001). We found that sites of gene loss coincide with fast-evolving intergenic regions more often than expected by chance: Five of the six most divergent intergenic regions between *P. sativum* and *L. sativus* are also the sites of five of their six gene losses (*ycf4*, *psaI*, *rps16*, *infA*, *rpl22*; $P = 2 \times 10^{-6}$ by the hypergeometric test).

Mutation rate in *ycf4* exceeds the rate in the nuclear genome

Early work on rates of nucleotide substitution in plant genomes concluded that the synonymous substitution rate (assumed to be equal to the mutation rate) is about four times higher in plant nuclear genomes than in the single-copy regions of chloroplast genomes (Wolfe et al. 1987, 1989; Gaut 1998; Muse 2000). Given the heterogeneity of synonymous rates seen within the *Lathyrus*

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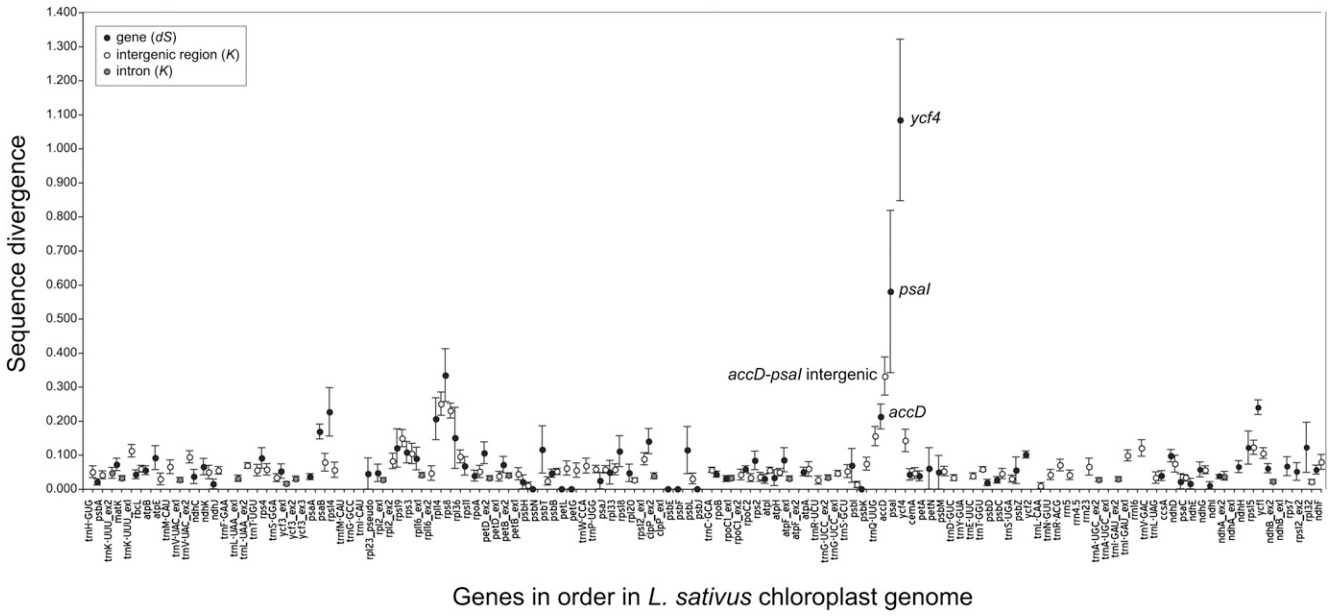


Figure 4. Sequence divergence between the *P. sativum* and *L. sativus* chloroplast genomes. The *x*-axis lists genes or exons in the order in which they occur in the *L. sativus* genome. Black filled circles show d_S (number of synonymous substitutions per synonymous site) for each orthologous protein gene pair, calculated using yn00 (Yang 2007). White and gray filled circles show divergence (*K*) for each intergenic region or intron, respectively, calculated by Kimura's two-parameter method (Kimura 1983). Vertical bars, d_S or $K \pm 1$ SE. Because *ycf4* is a pseudogene in *P. sativum* and *psaI* is not present in *L. sativus*, the d_S value plotted for *ycf4* is for a comparison between *L. sativus* and *L. palustris*, and the d_S value plotted for *psaI* is for a comparison between *P. sativum* and *L. palustris* (see text). No divergence values are plotted for intergenic regions that are not flanked by the same genes in the two species or that are shorter than 100 bp.

chloroplast genomes, we wondered how these rates compared with the rate in the nuclear genome. Relatively few nuclear genes have been sequenced from *Lathyrus* species, so we generated new expressed sequence tag (EST) data from *Lathyrus odoratus* (sweet-pea; see below) and identified putatively orthologous nuclear genes between these and database sequences from *P. sativum*. Among 56 putative orthologs, the median d_S is 0.131 (Supplemental Table S2), which is 2.4 times higher than the median d_S (0.055) for chloroplast genes compared between *P. sativum* and *L. sativus*. Thus in comparisons between *Lathyrus* and *P. sativum*, as in other flowering plant comparisons, the synonymous substitution divergence in most parts of the chloroplast genome is lower than in the nuclear genome. The synonymous divergence in *ycf4*, however, is at least 10 times greater than in the nuclear genome (the ratios of the d_S values given above, 1.084/0.131 = 8.3 and 1.522/0.131 = 11.6, are underestimates of the actual ratio because the numerators involve a shorter divergence time).

Transfer of *Trifolium accD* to the nucleus

We suspect that *ycf4* and *psaI* have been transferred to the nuclear genome in the *Lathyrus* species that lack them in cpDNA, because these species are fully photosynthetic and must have a functional photosystem I. However, we were unable to find nuclear copies of these genes. We made numerous unsuccessful attempts (see Methods) to amplify *ycf4* and *psaI* by PCR from genomic DNA of *L. odoratus* (which lacks both of them in its cpDNA and has a smaller *ycf4* pseudogene than *P. sativum*). We then made cDNA from young green leaves of *L. odoratus* and sequenced 8702 ESTs. None of the ESTs were derived from a nuclear *ycf4* or *psaI*, even though we did find ESTs corresponding to seven of the nine other nuclear-encoded subunits of photosystem I (Jolley et al. 2005), and to the older nuclear-transferred genes *infA* and *rpl22*. PsaI is a very small protein (34–40 amino acids) that is conserved between cyanobacteria and land plants and is physically located toward the exterior of photosystem I in *P. sativum*, where it interacts strongly with PsaH (Jolley et al. 2005; Amunts et al. 2007). It seems unlikely that photosystem I in *Lathyrus* could function efficiently without PsaI, although tobacco plants with a *psaI* knockout do not show a mutant phenotype under standard growth conditions (MA Schöttler and R Bock, pers. comm.). Most of the small membrane-spanning subunits of photosystem I appear to be nonessential, and knockout lines do not display visible mutant phenotypes (Varotto et al. 2002; Jensen et al. 2007; Schöttler et al. 2007). However, the loss of individual small membrane-spanning subunits usually affects the assembly of other subunits and results in lower

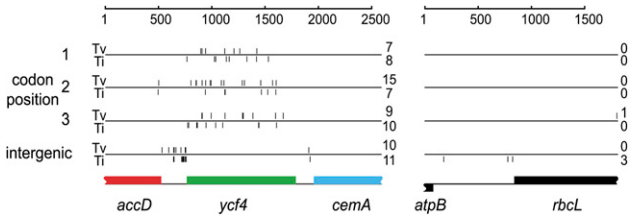


Figure 5. Sequence divergence between *L. latifolius* and *L. cirrhosus* in the *accD-ycf4-cemA* region (*left*) and the *atpB-rbcL* region (*right*). Vertical tickmarks indicate the locations of each nucleotide substitution, categorized according to whether it occurs at codon position 1, 2, or 3; or in intergenic DNA; and as a transversion (Tv; tickmarks *above* the horizontal lines) or a transition (Ti; tickmarks *below* the horizontal line). The total numbers of each type of substitution are shown on the *right*. Supplemental Figure S5 shows the nucleotide sequence alignment summarized in the *left* panel.

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efficiencies of excitation transfer and electron transfer (Varotto et al. 2002; Jensen et al. 2007; Schöttler et al. 2007), which would be evolutionarily deleterious. The only other known cases of loss of *psaI* from plastid DNA are in the parasitic species *Cuscuta gronovii* and *Cuscuta obtusiflora* which have reduced levels of photosynthesis but retain all other photosynthesis genes (Funk et al. 2007; McNeal et al. 2007), and in the nonphotosynthetic parasite *Epifagus* (Wolfe et al. 1992).

Although we have direct evidence for association between gene losses and a mutation hotspot only in the genus *Lathryus*, it is intriguing that other species in the IRLC legume clade show evolutionary losses of other genes that neighbor *ycf4* and *psaI* (Fig. 3). The loss of *rps16* in the common ancestor of the IRLC clade can be explained in terms of gene substitution by the nuclear gene for mitochondrial RPS16, as already demonstrated for *Medicago* (Ueda et al. 2008), and so does not necessitate a gene transfer to the nucleus. *Rps16* has been lost on multiple independent occasions during land plant evolution (Supplemental Table S1; Ohyama et al. 1986; Tsudzuki et al. 1992; Ueda et al. 2008), so it is possible that its multiple losses in legumes are simply the result of relatively easy and/or early substitution by the mitochondrial gene.

The other IRLC legume gene loss in the neighborhood of *ycf4* and *psaI* is the loss of *accD* in *Trifolium* (Fig. 3). *AccD* codes for a subunit of acetyl-CoA carboxylase, which functions in lipid synthesis and is an essential chloroplast gene in tobacco (Kode et al. 2005). The loss in *Trifolium* is one of five separate known instances of loss of *accD* in angiosperm cpDNAs (Supplemental Table S1). In grass species—the only case that has been studied in detail—the prokaryotic multisubunit carboxylase in the plastid has been completely replaced by a nuclear-encoded single-chain carboxylase of eukaryotic ancestry (Konishi et al. 1996; Gornicki et al. 1997). We identified an evolutionary transfer of *accD* to the nucleus in *Trifolium*. Using high-throughput EST sequence data from *Trifolium repens* (white clover), we found a cDNA structure consisting of a fusion between a gene for plastid lipoamide dehydrogenase (*LPD2*) and *accD* (Supplemental Fig. S6A–D). We confirmed the presence of a fused mRNA by reverse transcriptase PCR and Sanger sequencing (Supplemental Fig. S6E).

In plastids, lipoamide dehydrogenase is a component of pyruvate dehydrogenase, a complex that makes acetyl-CoA (Lutziger and Oliver 2000; Drea et al. 2001). The *T. repens* nuclear transcript codes for a predicted protein of 805 amino acids, with residues 1–512 (including a transit peptide) derived from *LPD2* and residues 513–805 derived from *accD*. By comparison to the known genomic structures of *LPD* genes in *M. truncatula*, we infer that in *T. repens* the *accD* sequence has replaced the final two exons (exons 14 and 15) of its *LPD2* gene, with the point of fusion occurring at the third codon of exon 14. We did not find any evidence for alternative splicing of the *LPD2–accD* fusion to form two products, as occurs with the *SOD–rpl32* fusion in mangrove trees (Cusack and Wolfe 2007). The fusion to *accD* probably rendered *LPD2* unable to code for functional lipoamide dehydrogenase, because the fusion protein lacks some conserved residues normally provided by exons 14 and 15, but *T. repens* retains and expresses a paralogous gene *LPD1* that also codes for plastid lipoamide dehydrogenase (Supplemental Fig. S6A). We found the transferred gene in *T. repens*, but we presume that the transfer is shared by other *Trifolium* species, including the two that have been demonstrated to have no *accD* in their cpDNAs (*T. subterraneum* and *Trifolium pratense*) (Doyle et al. 1995; Cai et al. 2008). We also found database ESTs for a nuclear *accD* in *T. pratense* (red clover), but they are too short to confirm that this species also has the *LPD2–accD* fusion. Phylogenetic analysis indicates that the *T. repens* and *T. pratense* nuclear sequences have a monophyletic origin and that the transfer of *accD* to the nucleus occurred within the IRLC clade (Supplemental Fig. S6F), consistent with the change in *LPD2* gene structure that occurred after *Trifolium* diverged from *Medicago* (Supplemental Fig. S6A). The *Trifolium* nuclear *accD* gene is transcribed in both *T. repens* and *T. pratense*, is predicted to have a functional transit peptide in *T. repens* (TargetP cTP score 0.976) (Emanuelsson et al. 2000), and shows evidence of selection to maintain its AccD-coding function (d_N/d_S = 0.26 between *T. repens* and *T. pratense* in the *accD* region of the transcript). Moreover, the *Trifolium* nuclear mRNAs code for a leucine residue at a site that undergoes an essential Ser → Leu mRNA edit in *P. sativum* plastids (Supplemental Fig. S6D; Sasaki et al. 2001; Inada et al. 2004).

Discussion

The genomic region around *ycf4* in *Lathyrus* is a dramatic hotspot for point mutations. It is difficult to quantify the factor by which its mutation rate is increased relative to the rest of the genome, but comparisons of synonymous site divergence indicate an increase of at least 20-fold, both in comparisons between *P. sativum* and *L. sativus* (Fig. 4) and among *Lathyrus* species (Table 1). Between *L. latifolius* and *L. cirrhosus*, the increase may be even greater (Fig. 5; Table 1). Even a 20-fold mutation rate increase only goes partway toward explaining how the protein sequence divergence between *L. palustris* and *L. cirrhosus* (with a divergence time of <10 Myr) (Kenicer et al. 2005) exceeds that between other angiosperms and cyanobacteria (separated by >1000 Myr); a relaxation of selective constraints on the Ycf4 protein in legumes must be involved too. Although there have been previous reports that the variance of synonymous substitution rates among genes in many eukaryotic genomes is greater than expected by chance (e.g., Baer et al. 2007; Fox et al. 2008), there are few if any precedents for the phenomenon that we describe here—a sharply localized mutation rate acceleration of great magnitude in one specific region of a genome. The existence of the hotspot violates the common assumption that the point mutation rate is approximately constant in all regions of the same genome (Kimura 1983), which underpins the silent molecular clock hypothesis (Ochman and Wilson 1987). Our results bear some similarities to the "mutation showers" (transient localized hypermutation events) that have been found in some studies on the genomic distribution of spontaneous mutations (Drake 2007; Wang et al. 2007; Nishant et al. 2009). As well as being a mutation hotspot, *ycf4* and its neighbors also appear to be a hotspot for the formation and turnover of minisatellite sequences in *Lathyrus*.

The previous study most relevant to our findings is that of Erixon and Oxelman (2008), who reported somewhat similar results for the chloroplast *clpP* gene in *Silene* and *Oenothera* species. For some interspecies comparisons in their study, both d_N and d_S were elevated in *clpP* compared with other chloroplast genes, although the d_S elevations were at most fivefold for *clpP*, compared with at least 20-fold for *ycf4* in *Lathyrus*. Also, insertions of repetitive amino acid sequence regions occurred in some of the fast-evolving taxa. Locus-specific rate accelerations affecting both d_N and d_S were reported in cpDNA of Geraniaceae, but in this case, the accelerations occurred in numerous genes (Guisinger et al. 2008). In all IR-containing cpDNAs, the synonymous rate is higher in single-copy genes than in IR-located genes, probably due to a copy-number effect during DNA repair (Wolfe et al. 1987; Birky and Walsh 1992; Perry and Wolfe 2002). Dramatic accelerations of

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synonymous rates have been found in the mitochondrial genomes of some plants, such as *Plantago*, *Pelargonium*, and certain *Silene* species (Cho et al. 2004; Parkinson et al. 2005; Mower et al. 2007; Sloan et al. 2009). Most of these mitochondrial accelerations appear to affect all genes in the genome similarly, but among-gene rate heterogeneity was found within the mtDNAs of a few species (Mower et al. 2007), including a 40-fold difference in synonymous rates between *atp9* and three other mitochondrial genes in *Silene* (Sloan et al. 2009). Because plant mitochondrial genomes are relatively large and do not show much gene order conservation, most studies have only examined individual genes so the sizes of the genomic regions affected by rate acceleration are not known.

Apart from these organellar examples, there are very few precedents for a mutation rate change that is so pronounced over such a short physical distance. One early study (Martin and Meyerowitz 1986) reported a 2-kb region of noncoding DNA near the glue gene cluster of three *Drosophila* species, which contained an abrupt boundary between a conserved region and a nonconserved region with a 10-fold elevated substitution rate, but this report has not been followed up with more extensive analyses based on complete genome sequence data. An abrupt boundary of evolutionary rates also occurs on the mammalian X chromosome at the junction between the pseudoautosomal region and the X-specific region. The pseudoautosomal part of the gene *Fxy*, which spans this junction in laboratory mice, has a synonymous rate about 60 times faster than the X-specific part of the gene, probably because the high recombination rate in the pseudoautosomal part leads to high levels of biased gene conversion (Perry and Ashworth 1999; Duret and Galtier 2009).

Is the chloroplast hypermutation phenomenon unique to *Lathyrus*? At present, *Lathyrus* is the only legume genus for which we have extensive sequence data from more than one species, so we are unable to say whether the same hotspot is present in legumes outside this genus. Therefore the only gene losses we can potentially attribute directly to hypermutation are those of *ycf4* in *L. odoratus* and of *psaI* in the ancestor of four *Lathyrus* species. *Ycf4* is also evolving fast in *Desmodium* and has been lost in three species of that genus. The losses of *ycf4* in *P. sativum*, of *accD* in *Trifolium*, and the older loss of *rps16* in the ancestor of the IRLC clade are suggestive, but we have no direct evidence that these loci were fast-evolving prior to the gene losses. It is possible that a hotspot has existed throughout legume evolution and was the cause of the *ycf4* acceleration seen in the common ancestor of Millettioids, Robinioids, and the IRLC (Fig. 1) but that the exact location of the hotspot (and its associated tandem repeat sequences) has varied somewhat among lineages, affecting *ycf4* in some taxa, but *accD* or *psaI* in others. We do not know the molecular basis for the increases in either the point mutation rate or the length mutation rate, but we speculate that they might be connected. We suggest that a correlation between the two rates could develop if, for some reason, the genomic region around *ycf4* was subject to repeated DNA breakage and repair (cf. Guisinger et al. 2008; Yang et al. 2008). In this regard, it is interesting to note that only a few angiosperm species have cpDNAs that are highly rearranged relative to the canonical gene order, but among these, there are several independent lineages that are both highly rearranged and contain rapidly-evolving protein genes (Jansen et al. 2007). These lineages include *Jasminum* (acceleration of *accD*; Lee et al. 2007), *Silene* (acceleration of *clpP*; Erixon and Oxelman 2008), and now *Lathyrus* (acceleration of *ycf4*). The phylogenetic diversity of these lineages suggests that hypermutable regions may exist in other angiosperm cpDNAs, and our findings may go some way toward explaining the apparent bursts of organelle-to-nucleus gene transfer seen in some angiosperms.

It is likely that many factors dictate whether a gene can be lost from an organelle genome. One property that is common to the gene transfer and gene substitution processes is that they both involve a phase during which the organelle gene and the nuclear gene coexist in the same species (Timmis et al. 2004). Analogous to a gene duplication, this two-gene phase can be resolved either by losing the organelle copy (resulting in a successful transfer of function) or by losing the nuclear copy (restoring the status quo). Intermediates in this process, and sister lineages where the two-gene phase was resolved in opposite ways, have been identified (Adams et al. 1999). Brandvain and Wade (2009) have shown theoretically that the ratio between the point mutation rates in the organelle and nuclear copies has a profound influence on the direction in which the two-gene phase is resolved. If the organelle mutation rate is lower than the nuclear mutation rate, as is true for most plant mitochondrial and chloroplast genes, then gene transfer will not occur unless there is a benefit to relocating the gene. By contrast, if the organelle rate exceeds the nuclear rate, then gene transfer is predicted to occur even in the absence of any benefit (Brandvain and Wade 2009). Therefore, in a genome such as *Lathyrus* cpDNA, in which the mutation rate exceeds the nuclear rate only in one hypermutable region, we should expect to see more transfers, substitutions, or losses of genes from the hypermutable region than from the rest of the genome. This argument provides a plausible explanation for the losses of *ycf4* and *psaI* seen in some *Lathyrus* species and, perhaps more generally, for the cluster of losses from the *rps16-accD-psaI-ycf4* region seen in other legume cpDNAs.

Methods

Plant material

Seeds of *Lathyrus sativus* (cv. Cicerchia Marchigiana) were purchased from B&T World Seeds. Seeds of *L. cirrhosus* (accession no. LAT17) were obtained from the Leibniz Institute of Plant Genetics and Crop Plant Research. Other *Lathyrus* species were purchased from Thompson & Morgan. Additional sequencing of *P. sativum* cpDNA was done using cv. Feltham First.

Nucleotide sequencing

The *P. sativum* (pea) chloroplast genome sequence was completed by S.A. and J.C.G. using the chain termination method (Sanger et al. 1977) with fluorescent dideoxynucleotides on PCR products amplified from cloned PstI fragments (Palmer and Thompson 1981), from cpDNA extracted from isolated chloroplasts, or from total DNA extracted from shoots of 8-d-old seedlings. Chloroplasts were isolated by the high-salt method (Bookjans et al. 1984), and DNA was extracted by the CTAB (hexadecyltrimethylammonium bromide) method (Milligan 1989). Previously published regions were not resequenced except at the borders or where there were discrepancies between publications. Newly sequenced regions were completed on both strands, and all the PstI sites used for cloning were confirmed by sequencing spanning PCR fragments. At the *ycf4* locus, there is a 2-bp deletion in the sequence reported by Nagano et al. (1991a), relative to the sequence reported by Smith et al. (1991), both of which were obtained from the same cloned 17.3-kb PstI fragment from *P. sativum* cv. Alaska. We confirmed that this 2-bp deletion exists, in both cv. Alaska and cv. Feltham First. This correction means that the reported ORF157 (Smith et al. 1991) does not exist.

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The *L. sativus* (grasspea) chloroplast genome sequence was determined by A.M.M., T.A.K., and K.H.W. Approximately 150 seeds were grown on soil in the greenhouse. Seedling shoots were harvested at 7 d post-germination, and cpDNA was prepared according to the method described by Milligan (1989) except that chloroplast lysis and cpDNA recovery procedures were modified. Chloroplasts were lysed by adding a 1/5 volume of 10% CTAB (Sigma-Aldrich) and heating for 20 min at 70°C. This was followed by a chloroform extraction, treatment with RNaseA (10 μg/mL), and isopropanol precipitation of cpDNA. A plasmid library of nebulized fragments was constructed from 5 μg of cpDNA by GATC-Biotech. The genome sequence was assembled from 1536 Sanger shotgun sequence reads with primer-walking to close gaps.

We tried unsuccessfully to amplify *ycf4* and *psaI* by PCR from *L. odoratus* genomic DNA using 16 and 9 primer combinations, respectively, and a range of amplification conditions. These primers were designed based on amino acid residues conserved among known Fabaceae Ycf4 and PsaI proteins, but primer design for these genes is difficult due to the fast rate of *ycf4* evolution and the short length of *psaI*, as well as the high A+T content of the region. To obtain EST data from *L. odoratus*, we isolated poly(A) mRNA from leaves of 3-d-old seedlings. A normalized cDNA library was constructed by GATC-Biotech, and the 3′ ends of 8702 cDNAs were sequenced by Agencourt Biosciences. ESTs were assembled into contigs, and putative orthologs between these contigs and *P. sativum* sequence data from GenBank were identified according the method of Sémon and Wolfe (2008).

The other new sequence data indicated in Figures 3 and 5 were generated by PCR amplification and sequencing (by primer walking) of at least three independent cloned products for each region. The cpDNA region that normally contains *ycf4* was PCR amplified from *L. latifolius*, *L. cirrhosus*, *L. odoratus*, and *L. palustris* using primers designed from the *P. sativum accD* (5′-AAACAGGCACAGG TCAASTAAATGG-3′) and *cemA* (5′-GACGGAGATACACGATTTA AATAACG-3′) genes. The *atpB–rbcL* region from *L. latifolius*, *L. cirrhosus*, and *L. palustris* was amplified with primers 5′-TGRAAAA RCTACATCGAGTACCGGAGG-3′ and 5′-TATGATCTCCACCAGA CATACG-3′. *T. repens* mRNA sequences coding for *LPD1* and the *LPD2–accD* fusion gene were identified among 700,000 ESTs obtained by high-throughput pyrosequencing of flower, leaf, and stolon mRNA from the inbred line S (7S.4.6.3.3.4.4.10) (DM and SB, unpubl.) and assembled manually. The structure of the *LPD2-accD* junction was confirmed by reverse transcriptase-PCR from *T. repens* leaf mRNA (commercial variety Nusiral) and Sanger sequencing.

Computational methods

Sequence divergence for most analyses was calculated using yn00 from the PAML package (Yang 2007) for coding regions and Kimura's two-parameter method (Kimura 1983) for noncoding regions. Gene sequences were aligned by reverse-translation of ClustalW alignments of the corresponding protein sequences. Noncoding sequences were aligned using ClustalW with manual adjustment for regions around *ycf4*. For the analysis in Figure 1 and Supplemental Figure S1, we first constructed a maximum likelihood phylogeny (in PAUP) from *matK* sequences using the HKY substitution model with a four category gamma rate distribution. The transition/transversion ratio and shape parameter were estimated iteratively until the topology converged. This analysis included legume *ycf4* sequences from Stefanovic et al. (2009; GenBank [http://www.ncbi.nlm.nih.gov/Genbank/] accession nos. EU717431–EU717464). The d_N and d_S branch lengths for the *matK*, *ycf4*, and *rbcL* trees were estimated based on the PAML/codeML free-ratio model, using the fixed topology obtained from the above *matK* ML analysis. Dot-matrix plots were made using DNAMAN (http://www.lynnon.com) (Huang and Zhang 2004).

Acknowledgments

We thank Gavin Conant for help with Figure S3, Shusei Sato for *Trifolium* cDNA clones, Greg Kenicer for prepublication access to sequence data, and Ralph Bock for discussion. S.A. and J.C.G. thank Chris Maddren (Department of Genetics, University of Cambridge) for DNA sequencing. This study was supported by Science Foundation Ireland (K.H.W., T.A.K.), European Commission FP5 Plastid Factory (J.C.G., T.A.K.), US National Institutes of Health (J.D.P.), and the METACyt Initiative of Indiana University, funded in part through a major grant from the Lilly Endowment, Inc. (J.D.P., D.W.R.).

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Received June 20, 2010; accepted in revised form September 20, 2010.