Supporting Information

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Table S1. Mitochondrial and plastid genome architectural diversity and its extremes

	Mitochondrial genomes		Plastid genomes	
Genomic trait	Species (lineage)	Notable feature	Species (lineage)	Notable feature
Nucleotide content	*Nakaseomyces bacillisporus* (pathogenic yeast)	GC poor (11%)	*Leucocytozoon caulleryi* (apicomplexan parasite)	GC poor (15%)
	Selaginella moellendorffii (lycophyte)	GC rich (68%)	*Trebouxiophyceae* sp. MX-AZ01 (trebouxiophyte green alga)	GC rich (58%)
Conformation	*Ochromonas danica* (stramenopile alga)	Linear-mapping genome with inverted-repeat telomeres	*Chromera velia* (autotrophic alveolate)	Linear-mapping genome with inverted repeat telomeres
	Chlamydomonas moewusii (chlorophycean green alga)	Circular monomeric genome	*Nicotiana tabacum* (angiosperm)	Multigenomic, linear-branched chromosomal structure
Chromosome number	*Diplonema papillatum* (euglenozoan)	>75 small (6–7 kb) circular DNAs with single-gene modules	*Karlodinium veneficum* (dinoflagellate with haptophyte-derived plastid)	Conventional plastid genome with a satellite fraction of fragmented miniature chromosomes
	Amoebidium parasiticum (ichthyosporean protist)	Several hundred (0.3–8.3 kb) linear chromosomes with one to multiple genes apiece	*Symbiodinium* sp. clade C3 (dinoflagellate with peridinin-containing plastid)	Multiple mini (2–3 kb) circular chromosomes with one to a few genes each
Size	*Silene conica* (angiosperm)	11,318-kb genome, ~99% noncoding	*Floydiella terrestris* (chlorophycean green alga)	521 kb genome, ~80% noncoding DNA
	Babesia bovis (apicomplexan parasite)	6-kb genome, >90% coding	*Helicosporidium* sp. (nonphotosynthetic, parasitic trebouxiophyte)	37.5 kb genome, ~95% coding
Introns	*Agaricus bisporus* (button mushroom)	43 group I and 3 group II introns distributed in 8 of 15 protein-coding genes. Introns represent 45% of the mtDNA sequence	*Euglena gracilis* (euglenozoan alga)	>150 introns, including 72 group II and 46 group III introns, many of which are twintrons (introns within introns). Introns represent ~40% of the ptDNA sequence
Genes	*Andalucia godoyi* (jakobid)	MtDNA encodes 66 proteins and 34 functional RNAs; no introns	*Porphyra purpurea* (multicellular red alga)	PtDNA encodes 212 proteins and 41 functional RNAs; no introns
	Hematodinium sp. (deep-branching, parasitic dinoflagellate)	MtDNA encodes three proteins and two functional RNAs; no introns	*Heterocapsa triquetra* (dinoflagellate with peridinin-containing plastid)	PtDNA encodes 10 proteins, ~3 functional RNAs; no introns
Fragmented genes	*Plasmodium falciparum* (apicomplexan parasite)	LSU and SSU rRNA genes are fragmented and scrambled into ≥27 coding modules	*Chlamydomonas reinhardtii* (chlorophycean green alga)	*psaA* gene is split in three separate exons in distant loci of the plastid genome
Gene expression	*Saccharomyces cerevisiae* (yeast)	Deviant genetic code: AUA is read as methionine, UGA as tryptophan, and CUN as threonine	*Lepidodinium chlorophorum* (dinoflagellate with green algal-derived plastid)	One codon reassignment: AUA is read as methionine instead of isoleucine
	Trypanosoma brucei (kinetoplastid)	~90% of codons experience uracil-insertion/deletion editing	*Anthoceros formosae* (hornwort)	509 C-to-U and 433 U-to-C editing sites
Foreign DNA	*Amborella trichopoda* (angiosperm)	Contains six genome equivalents of foreign mtDNA, acquired from green algae, mosses, and other angiosperms	*Daucus carota* (carrot)	Contains an ~1.5 kb of potential mitochondrial origin
	Physarum polycephalum (amboebozoan)	14.5-kb linear plasmid with defined telomeres in the mitochondrion	*Ernodesmis verticillata* (ulvophycean green alga)	Putative ~2.2-kb plasmid within the chloroplast

Table S1. Cont.

Genomic trait	Mitochondrial genomes: Species (lineage)	Mitochondrial genomes: Notable feature	Plastid genomes: Species (lineage)	Plastid genomes: Notable feature
Genome loss	*Encephalitozoon cuniculi* (microsporidian fungus)	Mitochondrial-derived organelle (mitosome) without DNA	*Polytomella* spp. (nonphotosynthetic chlorophycean green algae)	Genome and transcriptome sequencing suggest complete loss of plastid genome
	Trichomonas vaginalis (parabasalid excavate)	Mitochondrial-derived organelle (hydrogenosome) without DNA	*Rafflesia lagascae* (nonphotosynthetic, parasitic angiosperm)	Genome sequencing data suggest complete loss of plastid genome

Table S2. Convergent mitochondrial and plastid genomic architectures within the same lineage or species

Species (lineage)	Mitochondrial genomic architecture	Plastid genomic architecture
Selaginella moellendorffii (lycophyte)	Elevated GC content (68%). Reduced tRNA repertoire (none). Intron rich (37). Large number of C-to-U RNA-editing sites (thousands). Recombinant structure (dynamic organization, currently too complex to define).	Elevated GC content (52%). Reduced tRNA repertoire (13). Intron rich (11). Large number of C-to-U RNA-editing sites (hundreds). Recombinant structure (circular-mapping chromosome that is highly rearranged compared with ptDNAs of close relatives).
Amphidinium carterae strain CCAP 1102/6 (dinoflagellate with peridinin-containing plastid)	Complex structure (dynamic organization of highly recombinant heterogeneous mtDNA molecules). Reduced gene repertoire (3 proteins, no identifiable rRNAs, tRNAs, or introns). Fragmented genes. Extensive posttranscriptional modifications (Six types of RNA editing, transsplicing, and poly-A tails).	Complex structure (multiple miniature circular ptDNA molecules). Reduced gene repertoire (12 proteins, 3 functional RNAs, no introns). Fragmented genes. Extensive posttranscriptional modifications (poly-U tails, 5′ processing).
Cyanidioschyzon merolae (unicellular red alga)	Genomic compaction (~99% coding and no introns or repeats). AT rich (27.1%). Conventional architecture (circular-mapping monomeric genome, standard genetic code, and intact genes).	Genomic compaction (~90% coding and no introns or repeats). AT rich (37.6%). Conventional architecture (circular-mapping monomeric genome, standard genetic code, and intact genes).
Dunaliella salina (chlorophycean green alga)	Genomic expansion (~60% noncoding). Large numbers of introns (~1.5 introns/gene). Repeat rich (similar repeats in mtDNA and ptDNA). Gene fragmentation (rRNA genes). AT rich (34.4%).	Genomic expansion (~65% noncoding). Large numbers of introns (~0.4 introns/gene). Repeat rich (similar repeats in mtDNA and ptDNA). Gene fragmentation (*psaA*). AT rich (32.1%).