

Supplementary Figures and Tables

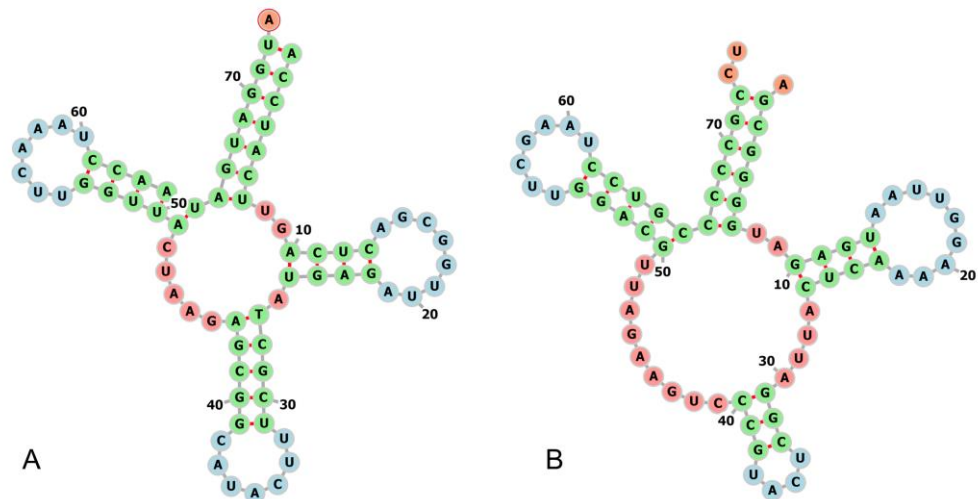


Figure S1. The secondary structure of tRNA. A and B are two different structures of *trnM-CAU*.

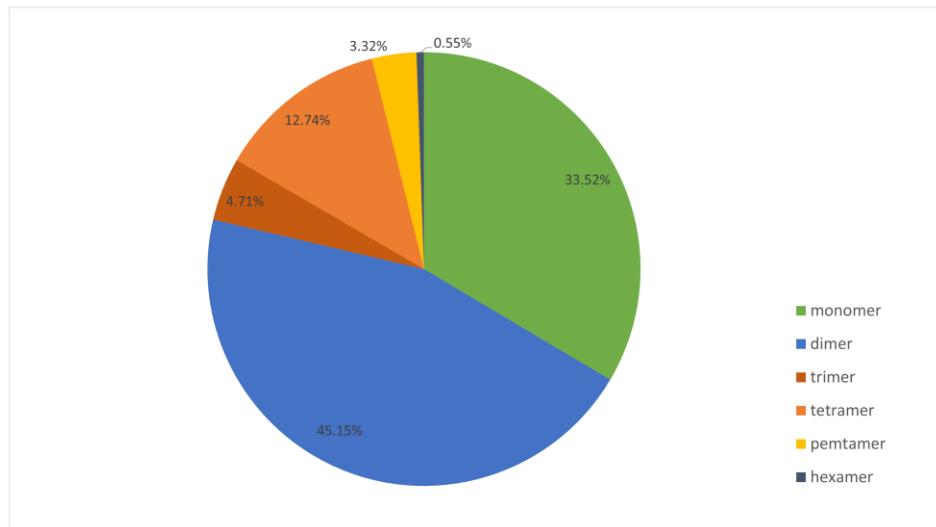


Figure S2. The distribution of SSRs in *S. glauca* mt genome. The colors represent different types of SSRs. The area on the pie chart indicates the percentages of different SSR types.

Table S1. The mt homologous genes in *S. glauca*, *A. thaliana*, *H. sapiens*, and *S. cerevisiae*.

	<i>S. glauca</i>	<i>A. thaliana</i>	<i>H. sapiens</i>	<i>S. cerevisiae</i>
NADH dehydrogenase	<i>nad1</i>	<i>nad1</i>	<i>ND1</i>	-
	<i>nad2</i>	<i>nad2</i>	<i>ND5</i>	-
	<i>nad3</i>	<i>nad3</i>	<i>ND3</i>	-
	<i>nad4L</i>	<i>nad4L</i>	-	-
	<i>nad5</i>	<i>nad5</i>	<i>ND5</i>	-
	<i>nad7</i>	<i>nad7</i>	-	-
	<i>nad9</i>	<i>nad9</i>	-	-
ATP synthase	<i>atp1</i>	<i>atp1</i>	-	-
	<i>atp4</i>	<i>atp4</i>	-	-
	<i>atp6</i>	<i>atp6</i>	-	-
	<i>atp8</i>	<i>atp8</i>	-	-
	<i>atp9</i>	<i>atp9</i>	-	-
Cytochrome c biogenesis	<i>ccmB</i>	<i>ccmB</i>	-	-
	<i>ccmC</i>	<i>ccmC</i>	-	-
	<i>ccmFC</i>	<i>ccmFC</i>	-	-
	<i>ccmFN</i>	<i>ccmFN2</i>	-	-
Cytochrome c oxidase	<i>cox1</i>	<i>cox1</i>	-	-
	<i>cox2^a</i>	<i>cox2</i>	<i>Cox2</i>	<i>Cox2</i>
	<i>cox3</i>	<i>cox3</i>	<i>Cox3</i>	<i>Cox3</i>
Maturases	<i>matR</i>	<i>matR</i>	-	-
Ubiquinol cytochrome c reductase	<i>cob</i>	<i>cob</i>	<i>CYTB</i>	<i>cob</i>
Ribosomal proteins (LSU)	<i>rpl5</i>	<i>rpl5</i>	-	-
Ribosomal proteins (SSU)	<i>rps3</i>	<i>rps3</i>	-	-
	<i>rps7</i>	<i>rps7</i>	-	-
	<i>rps12</i>	<i>rps12</i>	-	-
Transport membrane protein	<i>sdh4</i>	<i>sdh4</i>	-	-
Ribosomal RNAs	<i>rrn5</i>	<i>rrn5</i>	-	-
	<i>rrnS</i>	<i>rrn18</i>	-	-
	<i>rrnL(3)</i>	<i>rrn26</i>	-	-
Transfer RNAs	<i>trnA-UGC</i>	-	-	-
	<i>trnC-GCA</i>	<i>trnC-GCA</i>	-	-
	<i>trnE-UUC</i>	<i>trnE(UUC)</i>	-	-
	<i>trnF-GAA</i>	-	-	-
	<i>trnG-GCC</i>	<i>trnG(GCC)</i>	-	-
	<i>trnH-GUG</i>	<i>trnH(GUG)</i>	-	-
	<i>trnI-GAU</i>	<i>trnN(GUU)</i>	-	-
	<i>trnK-UUU</i>	<i>trnK(UUU)</i>	-	-
	<i>trnL-CAA</i>	-	-	-
	<i>trnM-CAU</i>	<i>trnM(CAU)</i>	-	-
	<i>trnN-GUU</i>	<i>trnN(GUU)</i>	-	-
	<i>trnP-UGG</i>	<i>trnP(UGG)</i>	-	-
	<i>trnQ-UUG</i>	<i>trnQ(UUG)</i>	-	-
	<i>trnR-ACG</i>	-	-	-
	<i>trnS-GCU</i>	<i>trnS(GCU)</i>	-	-
	<i>trnS-UGA</i>	<i>trnS(UGA)</i>	-	-
	<i>trnV-GAC</i>	<i>trnN(GUU)</i>	-	-
	<i>trnW-CCA</i>	<i>trnW(CCA)</i>	-	-
	<i>trnY-GUA</i>	<i>trnY(GUA)</i>	-	-

Note: “-” indicate the absence of the specific gene.

Table S2. The stop codes of protein-coding genes in *S. glauca* mt genome.

Stop codon	Number	Percentage
TAG	5	18.52%
TGA	10	37.04%
TAA	12	44.44%
Total	27	100%

Table S3. The abbreviations and NCBI accession numbers of mt genomes used in this study.

Species	Abbreviations	Accession Numbers
<i>Arabidopsis thaliana</i>	<i>A. thaliana</i>	NC_037304
<i>Bartramia pomiformis</i>	<i>B. pomiformis</i>	NC_024519
<i>Beta vulgaris</i>	<i>B. vulgaris</i>	NC_002511
<i>Brassica napus</i>	<i>B. napus</i>	NC_008285
<i>Buxbaumia aphylla</i>	<i>B. aphylla</i>	NC_024518
<i>Capsicum annuum</i>	<i>C. annuum</i>	NC_024624
<i>Chlamydomonas reinhardtii</i>	<i>C. reinhardtii</i>	NC_001638
<i>Chlorella heliozoae</i>	<i>C. heliozoae</i>	KY629615
<i>Chara vulgaris</i>	<i>C. vulgaris</i>	NC_005255
<i>Carica papaya</i>	<i>C. papaya</i>	NC_012116
<i>Citrullus lanatus</i>	<i>C. lanatus</i>	NC_014043
<i>Cucumis sativus</i>	<i>C. sativus</i>	NC_016005
<i>Cucurbita pepo</i>	<i>C. pepo</i>	NC_014050
<i>Cycas taitungensis</i>	<i>C. taitungensis</i>	NC_010303
<i>Daucus carota</i>	<i>D. carota</i>	NC_017855
<i>Ginkgo biloba</i>	<i>G. biloba</i>	NC_027976
<i>Glycine max</i>	<i>G. max</i>	NC_020455
<i>Homo sapiens</i>	<i>H. sapiens</i>	NC_012920
<i>Lotus japonicas</i>	<i>L. japonicas</i>	NC_016743
<i>Malus domestica</i>	<i>M. domestica</i>	NC_018554
<i>Millettia pinnata</i>	<i>M. pinnata</i>	NC_016742
<i>Marchantia palealea</i>	<i>M. palealea</i>	NC_001660
<i>Medicago truncatula</i>	<i>M. truncatula</i>	NC_029641
<i>Nicotiana tabacum</i>	<i>N. tabacum</i>	NC_006581
<i>Nitella hyalina</i>	<i>N. hyalina</i>	NC_017598
<i>Oryza sativa</i>	<i>O. sativa</i>	NC_007886
<i>Populus tremula</i>	<i>P. tremula</i>	NC_028096
<i>Raphanus sativus</i>	<i>R. sativus</i>	NC_018551
<i>Rhazya stricta</i>	<i>R. stricta</i>	NC_024293
<i>Saccharomyces cerevisiae</i>	<i>S. cerevisiae</i>	NC_001224
<i>Salix suchowensis</i>	<i>S. suchowensis</i>	NC_029317
<i>Sorghum bicolor</i>	<i>S. bicolor</i>	NC_008360
<i>Sphagnum palustre</i>	<i>S. palustre</i>	NC_024521
<i>Triticum aestivum</i>	<i>T. aestivum</i>	NC_007579
<i>Vigna angularis</i>	<i>V. angularis</i>	NC_021092
<i>Vitis vinifera</i>	<i>V. vinifera</i>	NC_012119
<i>Zea mays</i>	<i>Z.mays</i>	NC_008332
<i>Chenopodium quinoa</i>	<i>C. quinoa</i>	NC_041093
<i>Spinacia oleracea</i>	<i>S. oleracea</i>	NC_035618

Table S4. Protein-coding genes annotated in *S. glauca* mt genome in comparison to related species.

Gene	<i>B. vulgaris</i>	<i>S. glauca</i>	<i>C. quinoa</i>	<i>S. oleracea</i>
<i>atp1</i>	+	+	+	+
<i>atp4</i>	-	+	+	+
<i>atp6</i>	+	+	+	+
<i>atp8</i>	+	+	+	+
<i>atp9</i>	+	+	+	+
<i>ccmB</i>	+	+	+	+
<i>ccmC</i>	-	+	+	+
<i>ccmFc</i>	+	+	+	+
<i>ccmFn</i>	+	+	+	+
<i>cob</i>	+	+	+	+
<i>cox1</i>	+	+	+	+
<i>cox2</i>	+	+	+	+
<i>cox3</i>	+	+	+	+
<i>matR</i>	+	+	+	+
<i>nad1</i>	++	+	+	-
<i>nad2</i>	+	+	+	+
<i>nad3</i>	+	+	+	+
<i>nad4</i>	+	-	+	+
<i>nad4L</i>	+	+	+	+
<i>nad5</i>	+	+	+	+
<i>nad6</i>	+	-	+	+
<i>nad7</i>	+	++	+	+
<i>nad9</i>	+	+	+	+
<i>rpl5</i>	+	+	+	+
<i>rps3</i>	+	+	+	+
<i>rps4</i>	+	-	+	+
<i>rps12</i>	+	+	+	+
<i>rps13</i>	+	-	+	+
<i>rps7</i>	++	+	+	+
<i>sdh4</i>	+	+	-	-
<i>tatC</i>	+	-	+	+

Note: '+' indicates the presence of the gene in the specific species, and each '+' represents one copy number. '-' indicates the absence of the specific gene.