

Table S1. Base composition in the *E. strigosa*, *H. arbainense* and *H. longiflorum* plastomes.

Species	<i>E. strigosa</i>	<i>H. arbainense</i>	<i>H. longiflorum</i>
Genome size (bp)	155,174	154,709	154,496
IR (bp)	25,852	25,818	25,917
LSC (bp)	85,491	85,078	84,742
SSC (bp)	17,979	17,995	17,920
Total number of genes	134	134	134
rRNA	4	4	4
tRNA	30	30	30
Protein-coding genes	80	80	80
T (U) %	31.47	31.53	31.63
C %	19.27	19.23	19.04
A %	30.71	30.74	30.94
G %	18.53	18.47	18.37
Overall GC content %	37.80	37.70	37.41
GC content in LSC %	35.86	35.70	35.35
GC content in SSC %	31.84	31.73	31.13
GC content in IR %	43.10	43.10	42.95

Table S2. Gene contents in the plastomes of *E. strigosa*, *H. arbainense* and *H. longiflorum*.

Category	Gene groups	Gene Names
RNA genes	Ribosomal RNA genes (rRNA)	<i>rrn5^a</i> , <i>rrn4.5^a</i> , <i>rrn16^a</i> , <i>rrn23^a</i>
	Transfer RNA genes (tRNA)	<i>trnH-GUG</i> , <i>trnK-UUU⁺</i> , <i>trnQ-UUG</i> , <i>trnS-GCU</i> , <i>trnG-GCC⁺</i> , <i>trnG-UCC⁺</i> , <i>trnR-UCU</i> , <i>trnC-GCA</i> , <i>trnD-GUC</i> , <i>trnY-GUA</i> , <i>trnE-UUC</i> , <i>trnT-GGU</i> , <i>trnS-UGA</i> , <i>trnM-CAU</i> , <i>trnG-GCC</i> , <i>trnS-GGA</i> , <i>trnL-UAA⁺</i> , <i>trnT-UGU</i> , <i>trnF-GAA</i> , <i>trnV-UAC⁺</i> , <i>trnM-CAU</i> , <i>trnW-CCA</i> , <i>trnP-UGG</i> , <i>trnI-CAU^{+,a}</i> , <i>trnL-CAA^a</i> , <i>trnV-GAC^a</i> , <i>trnI-GAU^a</i> , <i>trnA-UGC^{+,a}</i> , <i>trnR-ACG^a</i> , <i>trnN-GUU^a</i> , <i>trnL-UAG</i>
Ribosomal proteins	Small sub-unit of ribosome	<i>rps2</i> , <i>rps3</i> , <i>rps4</i> , <i>rps7^a</i> , <i>rps8</i> , <i>rps11</i> , <i>rps12^{+,a}</i> , <i>rps14</i> , <i>rps15</i> , <i>rps16⁺</i> , <i>rps18</i> , <i>rps19</i>
Transcription Genes	Large sub-unit of ribosome	<i>rpl2^{+,a}</i> , <i>rpl14</i> , <i>rpl16⁺</i> , <i>rpl20</i> , <i>rpl22</i> , <i>rpl23^a</i> , <i>rpl32</i> , <i>rpl33</i> , <i>rpl36</i>
	DNA-dependent RNA polymerase	<i>rpoA</i> , <i>rpoB</i> , <i>rpoC1⁺</i> , <i>rpoC2</i>
Protein-coding genes	Photosystem I	<i>psaA</i> , <i>psaB</i> , <i>psaC</i> , <i>psaI</i> , <i>psaJ</i> , <i>ycf3⁺⁺</i>
	Photosystem II	<i>psbA</i> , <i>psbB</i> , <i>psbC</i> , <i>psbD</i> , <i>psbE</i> , <i>psbF</i> , <i>psbH</i> , <i>psbI</i> , <i>psbJ</i> , <i>psbK</i> , <i>psbL</i> , <i>psbM</i> , <i>psbN</i> , <i>psbT</i> , <i>psbZ</i>
	Sub-unit of cytochrome	<i>petA</i> , <i>petB⁺</i> , <i>petD⁺</i> , <i>petG</i> , <i>petL</i> , <i>petN</i>
	Sub-unit of synthase	<i>atpA</i> , <i>atpB</i> , <i>atpE</i> , <i>atpF⁺</i> , <i>atpH</i> , <i>atpI</i>
	Large sub-unit of rubisco	<i>rbcL</i>
	NADH dehydrogenase	<i>ndhA⁺</i> , <i>ndhB^{+,a}</i> , <i>ndhC</i> , <i>ndhD</i> , <i>ndhE</i> , <i>ndhF</i> , <i>ndhG</i> , <i>ndhH</i> , <i>ndhI</i> , <i>ndhJ</i> , <i>ndhK</i>
	ATP-dependent protease subunit P	<i>clpP⁺⁺</i>
Other genes	Cp envelope membrane protein	<i>cemA</i>
	Maturase	<i>matK</i>
	Sub-unit acetyl-coA carboxylase	<i>accD</i>
	C-type cytochrome synthesis	<i>ccsA</i>
	Translation initiation factor	<i>infA</i>
	Hypothetical proteins	<i>ycf2^a</i> , <i>ycf4</i> , <i>ycf15^a</i>
	Component of TIC complex	<i>ycf1^a</i>

* + Gene with one intron, ++ Gene with two introns and **a** Gene with multiple copies. *trnG-GCC* gene was absent in *E. strigosa* and *H. longiflorum*. while *trnG-UCC* gene was absent in *H. arbainense*.

Table S3. Length of introns and exons in the of *E. strigosa*, *H. arbainense* and *H. longiflorum* plastomes.

Gene	Location	Exon I (bp)			Intron I (bp)			Exon II (bp)			Intron II (bp)			Exon III (bp)		
		<i>E. s</i>	<i>H. a</i>	<i>H. l</i>	<i>E. s</i>	<i>H. a</i>	<i>H. l</i>	<i>E. s</i>	<i>H. a</i>	<i>H. l</i>	<i>E. s</i>	<i>H. a</i>	<i>H. l</i>	<i>E. s</i>	<i>H. a</i>	<i>H. l</i>
<i>trnK-UUU</i>	LSC	34	34	34	2487	2488	2472	36	36	36						
<i>rps16</i>	LSC	226	226	226	874	861	892	39	39	39						
<i>trnG-GCC</i>	LSC	*	22	*	*	667	*	*	47	*						
<i>trnG-UCC</i>	LSC	22	*	22	668	*	699	47	*	47						
<i>atpF</i>	LSC	410	410	410	704	703	695	143	143	143						
<i>rpoC1</i>	LSC	1612	1612	1612	757	754	764	429	450	429						
<i>ycf3</i>	LSC	154	154	154	747	739	767	227	227	227	728	726	751	123	123	123
<i>trnL-UAA</i>	LSC	34	34	34	500	502	509	49	49	49						
<i>trnV-UAC</i>	LSC	-	36	-	-	599	-	-	37	-						
<i>clpP1</i>	LSC	227	227	233	621	611	597	291	291	291	771	765	801	70	70	70
<i>petB</i>	LSC	5	5	5	782	790	696	641	641	641						
<i>petD</i>	LSC	7	7	7	681	693	687	474	474	474						
<i>rpl16</i>	LSC	398	398	398	1059	1059	787	8	8	8						
<i>rpl2</i>	IR	433	433	433	660	660	658	390	390	390						
<i>ndhB</i>	IR	757	755	757	678	678	677	774	776	774						
<i>rps12</i>	IR	25	25	25	534	534	535	231	231	231						
<i>trnI-GAU</i>	IR	36	36	36	945	944	948	34	34	34						
<i>trnA-UGC</i>	IR	37	37	37	811	811	817	34	34	34						
<i>ndhA</i>	SSC	538	538	538	1102	1105	1083	552	552	552						

Table S4. Codon-anticodon recognition patterns and codon usage of the *E. strigosa* plastome.

Codon	Amino Acid	RSCU	tRNA	Codon	Amino Acid	RSCU	tRNA
UUU	Phe	1.18	trnF-GAA	UAU(Y)	Tyr	1.32	trnY-GUA
UUC	Phe	0.82		UAC(Y)	Tyr	0.68	
UUA	Leu	1.3	trnL-UAA	UAA(*)	Stop	0.99	
UUG	Leu	1.31	trnL-CAA	UAG(*)	Stop	0.94	
CUU	Leu	1.14	trnL-UAG	CAU(H)	His	1.29	trnH-GUG
CUC	Leu	0.61		CAC(H)	His	0.71	
CUA	Leu	0.97		CAA(Q)	Gln	1.24	trnQ-UUG
CUG	Leu	0.66		CAG(Q)	Gln	0.76	
AUU	Ile	1.24	trnI-GAU	AAU(N)	Asn	1.31	trnN-GUU
AUC	Ile	0.82		AAC(N)	Asn	0.69	
AUA	Ile	0.93	trnI-CAU	AAA(K)	Lys	1.22	trnK-UUU
AUG	Met	1	trnM-CAU	AAG(K)	Lys	0.78	
GUU	Val	1.36	trnV-GAC	GAU(D)	Asp	1.36	trnD-GUC
GUC	Val	0.65		GAC(D)	Asp	0.64	
GUA	Val	1.24		GAA(E)	Glu	1.3	trnE-UUC
GUG	Val	0.75	trnV-UAC	GAG(E)	Glu	0.7	
UCU	Ser	1.24	trnS-GGA	UGU(C)	Cys	1.06	trnC-GCA
UCC	Ser	0.93		UGC(C)	Cys	0.94	
UCA	Ser	1.43		UGA(*)	Stop	1.07	
UCG	Ser	0.84	trnS-UGA	UGG(W)	Trp	1	trnW-CCA
CCU	Pro	1.01	trnP-UGG	CGU(R)	Arg	0.55	trnR-ACG
CCC	Pro	0.81		CGC(R)	Arg	0.4	trnR-UCU
CCA	Pro	1.25		CGA(R)	Arg	0.91	
CCG	Pro	0.93		CGG(R)	Arg	0.84	
ACU	Thr	1.08		AGA(R)	Arg	1.98	
ACC	Thr	0.82		AGG(R)	Arg	1.32	
ACA	Thr	1.33	trnT-GGU	AGU(S)	Ser	0.84	trnS-GCU
ACG	Thr	0.77	trnT-UGU	AGC(S)	Ser	0.73	
GCU	Ala	1.31	trnA-UGC	GGU(G)	Gly	0.96	trnG-GCC
GCC	Ala	0.83		GGC(G)	Gly	0.63	
GCA	Ala	1.14		GGA(G)	Gly	1.32	
GCG	Ala	0.72		GGG(G)	Gly	1.09	trnG-UCC

Table S5. Codon-anticodon recognition patterns and codon usage of the *H. arbainense* plastome.

Codon	Amino Acid	RSCU	tRNA	Codon	Amino Acid	RSCU	tRNA
UUU	Phe	1.15	trnF-GAA	UAU(Y)	Tyr	1.35	trnY-GUA
UUC	Phe	0.85		UAC(Y)	Tyr	0.65	
UUA	Leu	1.33	trnL-UAA	UAA(*)	Stop	0.94	
UUG	Leu	1.32	trnL-CAA	UAG(*)	Stop	1.06	
CUU	Leu	1.15	trnL-UAG	CAU(H)	His	1.33	trnH-GUG
CUC	Leu	0.65		CAC(H)	His	0.67	
CUA	Leu	0.91		CAA(Q)	Gln	1.29	trnQ-UUG
CUG	Leu	0.63		CAG(Q)	Gln	0.71	
AUU	Ile	1.2	trnI-GAU	AAU(N)	Asn	1.35	trnN-GUU
AUC	Ile	0.8		AAC(N)	Asn	0.65	
AUA	Ile	1	trnI-CAU	AAA(K)	Lys	1.25	trnK-UUU
AUG	Met	1	trnM-CAU	AAG(K)	Lys	0.75	
GUU	Val	1.41	trnV-GAC	GAU(D)	Asp	1.43	trnD-GUC
GUC	Val	0.63		GAC(D)	Asp	0.57	
GUA	Val	1.18		GAA(E)	Glu	1.37	trnE-UUC
GUG	Val	0.78	trnV-UAC	GAG(E)	Glu	0.63	
UCU	Ser	1.48	trnS-GGA	UGU(C)	Cys	1.22	trnC-GCA
UCC	Ser	0.89		UGC(C)	Cys	0.78	
UCA	Ser	1.33		UGA(*)	Stop	1	
UCG	Ser	0.82	trnS-UGA	UGG(W)	Trp	1	trnW-CCA
CCU	Pro	1.09	trnP-UGG	CGU(R)	Arg	0.68	trnR-ACG
CCC	Pro	0.81		CGC(R)	Arg	0.37	trnR-UCU
CCA	Pro	1.26		CGA(R)	Arg	1.06	
CCG	Pro	0.83		CGG(R)	Arg	0.79	
ACU	Thr	1.22		AGA(R)	Arg	1.97	
ACC	Thr	0.77		AGG(R)	Arg	1.13	
ACA	Thr	1.32	trnT-GGU	AGU(S)	Ser	0.94	trnS-GCU
ACG	Thr	0.69	trnT-UGU	AGC(S)	Ser	0.54	
GCU	Ala	1.39	trnA-UGC	GGU(G)	Gly	1.04	trnG-GCC
GCC	Ala	0.75		GGC(G)	Gly	0.55	
GCA	Ala	1.16		GGA(G)	Gly	1.35	
GCG	Ala	0.7		GGG(G)	Gly	1.05	trnG-UCC

Table S6. Codon-anticodon recognition patterns and codon usage of the *H. longiflorum* plastome.

Codon	Amino Acid	RSCU	tRNA	Codon	Amino Acid	RSCU	tRNA
UUU	Phe	1.2	trnF-GAA	UAU(Y)	Tyr	1.34	trnY-GUA
UUC	Phe	0.8		UAC(Y)	Tyr	0.66	
UUA	Leu	1.37	trnL-UAA	UAA(*)	Stop	1.05	
UUG	Leu	1.35	trnL-CAA	UAG(*)	Stop	0.94	
CUU	Leu	1.14	trnL-UAG	CAU(H)	His	1.43	trnH-GUG
CUC	Leu	0.66		CAC(H)	His	0.57	
CUA	Leu	0.85		CAA(Q)	Gln	1.3	trnQ-UUG
CUG	Leu	0.63		CAG(Q)	Gln	0.7	
AUU	Ile	1.24	trnI-GAU	AAU(N)	Asn	1.35	trnN-GUU
AUC	Ile	0.78		AAC(N)	Asn	0.65	
AUA	Ile	0.97	trnI-CAU	AAA(K)	Lys	1.25	trnK-UUU
AUG	Met	1	trnM-CAU	AAG(K)	Lys	0.75	
GUU	Val	1.33	trnV-GAC	GAU(D)	Asp	1.4	trnD-GUC
GUC	Val	0.74		GAC(D)	Asp	0.6	
GUA	Val	1.2		GAA(E)	Glu	1.29	trnE-UUC
GUG	Val	0.72	trnV-UAC	GAG(E)	Glu	0.71	
UCU	Ser	1.44	trnS-GGA	UGU(C)	Cys	1.15	trnC-GCA
UCC	Ser	0.9		UGC(C)	Cys	0.85	
UCA	Ser	1.24		UGA(*)	Stop	1.01	
UCG	Ser	0.86	trnS-UGA	UGG(W)	Trp	1	trnW-CCA
CCU	Pro	1.1	trnP-UGG	CGU(R)	Arg	0.71	trnR-ACG
CCC	Pro	0.85		CGC(R)	Arg	0.33	trnR-UCU
CCA	Pro	1.15		CGA(R)	Arg	0.97	
CCG	Pro	0.89		CGG(R)	Arg	0.72	
ACU	Thr	1.16		AGA(R)	Arg	2	
ACC	Thr	0.82		AGG(R)	Arg	1.27	
ACA	Thr	1.26	trnT-GGU	AGU(S)	Ser	0.93	trnS-GCU
ACG	Thr	0.76	trnT-UGU	AGC(S)	Ser	0.65	
GCU	Ala	1.35	trnA-UGC	GGU(G)	Gly	0.95	trnG-GCC
GCC	Ala	0.82		GGC(G)	Gly	0.6	
GCA	Ala	1.08		GGA(G)	Gly	1.37	
GCG	Ala	0.76		GGG(G)	Gly	1.08	trnG-UCC

Table S7. Predicted RNA editing site in the *E. strigosa* plastome.

Gene	Nucleotide position	Amino acid position	Triplet position within codon	Base conversion	Codon change	Amino acid conversion
<i>matK</i>	655	219	1	C→U	CAU→UAU	H→Y
<i>atpF</i>	92	31	2	C→U	CCA→CUA	P→L
<i>rps2</i>	248	83	2	C→U	UCA→UUA	S→L
<i>rpoC1</i>	65	22	2	C→U	UCA→UUA	S→L
<i>rpoB</i>	338	113	2	C→U	UCU→UUU	S→F
	473	158	2	C→U	UCA→UUA	S→L
	551	184	2	C→U	UCA→UUA	S→L
	2432	811	2	C→U	UCA→UUA	S→L
<i>psbZ</i>	50	17	2	C→U	UCA→UUA	S→L
<i>rps14</i>	80	27	2	C→U	UCA→UUA	S→L
<i>rps14</i>	149	50	2	C→U	CCA→CUA	P→L
<i>psbL</i>	2	1	2	C→U	ACG→AUG	T→M
<i>psbE</i>	214	72	1	C→U	CCU→UCU	P→S
<i>petB</i>	611	204	2	C→U	CCA→CUA	P→L
<i>rpoA</i>	842	281	2	C→U	UCA→UUA	S→L
<i>rpl23</i>	71	24	2	C→U	UCU→UUU	S→F
	89	30	2	C→U	UCA→UUA	S→L
<i>ndhB</i>	53	18	2	C→U	UCA→UUA	S→L
	59	20	2	C→U	UCA→UUA	S→L
	95	32	2	C→U	UCA→UUA	S→L
	149	50	2	C→U	UCA→UUA	S→L
	467	156	2	C→U	CCA→CUA	P→L
	586	196	1	C→U	CAU→UAU	H→Y
	704	235	2	C→U	CCA→CUA	P→L
	737	246	2	C→U	CCA→CUA	P→L
<i>ndhF</i>	290	97	2	C→U	UCA→UUA	S→L
<i>ndhD</i>	2	1	2	C→U	ACG→AUG	T→M
	599	200	2	C→U	UCA→UUA	S→L
	674	225	2	C→U	UCG→UUG	S→L
	878	293	2	C→U	UCA→UUA	S→L
	1298	433	2	C→U	UCA→UUA	S→L
<i>ndhA</i>	341	114	2	C→U	UCA→UUA	S→L
	409	137	1	C→U	CCU→UCU	P→S
	521	174	2	C→U	UCC→UUC	S→F

Table S8. Predicted RNA editing site in the *H. arbainense* and *H. longiflorum* plastomes.

Gene	Nucleotide position	Amino acid position	Triplet position within codon	Base conversion	Codon change	Amino acid conversion
<i>matK</i>	655	219	1	C→U	CAU→UAU	H→Y
<i>atpF</i>	92	31	2	C→U	CCA→CUA	P→L
<i>rps2</i>	248	83	2	C→U	UCA→UUA	S→L
<i>rpoC1</i>	65	22	2	C→U	UCA→UUA	S→L
<i>rpoB</i>	338	113	2	C→U	UCU→UUU	S→F
	473	158	2	C→U	UCA→UUA	S→L
	551	184	2	C→U	UCA→UUA	S→L
	2432	811	2	C→U	UCA→UUA	S→L
<i>psbZ</i>	50	17	2	C→U	UCA→UUA	S→L
<i>rps14</i>	80	27	2	C→U	UCA→UUA	S→L
	149	50	2	C→U	CCA→CUA	P→L
<i>psbE</i>	214	72	1	C→U	CCU→UCU	P→S
<i>petB</i>	611	204	2	C→U	CCA→CUA	P→L
<i>rpoA</i>	200	67	2	C→U	UCU→UUU	S→F
<i>rpoA</i>	842	281	2	C→U	UCA→UUA	S→L
<i>rpl23</i>	71	24	2	C→U	UCU→UUU	S→F
	89	30	2	C→U	UCA→UUA	S→L
<i>ndhB</i>	53	18	2	C→U	UCA→UUA	S→L
	59	20	2	C→U	UCA→UUA	S→L
	95	32	2	C→U	UCA→UUA	S→L
	149	50	2	C→U	UCA→UUA	S→L
	467	156	2	C→U	CCA→CUA	P→L
	586	196	1	C→U	CAU→UAU	H→Y
	704	235	2	C→U	CCA→CUA	P→L
	737	246	2	C→U	CCA→CUA	P→L
<i>ndhF</i>	290	97	2	C→U	UCA→UUA	S→L
<i>ndhD</i>	2	1	2	C→U	ACG→AUG	T→M
	599	200	2	C→U	UCA→UUA	S→L
	878	293	2	C→U	UCA→UUA	S→L
	1298	433	2	C→U	UCA→UUA	S→L
<i>ndhA</i>	341	114	2	C→U	UCA→UUA	S→L
	409	137	1	C→U	CCU→UCU	P→S
	521	174	2	C→U	UCC→UUC	S→F

*The Prediction of RNA editing site in *psbE* gene was only found in *H. longiflorum*.

Table S9. Repeat sequences present in the *E. strigosa* plastome.

SN	Repeat Size	Repeat Position 1	Repeat Type	Repeat Location 1	Repeat Position 2	Repeat Location 2	E-Value
1	44	75616	P	IGS	75616	IGS	0 2.19e-17
2	40	9824	P	IGS	9824	IGS	0 5.60e-15
3	29	8177	P	IGS	45753	trnS-GGA	0 2.35e-08
4	29	114600	F	ndhF	114626	IGS	0 2.35e-08
5	26	89128	P	ycf2	89128	ycf2	0 1.50e-06
6	26	89128	F	ycf2	151511	ycf2	0 1.50e-06
7	26	121786	P	ndhA - intron	121786	ndhA - intron	0 1.50e-06
8	26	151511	P	ycf2	151511	ycf2	0 1.50e-06
9	24	32169	F	IGS	32191	IGS	0 2.41e-05
19	24	39503	F	psaB	41727	psaA	0 2.41e-05
11	24	55945	F	IGS	55968	IGS	0 2.41e-05
12	24	126151	P	ycf1	126151	ycf1	0 2.41e-05
13	23	27891	F	IGS	27914	IGS	0 9.62e-05
14	22	9750	F	trnG-UCC	37284	trnG-GCC	0 3.85e-04
15	22	95208	P	IGS	95234	IGS	0 3.85e-04
16	22	95208	F	IGS	145409	IGS	0 3.85e-04
17	22	95234	F	IGS	145435	IGS	0 3.85e-04
18	22	145409	P	IGS	145435	IGS	0 3.85e-04
19	21	241	P	IGS	291	IGS	0 1.54e-03
20	21	6805	R	IGS	6805	IGS	0 1.54e-03
21	21	8182	F	trnS-GCU	36364	trnS-UGA	0 1.54e-03
22	21	30305	P	IGS	30336	IGS	0 1.54e-03
23	21	36364	P	trnS-UGA	45756	trnS-GGA	0 1.54e-03
24	21	37498	F	trnM-CAU	67949	trnP-UGG	0 1.54e-03
25	21	92777	F	ycf2	92795	ycf2	0 1.54e-03
26	21	92777	P	ycf2	147849	ycf2	0 1.54e-03
27	21	92795	P	ycf2	147867	ycf2	0 1.54e-03
28	21	99797	F	IGS	121412	ndhA - intron	0 1.54e-03
29	21	121412	P	ndhA - intron	140847	IGS	0 1.54e-03
30	21	147849	F	ycf2	147867	ycf2	0 1.54e-03
31	20	8407	F	IGS	8425	IGS	0 6.16e-03
32	20	29669	F	IGS	29688	IGS	0 6.16e-03
33	20	31977	P	IGS	31977	IGS	0 6.16e-03
34	20	50956	R	ndhC	50956	ndhC	0 6.16e-03
35	20	52906	P	trnV-UAC	104513	trnA-UGC	0 6.16e-03
36	20	52906	F	trnV-UAC	136132	trnA-UGC	0 6.16e-03
37	19	2818	R	trnK-UUU - intron	114895	IGS	0 2.46e-02
38	19	6304	R	IGS	46714	IGS	0 2.46e-02
39	19	6306	F	IGS	6326	IGS	0 2.46e-02
40	19	15199	R	IGS	15199	IGS	0 2.46e-02
41	19	16768	P	rpoC2	60777	IGS	0 2.46e-02
42	19	43091	F	IGS	111358	ycf1	0 2.46e-02
43	19	51380	F	IGS	51397	IGS	0 2.46e-02
44	19	55702	C	IGS	92182	ycf2	0 2.46e-02
45	19	55702	R	IGS	148464	ycf2	0 2.46e-02
46	19	61751	F	IGS	72876	clpP1 - intron	0 2.46e-02
47	19	118218	P	IGS	118243	IGS	0 2.46e-02
48	18	8620	F	IGS	28888	IGS	0 9.85e-02
49	18	31641	P	IGS	45149	ycf3 - intron	0 9.85e-02

Table S10. Repeat sequences present in the *H. arbainense* plastome.

SN	Repeat Size	Repeat Position 1	Repeat Type	Repeat Location 1	Repeat Position 2	Repeat Location 2	E-Value
1	40	9555	P	IGS	9555	IGS	0 5.57e-15
2	29	7942	P	IGS	45552	trnS-GGA	0 2.34e-08
3	26	88679	P	ycf2	88679	ycf2	0 1.49e-06
4	26	88679	F	ycf2	151082	ycf2	0 1.49e-06
5	26	121326	P	ndhA - Intron	121326	ndhA - Intron	0 1.49e-06
6	26	151082	P	ycf2	151082	ycf2	0 1.49e-06
7	25	26984	F	IGS	27008	IGS	0 5.98e-06
8	24	39337	F	psaB	41561	psaA	0 2.39e-05
9	24	111676	R	ndhF	111676	ndhF	0 2.39e-05
19	22	9486	F	trnG-GCC	37121	trnG-GCC	0 3.83e-04
11	22	82589	P	rpl16 - Intron	82589	rpl16 - Intron	0 3.83e-04
12	22	94770	P	IGS	94796	IGS	0 3.83e-04
13	22	94770	F	IGS	144969	IGS	0 3.83e-04
14	22	94796	F	IGS	144995	IGS	0 3.83e-04
15	22	144969	P	IGS	144995	IGS	0 3.83e-04
16	21	101	R	IGS	101	IGS	0 1.53e-03
17	21	286	P	IGS	336	IGS	0 1.53e-03
18	21	7947	F	trnS-GCU	36169	trnS-UGA	0 1.53e-03
19	21	29990	P	IGS	30021	IGS	0 1.53e-03
20	21	33245	F	IGS	33266	IGS	0 1.53e-03
21	21	36169	P	trnS-UGA	45555	trnS-GGA	0 1.53e-03
22	21	37331	F	trnM-CAU	67517	trnP-UGG	0 1.53e-03
23	21	92334	F	ycf2	92352	ycf2	0 1.53e-03
24	21	92334	P	ycf2	147414	ycf2	0 1.53e-03
25	21	92352	P	ycf2	147432	ycf2	0 1.53e-03
26	21	99359	F	IGS	120943	ndhA - Intron	0 1.53e-03
27	21	120943	P	ndhA - Intron	140407	IGS	0 1.53e-03
28	21	147414	F	ycf2	147432	ycf2	0 1.53e-03
29	20	31657	P	IGS	31657	IGS	0 6.12e-03
30	20	50676	R	ndhC	50676	ndhC	0 6.12e-03
31	20	52593	P	trnV-UAC	104067	trnA-UGC	0 6.12e-03
32	20	52593	F	trnV-UAC	135700	trnA-UGC	0 6.12e-03
33	19	119	R	IGS	115293	ccsA	0 2.45e-02
34	19	14927	R	atpI	14927	atpI	0 2.45e-02
35	19	30148	F	IGS	30162	IGS	0 2.45e-02
36	19	32524	C	IGS	55519	IGS	0 2.45e-02
37	19	42925	F	IGS	110911	ndhF	0 2.45e-02
38	19	75154	P	IGS	75179	IGS	0 2.45e-02
39	19	111683	R	ndhF	111683	ndhF	0 2.45e-02
40	19	116195	R	IGS	116195	IGS	0 2.45e-02
41	19	117758	P	IGS	117783	IGS	0 2.45e-02
42	19	121239	F	ndhA - Intron	121258	ndhA - Intron	0 2.45e-02
43	18	6483	F	IGS	47194	IGS	0 9.80e-02
44	18	16475	P	rpoC2	60408	IGS	0 9.80e-02
45	18	27899	R	IGS	27899	IGS	0 9.80e-02
46	18	36364	F	IGS	36382	IGS	0 9.80e-02
47	18	47349	R	IGS	47349	IGS	0 9.80e-02
48	18	57348	F	IGS	57368	IGS	0 9.80e-02
49	18	63960	P	IGS	108551	IGS	0 9.80e-02

Table S11. Repeat sequences present in the *H. longiflorum* plastome.

SN	Repeat Size	Repeat Position 1	Repeat Type	Repeat Location 1	Repeat Position 2	Repeat Location 2	E-Value
1	48	75187	P	IGS	75187	IGS	8.47E-20
2	40	99085	F	IGS	120662	ndhA - Intron	5.55E-15
3	40	120662	P	ndhA - Intron	140113	IGS	5.55E-15
4	38	113438	F	IGS	113458	IGS	8.88E-14
5	29	8381	P	IGS	45931	trnS-GGA	2.33E-08
6	26	39349	F	psaB	41573	psaA	1.49E-06
7	26	81405	R	IGS	81405	IGS	1.49E-06
8	26	88412	P	ycf2	88412	ycf2	1.49E-06
9	26	88412	F	ycf2	150800	ycf2	1.49E-06
19	26	150800	P	ycf2	150800	ycf2	1.49E-06
11	23	4297	R	IGS	4297	IGS	9.54E-05
12	23	33269	F	IGS	33290	IGS	9.54E-05
13	23	64638	F	IGS	64660	IGS	9.54E-05
14	22	9660	F	trnG-UCC	37145	trnG-GCC	3.82E-04
15	22	55554	C	IGS	81411	IGS	3.82E-04
16	22	94504	P	IGS	94530	IGS	3.82E-04
17	22	94504	F	IGS	144686	IGS	3.82E-04
18	22	94530	F	IGS	144712	IGS	3.82E-04
19	22	144686	P	IGS	144712	IGS	3.82E-04
20	21	98	F	IGS	119	IGS	1.53E-03
21	21	8386	F	trnS-GCU	36185	trnS-UGA	1.53E-03
22	21	33047	R	IGS	33047	IGS	1.53E-03
23	21	36185	P	trnS-UGA	45934	trnS-GGA	1.53E-03
24	21	37346	F	trnM-CAU	67578	trnP-UGG	1.53E-03
25	21	55554	P	IGS	121069	ndhA - Intron	1.53E-03
26	21	81411	R	IGS	121069	ndhA - Intron	1.53E-03
27	21	92061	F	ycf2	92079	ycf2	1.53E-03
28	21	92061	P	ycf2	147138	ycf2	1.53E-03
29	21	92079	P	ycf2	147156	ycf2	1.53E-03
30	21	147138	F	ycf2	147156	ycf2	1.53E-03
31	20	28959	F	IGS	28979	IGS	6.11E-03
32	20	31773	P	IGS	31773	IGS	6.11E-03
33	20	51180	R	ndhC	51180	ndhC	6.11E-03
34	20	55554	P	IGS	81405	IGS	6.11E-03
35	20	81405	F	IGS	121070	ndhA - Intron	6.11E-03
36	20	125563	P	ycf1	125563	ycf1	6.11E-03
37	19	4336	P	IGS	121074	ndhA - Intron	2.44E-02
38	19	12278	P	atpF - Intron	81953	IGS	2.44E-02
39	19	14971	R	atpI	14971	atpI	2.44E-02
40	19	16241	P	IGS	45334	IGS	2.44E-02
41	19	18418	R	rpoC2	32902	IGS	2.44E-02
42	19	50997	R	IGS	127061	ycf1	2.44E-02
43	18	224	P	IGS	270	IGS	9.77E-02
44	18	4603	F	IGS	72191	clpP1 - Intron	9.77E-02
45	18	8451	F	trnS-GCU	36251	trnS-UGA	9.77E-02
46	18	15300	P	IGS	126815	ycf1	9.77E-02
47	18	22832	C	rpoC1 - Intron	51796	IGS	9.77E-02
48	18	24721	C	rpoB	28778	IGS	9.77E-02
49	18	31227	C	IGS	114405	IGS	9.77E-02

Table S12. Simple sequence repeats in the plastome of *E. strigosa*.

Repeat	Length (bp)	Number	Start position
A	8	27	1568; 8628; 9183; 12201; 15530; 18806; 21256; 22463; 28896; 29962; 38134; 43104; 46875; 47521; 55855; 63636; 65639; 72077; 72539; 76746; 83953; 89780; 98163; 115759; 121630; 129336; 155087
	9	20	4214; 4524; 8628; 30975; 37113; 49012; 55855; 69256; 69770; 79202; 90954; 109523; 114779; 118269; 136763; 140710; 141794; 145694; 155087; 155162
	10	6	8150; 49151; 60788; 64721; 94771; 115214
	11	6	86; 36591; 44559; 67287; 82441; 114169
	12	2	48147; 66831
	13	1	83246
	16	1	13640
C	8	1	16769
	9	1	37402
G	8	1	63098
	10	1	78232
T	8	34	2166; 4524; 7512; 8628; 15530; 16472; 22771; 26247; 26358; 28134; 29631; 43104; 49361; 50771; 51273; 51579; 52350; 61029; 62110; 64373; 71848; 76618; 83246; 84099; 85504; 111323; 114998; 116091; 117281; 127092; 129096; 142496; 150879
	9	27	7908; 16769; 44145; 49012; 55254; 59752; 67414; 69770; 75377; 78232; 84809; 85259; 85504; 85579; 94964; 98864; 99948; 103895; 114169; 116577; 121630; 124352; 127321; 127400; 127695; 131135; 149704
	10	6	30604; 55254; 57971; 70445; 71848; 145886
	11	7	9933; 13084; 32719; 52053; 60452; 61756; 72881
	12	1	66370
	13	3	12425; 18663; 81912
	17	1	32874
AT	5	4	20027; 31110; 86198; 154459
	6	1	6103
TA	5	2	32184; 32215
ATA	4	2	45525; 67849
TAT	4	1	64721
AAAC	3	1	69256
TCTT	3	1	30335

Table S13. Simple sequence repeats in the plastome of *H. arbainense*.

Repeat	Length (bp)	Number	Start position
A	8	26	108; 1622; 8364; 15258; 18512; 20977; 22184; 23478; 28602; 29635; 46645; 60419; 63262; 64352; 65238; 68831; 69340; 72082; 72102; 89331; 97725; 115300; 117809; 128905; 136331; 145260
	9	20	108; 4569; 30682; 36899; 36958; 37967; 44372; 47285; 47913; 48907; 65968; 82805; 83513; 90511; 109076; 114742; 121220; 140270; 141354; 154647
	10	11	4263; 4569; 7921; 8364; 31826; 55520; 66880; 76282; 78710; 94328; 113732
	11	2	4569; 55520
	13	3	13380; 114315; 154647
	15	1	66421
C	8	2	16475; 37239
G	10	1	77777
T	8	42	4569; 7292; 7495; 8364; 16190; 25965; 26076; 27847; 27912; 31343; 43007; 48771; 49110; 50491; 50993; 51273; 60658; 61186; 61733; 71395; 76156; 77777; 78710; 82805; 83513; 84818; 94521; 103450; 110876; 113732; 114315; 115632; 116821; 119478; 124729; 125712; 126519; 126640; 128659; 142056; 150450
	9	25	7689; 15258; 16475; 29271; 30303; 43958; 51747; 59406; 67006; 70014; 71395; 84368; 85094; 98426; 99510; 114541; 123886; 124915; 126869; 126948; 127243; 130704; 149269
	10	10	9664; 12151; 30817; 47913; 52042; 54941; 60101; 72425; 74913; 145451
	11	3	12813; 57634; 65968
	12	3	22489; 32523; 61387
	13	3	18369; 85094; 116199
	14	2	32679; 81448
AT	5	4	19742; 30817; 85749; 154030
TA	6	1	32009
AAAC	3	1	68831
ATAA	3	1	83358
TCTT	3	1	30020
TTAA	4	1	82593
AATAA	3	1	130413
TTTAT	3	1	109360

Table S14. Simple sequence repeats in the plastome of *H. longiflorum*.

Repeat	Length (bp)	Number	Start position
A	8	23	4510; 8362; 18564; 22234; 28551; 31238; 36898; 37979; 42902; 43507; 44475; 48182; 63517; 65531; 66504; 66822; 80329; 83220; 108775; 111364; 114091; 136026; 154430
	9	19	4158; 4510; 4679; 6252; 29603; 36898; 47042; 64576; 64973; 72075; 72201; 74990; 76356; 90238; 94054; 97463; 130410; 141066; 154430
	10	9	3699; 7056; 8702; 45342; 47888; 60171; 69325; 81959; 117539
	11	5	9253; 15303; 36425; 78723; 82549
	12	3	13501; 32215; 81959
	13	1	22832
	14	1	4283
	16	1	55553
C	9	1	99171
	12	1	100765
	13	1	36898
G	9	2	43507; 140060
	12	1	138463
T	8	22	7281; 26025; 26136; 27215; 27870; 29453; 32215; 36047; 42902; 45342; 50995; 64576; 66242; 67086; 84769; 103206; 115355; 116552; 121068; 126344; 128363; 130410;
	9	25	4510; 10016; 16530; 22832; 30248; 48300; 49225; 61648; 61674; 66242; 71435; 74854; 83724; 84523; 84769; 98165; 108775; 113228; 123606; 125380; 126573; 126821; 141768; 145177; 148993
	10	10	2126; 4283; 8129; 12283; 16244; 47607; 54997; 59625; 77733; 114416
	11	7	8702; 44064; 57815; 72314; 78968; 126821; 126958
	12	3	51797; 72314; 115930
	13	2	18421; 32907
	14	2	81412; 121068
AT	5	3	14480; 19794; 48300
TA	5	1	8543
GCT	4	1	57152
TTC	4	1	35839
AAAC	3	1	68897
AAAT	3	1	49558
TAAA	3	1	4283
TTTA	3	1	51600
TTTG	3	1	5460
TTCTTT	3	1	44064