

Suppl. Table 1. Mitochondrial genome features of *Stylosanthes*

	<i>S. hamata</i>	<i>S. viscosa</i>	<i>S. pilosa</i>	<i>S. capitata</i>	<i>S. scabra</i>	<i>S. macrocephala</i>	<i>S. capitata</i> RS024	<i>S. guianensis</i>	<i>S. seabrana</i>
Total size (bp)	503,967	353,136	433,649	456,448	492,899	350,377	345,666	468,896	523,870
Size of coding regions (bp)	39,000	35,478	35,772	35,130	38,484	32,690	21,760	35,892	37,896
Size of protein-coding regions (bp)	43,500	42,643	37,355	34,338	40,699	36,565	34,630	44,041	43,821
Size of rRNA (bp)	5,042	5,042	5,038	2,945	5,042	5,042	5,047	5,033	5,042
Size of tRNA (bp)	1,336	1,347	1,665	1,601	1,422	1,275	1,150	1,561	1,413
Size of intergenic regions (bp)	416,179	271,902	357,050	382,107	406,738	276,311	269,804	380,816	435,298
No. of different genes	33	33	33	31	33	30	32	32	32
No. of different protein-coding genes	47	46	47	42	47	45	47	47	47
No. of different tRNA genes	16	16	16	15	15	15	15	16	16
No. of different rRNA genes	3	3	3	1	3	3	3	3	3

No. of different duplicated genes	5	3	4	4	5	3	1	5	5
No. of different genes with introns	6	6	6	5	6	5	7	6	6
Overall % GC content	44.9	45.1	45.2	45.0	45.1	45.2	45.3	45.0	44.9
% GC content in protein-coding regions	46.4	46.4	45.7	45.8	46.5	45.3	46.0	46.3	46.4
% GC content in intergenic regions	46.5	46.5	46.1	46.2	46.5	45.9	45.4	46.6	46.6
% GC content in rRNA	52.1	52.1	52.0	51.1	52.1	52.1	44.0	52.1	52.1
% GC content in tRNA	51.5	52.2	49.1	49.7	52.4	52.2	49.5	52.1	52.1

Suppl. Table 2. Genes of *Stylosanthes* mitochondrial genomes.

GENE GROUP		GENE NAME								
		<i>S. hamata</i>	<i>S. viscosa</i>	<i>S. scabra</i>	<i>S. capitata</i> CG	<i>S. pilosa</i>	<i>S. macrocephala</i>	<i>S. capitata</i> 24	<i>S. seabraana</i>	<i>S. guianensis</i>
Transfer RNAs		trnA-UGC, trnD-cp, trnE, trnF, trnfM, trnF, trnfM (2x), trnG, trnH, trnl, trnK (2x), trnM- cp, trnN-cp, trnP (2x), trnQ, trnS, trnP, trnQ, trnS, trnW-cp, trnY.	trnD-cp, trnE, trnF, trnfM (3x), trnG, trnH, trnl, trnK (2x), trnM- cp, trnN-cp, trnP (2x), trnQ, trnS, trnW-cp, trnY.	trnD-cp, trnE, trnF, trnfM (2x), trnG, trnH, trnl, trnK (2x), trnM- cp, trnN-cp, trnP (2x), trnQ, trnS, trnW-cp, trnY.	trnA, trnD-cp, trnE, trnF, trnM, trnG, trnH, trnI, trnK, trnM-cp , trnN- cp, trnP (2x), trnQ, trnS, trnW-cp (2x), trnY	trnD-cp, trnE, trnF, trnfM (2x), trnG, trnH, trnl, trnK, trnM-cp, trnN-cp, trnP (2x), trnQ, trnS, trnW-cp, trnY	trnD-cp, trnE, trnF, trnfM (2x), trnG, trnH, trnl, trnK , trnM-cp, trnN-cp, trnP, trnQ, trnS, trnW-cp, trnY.	trnD-cp, trnE, trnF, trnfM (2x), trnG, trnH-, GUG, trnl, trnK (2x), trnM-cp, (2x), trnQ, trnS, (2x), trnQ-UUG, trnS, trnY, trnY- GUA.	trnD-GUC, trnE-UUC, trnF- GAA, trnF- GAA, trnfM (2x), trnG-GCC, trnH-GUG, trnl, trnK-UUU (2x), trnM-CAU, trnN-GUU, trnP (3x), trnP-UGG, trnQ-UUG, trnS-GCU, trnW-CCA, trnY-GUA.	
RNA polymerase		rrn5, rrn18, rrn26.	rrn5, rrn18, rrn26.	rrn5, rrn18, rrn26.	rrn26	rrn5, rrn18, rrn26	rrn5, rrn18, rrn26	rrn5, rrn18, rrn26.	rrn26.	rrn5S, rrn18, rrn26.
Ribosomal Protein small subunit		rps1, rps3 (2x), rps4, rps10, rps12 (2x), rps14.	rps1, rps3 (2x), rps4, rps10, rps12.	rps1, rps3, rps4, rps10, rps12, rps14.	rps1, rps3, rps4, rps10, rps12, rps14	rps1, rps3 (2x), rps4, rps10, rps12	rps1, rps3 (2x), rps4, rps10, rps12	rps1, rps3 (2x), rps4, rps10, rps12 (3x), rps14.	rps1, rps3 (2x), rps4, rps10, rps12, rps14.	
Ribosomal Protein large subunit		rpl5, rpl16.	rpl5, rpl16.	rpl5, rpl16.	rpl5, rpl16	rpl5, rpl16	rpl5, rpl16	rpl5, rpl16.	rpl5, rpl16.	
ATP synthase		atp4, atp6, atp8, atp9, atpA.	Atp4, atp6, atp8, atp9, atpA.	Atp4, atp6, atp8, atp9, atpA.	Atp4, atp6, atp8, atp9.	Atp4, atp6, atp8, atp9, atpA	Atp4, atp6, atp8, atp9, atpA	Atp4, atp6, atp8, atp9, atpA.	Atp4, atp6, atp8, atp9, atpA.	
Maturase		matR	matR	matR	matR	matR	matR	matR	matR	
Complex I (NADH dehydrogenase)		nad3, nad4L, nad6, nad7, nad9	nad3, nad4L, nad6, nad7, nad9	nad3, nad4L, nad6, nad7, nad9	nad3, nad4L, nad6, nad7, nad9	nad3, nad4L, nad6, nad7, nad9	nad3, nad4L, nad6, nad7, nad9	nad3, nad4L, nad6, nad7, nad9	nad3, nad4, nad6, nad7, nad9	
Complex II		sdh4	sdh4	sdh4 (2x)	sdh4	sdh4	sdh4	sdh4	sdh4	

Complex III (Ubichinol cytochrome c reductase)	cob	cob	cob	-	cob	cob	cob	-	cob
Complex IV (cytochrome c oxidase)	cox1, cox2, cox3.	cox1, cox2, cox3.	cox1, cox2, cox3 (2x).	cox1, cox2, cox3.	cox1, cox2 (2x), cox3	cox1, cox2, cox3	cox1, cox2, cox3.	cox1, cox2, cox3.	cox1, cox2 (2x), cox3.
Other genes	ccmB, ccmC, ccmFc, ccmFn, tatC.	ccmB, ccmC, ccmFn, tatC.	ccmB, ccmC, ccmFc, ccmFn, tatC.	ccmB, ccmC, ccmFc, ccmFn, tatC.	ccmB, ccmC, ccmFc, ccmFn, tatC.				

Suppl. Table 3. Plastome features of *Stylosanthes*.

Suppl. Table 4. Genes of *Stylosanthes* chloroplast genomes.

Gene group	<i>S. hamata</i>	<i>S. viscosa</i>	<i>S. scabra</i>	<i>S. capitata</i> GC	<i>S. pilosa</i>	<i>S. macrocephala</i>	<i>S. capitata</i> RS024	<i>S. seabrana</i>	<i>S. guianensis</i>	
Protein synthesis and DNA replication	trnA-UGC (2x), trnC- GCA, trnD- GUC, trnE- UUC, trnF- GAA, trnfM- CAU, trnG- UCC, trnH- GUG, trnI- CAU (2x), trnI-GAU (2x), trnK- UUU, trnL- CAA (2x), trnL-UAA, trnL-UAG, trnM-CAU, trnN-GUU (2x), trnP- UGG, trnQ- UUG, trnR- ACG (2x), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2x), trnV- UAC, trnW- CCA, trnY- GUA	trnA-UGC (2x), trnC- GCA, trnD- GUC, trnE- UUC, trnF- GAA, trnfM- CAU, trnG- UCC, trnH- GUG, trnI- CAU (2x), trnI-GAU (2x), trnK- UUU, trnL- CAA (2x), trnL-UAA, trnL-UAG, trnM-CAU, trnN-GUU (2x), trnP- UGG, trnQ- UUG, trnR- ACG (2x), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2x), trnV- UAC, trnW- CCA, trnY- GUA	trnA-UGC (2x), trnC- GCA, trnD- GUC, trnE- UUC, trnF- GAA, trnfM- CAU, trnG- UCC, trnH- GUG, trnI- CAU (2x), trnI-GAU (2x), trnK- UUU, trnL- CAA (2x), trnL-UAA, trnL-UAG, trnM-CAU, trnN-GUU (2x), trnP- UGG, trnQ- UUG, trnR- ACG (2x), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2x), trnV- UAC, trnW- CCA, trnY- GUA	trnA-UGC (2x), trnC- GCA, trnD- GUC, trnE- UUC, trnF- GAA, trnfM- CAU, trnG- UCC, trnH- GUG, trnI- CAU (2x), trnI-GAU (2x), trnK- UUU, trnL- CAA (2x), trnL-UAA, trnL-UAG, trnM-CAU, trnN-GUU (2x), trnP- UGG, trnQ- UUG, trnR- ACG (2x), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2x), trnV- UAC, trnW- CCA, trnY- GUA	trnA-UGC (2x), trnC- GCA, trnD- GUC, trnE- UUC, trnF- GAA, trnfM- CAU, trnG- UCC, trnH- GUG, trnI- CAU (2x), trnI-GAU (2x), trnK- UUU, trnL- CAA (2x), trnL-UAA, trnL-UAG, trnM-CAU, trnN-GUU (2x), trnP- UGG, trnQ- UUG, trnR- ACG (2x), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2x), trnV- UAC, trnW- CCA, trnY- GUA	trnA-UGC (2x), trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA, trnG-CAU, trnH-GUG, trnI-GAU (2x), trnK-UUU, trnL-CAA (2x), trnL-UAA, trnM-CAU, trnN-GUU (2x), trnP-UGG, trnQ-UUG, trnR-UUG, trnR-ACG (2x), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2x), trnV-UAC, trnW-CCA, trnY-GUA	trnA-UGC (2x), trnC- GCA, trnD- GUC, trnE- UUC, trnF- GAA, trnfM- CAU, trnG- UCC, trnH- GUG, trnI- CAU (2x), trnI-GAU (2x), trnK- UUU, trnL- CAA (2x), trnL-UAA, trnM-CAU, trnN-GUU (2x), trnP- UGG, trnQ- UUG, trnR- ACG (2x), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2x), trnV-UAC, trnW-CCA, trnY-GUA	trnA-UGC (2x), trnC- GCA, trnD- GUC, trnE- UUC, trnF- GAA, trnfM- CAU, trnG- UCC, trnH- GUG, trnI- CAU (2x), trnI-GAU (2x), trnK- UUU, trnL- CAA (2x), trnL-UAA, trnM-CAU, trnN-GUU (2x), trnP- UGG, trnQ- UUG, trnR- ACG (2x), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2x), trnV-UAC, trnW-CCA, trnY-GUA	trnA-UGC (2x), trnC- GCA, trnD- GUC, trnE- UUC, trnF- GAA, trnfM- CAU, trnG- UCC, trnH- GUG, trnI- CAU (2x), trnI-GAU (2x), trnK- UUU, trnL- CAA (2x), trnL-UAA, trnM-CAU, trnN-GUU (2x), trnP- UGG, trnQ- UUG, trnR- ACG (2x), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2x), trnV-UAC, trnW-CCA, trnY-GUA	trnA-UGC (2x), trnC- GCA, trnD- GUC, trnE- UUC, trnF- GAA, trnfM- CAU, trnG- UCC, trnH- GUG, trnI- CAU (2x), trnI-GAU (2x), trnK- UUU, trnL- CAA (2x), trnL-UAA, trnM-CAU, trnN-GUU (2x), trnP- UGG, trnQ- UUG, trnR- ACG (2x), trnR-UCU, trnS-GCU, trnS-GGA, trnS-UGA, trnT-GGU, trnT-UGU, trnV-GAC (2x), trnV-UAC, trnW-CCA, trnY-GUA

	Cytochrome b/f complex	petA, petB, petD, petG, petL, petN							
	ATP synthase	atpA, atpB, atpE, atpF, atpH, atpI							
Photosynthesis	NADH-dehydrogenase	ndhA, ndhB (2x), ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI, ndhJ, ndhK							
	Large subunit RUBISCO	rbcL							
	Acetyl-CoA carboxylase	accD							
	Cytochrome c biogenesis	ccsA							
	Maturase	matK							
Miscellaneous	ATP-dependent protease	clpP							
	Inner membrane protein	cemA							
Pseudogene unknown function	Conserved hypothetical chloroplast ORFs	ycf1, ycf2 (2x), ycf3, ycf4	ycf1, ycf2 (2x), ycf3, ycf4	ycf1, ycf2 (2x), ycf3, ycf4	ycf1 (3x), ycf2 (2x), ycf3, ycf4	ycf1 (3x), ycf2 (2x), ycf3, ycf4	ycf1 (3x), ycf2 (2x), ycf3, ycf4	ycf1 (2x), ycf2 (2x), ycf3, ycf4	ycf1 (2x), ycf2 (2x), ycf3, ycf4