

Table S1. Characterization of the mitogenome of selected genotypes of *C. picta* (457-1, S7) and *C. melanoneura* (498-2, AO282)

Region		<i>C. picta</i> (457-1, S7)			<i>C. melanoneura</i> (498-2)		<i>C. melanoneura</i> (AO282)		
		Start	End	Length [bp]	Start	End	Start	End	Length [bp]
trnI(gat)	Fw	1	66	66	1	66	1	66	66
trnQ(ttg)	Rev	71	136	66	71	136	71	136	66
trnM(cat)	Fw	142	205	64	142	207	142	207	66
ND2	Fw	206	1,177	972	208	1,179	208	1,179	972
trnW(tca)	Fw	1,176	1,237	62	1,178	1,240	1,178	1,240	63
trnC(gca)	Rev	1,240	1,302	63	1,243	1,305	1,243	1,305	63
trnY(gta)	Rev	1,303	1,365	63	1,306	1,367	1,306	1,367	62
COI	Fw	1,367	2,896	1,53	1,369	2,901	1,369	2,901	1,533
trnL2(taa)	Fw	2,896	2,959	64	2,901	2,965	2,901	2,965	65
COII	Fw	2,960	3,623	664	2,966	3,629	2,966	3,629	664
trnK(ctt)	Fw	3,624	3,693	70	3,630	3,699	3,630	3,699	70
trnD(gtc)	Fw	3,692	3,753	62	3,701	3,761	3,701	3,761	61
ATP8	Fw	3,754	3,903	150	3,762	3,914	3,762	3,914	153
ATP6	Fw	3,903	4,574	672	3,911	4,582	3,911	4,582	672
COIII	Fw	4,574	5,351	778	4,582	5,359	4,582	5,359	778
trnG(tcc)	Fw	5,352	5,409	58	5,360	5,419	5,360	5,419	60
ND3	Fw	5,410	5,760	351	5,420	5,77	5,420	5,770	351
trnA(tgc)	Fw	5,762	5,822	61	5,770	5,829	5,770	5,829	60
trnR(tcg)	Fw	5,827	5,887	61	5,840	5,900	5,840	5,900	61
trnN(gtt)	Fw	5,887	5,952	66	5,900	5,964	5,900	5,964	65
trnS1(gct)	Fw	5,953	6,006	54	5,965	6,018	5,965	6,018	54
trnE(ttc)	Fw	6,007	6,067	61	6,019	6,079	6,019	6,078	60
trnF(gaa)	Rev	6,056	6,118	63	6,068	6,13	6,067	6,129	63
ND5	Rev	6,119	7,736	1,618	6,131	7,748	6,13	7,747	1,618
trnH(gtg)	Rev	7,737	7,797	61	7,749	7,809	7,748	7,808	61
ND4	Rev	7,798	9,046	1,249	7,81	9,055	7,809	9,054	1,246
ND4l	Rev	9,040	9,327	288	9,049	9,336	9,048	9,335	288
trnT(tgt)	Fw	9,329	9,389	61	9,338	9,397	9,337	9,396	60
trnP(tgg)	Rev	9,390	9,452	63	9,398	9,463	9,397	9,462	66
ND6	Fw	9,455	9,940	486	9,466	9,951	9,465	9,950	486
CYTB	Fw	9,940	11,076	1,137	9,951	11,087	9,950	11,086	1,137
trnS2(tga)	Fw	11,078	11,141	64	11,091	11,153	11,09	11,152	63
GCCTA motif	Rev	11,153	11,157	5	11,165	11,169	11,164	11,168	5
ND1	Rev	11,169	12,083	915	11,181	12,095	11,18	12,094	915
trnL1(tag)	Rev	12,084	12,147	64	12,096	12,158	12,095	12,157	63
16S rRNA	Rev	12,148	13,304	1,157	12,159	13,31	12,158	13,309	1,152
trnV(tac)	Rev	13,305	13,366	62	13,311	13,373	13,310	13,372	63
12S rRNA	Rev	13,367	14,113	747	13,375	14,122	13,374	14,121	748
A+T rich	--	14,114	14,802	689	14,123	14,879	14,122	14,879	758, 757
polyT motif	--	14,532	14,551	20	14,606	14,628	14,607	14,629	23

Abbreviations used as follows: ND2 - NADH dehydrogenase subunit 2 , COI - cytochrome c oxidase subunit I, COII - cytochrome c oxidase subunit II, ATP8 - ATP synthase membrane subunit 8, ATP6 - ATP synthase membrane subunit 6, COIII - cytochrome c oxidase subunit III, ND3 - NADH dehydrogenase subunit 3, ND5 - NADH dehydrogenase subunit 5, ND4 - NADH dehydrogenase subunit 4, ND4L - NADH dehydrogenase subunit 4L, ND6 - NADH dehydrogenase subunit 6, ND1 - NADH dehydrogenase subunit 1, CYTB – cytochrom b, A+T rich – A+T rich control region, trn – tRNA (amino acids marked by IUPAC code); Fw – forward orientation, Rev- reverse orientation.