

Natural hybridization in heliconiine butterflies: the species boundary as a continuum

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Additional file 3 – Distance measures for mtDNA among species of Heliconiina

The figures given are for average uncorrected (raw) % divergence between pairs of species which overlap, or average divergences among individuals of the same species sampled. Based on 1569 bp of CoI/CoII mtDNA sequences (Beltran et al. 2006).

A. *Heliconius erato-sara* group

	Heliconius												KEY				
	ant	hew	con	eleu	sap	sar	leu	dem	ric	cha	per	era	him	cly	hor	hecs	tel
antiochus	1.35																
hewitsoni	x	0.00															
congener	x	x	x														
eleuchia	x	x	x	0.00													
sapho	6.77	x	x	7.73	0.32												
sara	5.90	5.77	7.19	7.48	6.80	0.78											
leucadia	7.35	x	x	x	x	x	5.87	x									
demeter	8.43	x	x	x	x	x	8.56	9.71	0.26								
ricini	7.80	x	x	x	x	x	7.96	x	x	x	0.39						
charithonia	x	x	x	x	x	x	7.37	x	x	x	x	0.60					
peruvianus	x	x	x	x	x	x	x	x	x	x	x	3.76	0.06				
erato	8.28	8.62	9.96	9.66	9.07	8.26	9.17	8.93	8.43	7.58	x	2.30					
himera	x	x	x	x	x	x	x	x	x	x	x	7.51	8.52	3.20	0.77		
clytostomus	x	x	x	x	x	x	x	x	x	x	x	7.12	x	7.08	x	0.64	
hortense	x	x	x	x	x	x	8.84	x	x	x	x	7.49	x	6.98	x	x	
hecalesia	x	x	x	9.90	9.19	8.38	x	x	x	x	x	7.54	x	5.74	x	7.22	
telesiphe	x	x	10.72	x	x	x	x	x	x	x	x	7.37	x	7.40	x	5.67	

KEY	
5.28	= Av. % divergence (uncorrected)
x	= no data available, or not sympatric
1.02	= intraspecific divergence
4.56	= interspecific divergence, hybrids known
6.55	= interspecific divergence

B. *Heliconius melpomene-cydno-silvaniform* group

C. Eueides species

procula	0.84							
vibilia	4.99	0.32						
pavana	x	2.87	x					
isabella	4.19	4.09	3.73	0.13				
lineata	5.35	6.73	x	6.12	x			
aliphera	5.54	6.47	6.09	5.80	6.86	0.13		
lybia	6.76	7.15	6.70	6.47	7.44	5.94	1.93	
tales	x	8.26	x	7.90	x	6.77	7.25	2.17
	proc	vib	pav	isa	lin	ali	lyb	tal
	Eueides							