

Table S2: Genetic distances (Kimura 2-parameter (K2P) model) between and within (grey) populations of *Megaloprepus* (all bold) and as a measure of gene flow between populations the F_{ST} -values (italics) are shown on the upper right. The analysis has been performed for 16S rRNA (Alignment 1: N = 49, 577 bp; Alignment 2: N = 39, 325 bp; Alignment 3: N = 145, 321 bp) and CO1 (Alignment 1: N = 61, 419 bp; Alignment 2: N = 29, 395 bp; Alignment 3: N = 135, 395 bp).

16S rRNA									COI*							
Alignment 1*		BCI	RBLT	LS	CAN	HN	NI	NI-b		BCI	CNP	RBLT	LS	CAN	NI	NI-b
	BCI	1.75	0.74*	0.61*	0.26	0.18	0.74*	0.28	BCI	0.07	/	/	/	/	/	/
	RBLT	5.56	0.58	0.93*	0.87	0.88	0.88*	0.85*	CNP	10.15	0.09	/	/	/	/	/
	LS	2.32	4.89	0.28	-0.33	0.93	0.89*	0.22	RBLT	9.38	10.46	0.54	/	/	/	/
	CAN	2.20	4.74	0.14	0.00	1.00	0.84*	0.00	LS	1.67	11.46	9.29	0.74	/	/	/
	HN	1.86	4.92	2.30	2.21	n/c	0.89	0.85	CAN	2.38	11.63	9.31	1.27	0.51	/	/
	NI	10.71	10.17	11.09	10.94	4.06	0.54	0.83*	NI	10.74	1.83	9.33	12.02	12.19	0.46	/
	NI-b	8.29	11.03	6.64	6.50	2.57	5.84	0.85	NI-b	1.71	11.19	9.01	0.75	0.64	11.78	0.76
Alignment 2		BCI	RBLT	LS	CAN	NI	NI-b		BCI	RBLT	LS	CAN	NI	NI-b	CNP	
	BCI	0.31	0.95*	0.86*	0.78	0.98*	0.82	BCI	0.17	0.98	0.85*	0.92	1.00*	0.88	0.99*	
	RBLT	4.89	0.00	0.96*	1.00	1.00*	1.00	RBLT	9.43	n/c	0.97	1.00	1.00	1.00	1.00	
	LS	1.95	5.45	0.08	-0.30	0.97*	0.12	LS	1.51	8.97	0.26	0.60	0.99	-1.00	0.99*	
	CAN	1.90	5.40	0.04	n/c	1.00	1.00	CAN	2.18	8.97	0.64	n/c	1.00*	1.00	1.00	
	NI	4.44	5.38	5.38	5.33	0.00	1.00*	NI	10.41	9.12	10.36	11.36	0.00	1.00	1.00*	
	NI-b	1.91	5.40	0.04	0.00	5.33	0.00	NI-b	1.38	8.97	0.13	0.77	11.36	n/c	1.00	
	CNP							CNP	10.02	10.50	10.96	10.96	1.56	10.96	0.00	
Alignment 3		BCI	RBLT	LS	CAN	NI	NI-b	CNP		BCI	RBLT	LS	CAN	NI	NI-b	CNP
	BCI	0.18	0.95*	0.85*	0.88	0.96*	0.87	0.97*	BCI	0.20	0.97*	0.92*	0.91	0.98*	0.86	0.99*
	RBLT	4.68	0.10	0.95*	0.97	0.98*	0.97	0.98*	RBLT	9.14	0.28	0.98*	0.96	0.98*	0.96	0.99*
	LS	1.81	5.22	0.06	0.40	0.96*	0.21	0.96*	LS	1.43	8.65	0.04	0.94	1.00*	-1.00	1.00*
	CAN	1.78	5.18	0.04	n/c	1.00	1.00	1.00*	CAN	2.21	8.65	0.75	n/c	1.00	1.00	1.00
	NI	4.53	5.16	5.45	5.40	0.00	1.00	0.99*	NI	10.44	9.07	11.36	11.36	0.00	1.00	1.00*
	NI-b	1.78	5.18	0.04	0.00	5.40	0.00	1.00*	NI-b	1.41	8.65	0.02	0.77	11.36	n/c	1.00
	CNP	4.54	5.18	5.10	5.06	1.30	5.06	0.02	CNP	10.06	10.44	10.96	10.96	1.56	10.96	0.00

* The F_{ST} -values for the CO1 Alignment 1 are missing as the alignment could not be analyzed in Arlequin.

** Sampling localities from north to south are: RBLT (Biosphere Reserve Los Tuxtlas, Veracruz, Mexico), HN (Cusuco National Park, Honduras), NI (El Jaguar reserve, Nicaragua), NI-b Biological Reserve Indio Maíz “Bartola Reserve”, Nicaragua, LS (Biological Research Station La Selva, Costa Rica), CNP (Corcovado National Park “Sirena Field Station”, Costa Rica), BCI (Barro Colorado Island, Panama) and CAN (Rio Canande Reserve, Esmeraldas Province, Ecuador).