

Electronic Supplementary Material

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Extremely low genetic diversity and weak population differentiation in the endangered Colombian river turtle *Podocnemis lewyana* (Testudines: Podocnemididae)

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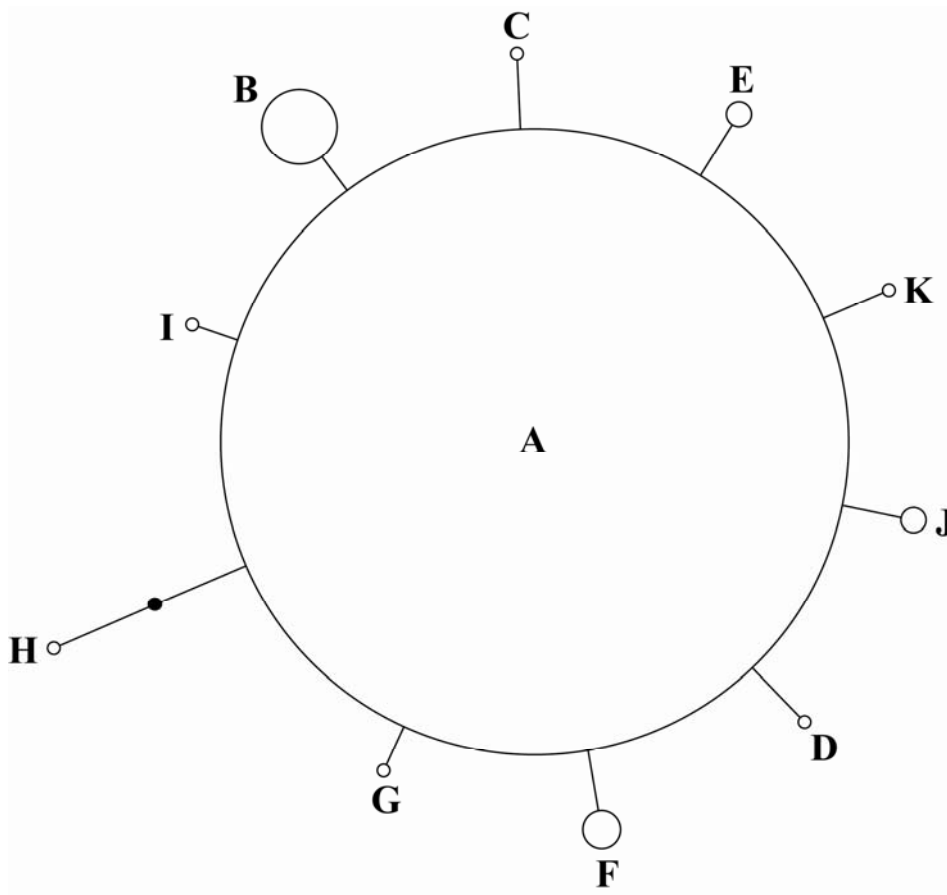


Fig. S1 Parsimony network for mtDNA haplotypes of *Podocnemis lewyana* (691 bp of control region). Circle size approximately reflects haplotype frequency. Missing haplotype, small black circle. Each line connecting haplotypes corresponds to one mutational step. Haplotype frequencies are A: $n = 100$; B: $n = 6$; F: $n = 3$; (E, J): $n = 2$; all other haplotypes were found only once

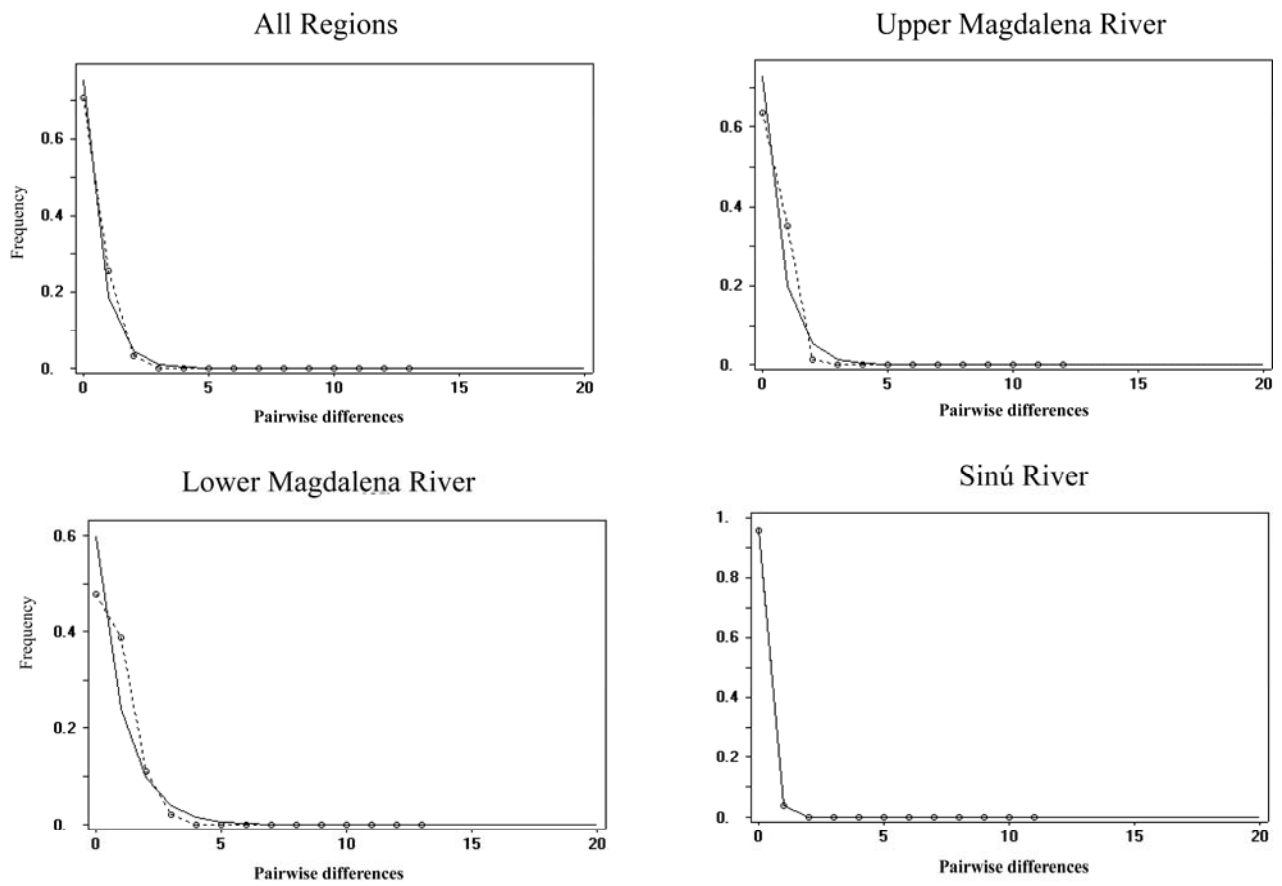


Fig. S2 Pairwise mismatch distributions for all regions together, the Upper and Lower Magdalena and Sinú River Basins. Dotted lines represent the observed frequencies of pairwise differences among haplotypes; solid lines, expected values for populations that experienced historical demographic expansion. The mismatch distributions for all regions lumped and for each region separately (San Jorge River and Lower Cauca River not shown) suggest population expansion

Table S1 Polymorphic microsatellite loci analyzed, number of alleles per locus, and allele size range. For Puni1B2, Puni1B10 and Puni2A9 only two alleles were found

Loci	Alleles	Allele size range
Puni1B2	2	319, 321
Puni1B10	2	205, 215
Puni1B11	5	242-266
Puni1F10	5	175-187
Puni2A9	2	125, 131
Puni2D9	12	194-230
Puni2C11	9	236-270
PE519	21	181-319
Sat62	7	171-205
Sat128	4	129-137
Total	69	125-321

Table S2 Pairwise F_{ST} values among *Podocnemis lewyana* regions calculated in ARLEQUIN using 10 microsatellite loci (below diagonal) and CR sequence fragments (mtDNA; above diagonal)

	I	II	III	IV	V	VI	VII
I – Upper Magdalena	—	0.074*	0.188	0.068	0.089	0.061	0.102
II – Lower Magdalena	0.101*	—	0.035	-0.022	0.011	-0.018	0.013
III – Lower Cauca	0.070*	-0.004	—	-0.098	0.284	0.270	0.433
IV – San Jorge	0.119*	0.014	-0.016	—	0.080	0.108	0.225
V – Lower Sinú	0.081*	0.084*	0.096	0.095	—	-0.031	0.002
VI – Middle Sinú	0.085*	0.045*	0.053	0.046	0.001	—	0
VII – Upper Sinú	0.093*	0.070*	0.063	0.075	0.018	0.005	—

F_{ST} values with asterisk are significantly different from zero

Table S3 Mean lnP(D) values for different K s, their standard deviations and ΔK values. Maximum values with asterisk

K	Mean lnP(D)	lnP(D) SD	ΔK
1	-2156.15	0.07	—
2	-2150.23	14.19	1.40
3	-2131.26*	8.90	3.28*
4	-2132.94	31.21	1.91
5	-2132.14	57.23	1.70
6	-2148.35	59.96	2.33
7	-2246.90	72.80	1.80
8	-2263.65	52.95	1.98
9	-2316.75	55.90	1.99
10	-2335.20	38.80	—

Table S4 Population assignment test performed with BAYESASS (assignment percentage)

Assigned from	Cluster								
	1 Upper Magdalena			2 Lower Magdalena + Lower Cauca + San Jorge			3 Sinú		
	No migrant	Migrant	Migrant's offspring	No migrant	Migrant	Migrant's offspring	No migrant	Migrant	Migrant's offspring
1	94.5	—	—	—	9.40	20.50	—	0.20	0.89
2	—	0.27	0.82	16.32	—	—	—	0.13	1.39
3	—	0.52	3.89	—	18.61	35.17	97.39	—	—

Table S5 Geographic distribution of control region haplotypes in *Podocnemis lewyana*.

The respective number of individuals is listed under each region

Haplotype	Region							Total
	I (Upper Magdalena)	II (Lower Magdalena)	III (Lower Cauca)	IV (San Jorge)	V (Lower Sinú)	VI (Middle Sinú)	VII (Upper Sinú)	
A	26	18	2	5	15	12	22	100
B	6	—	—	—	—	—	—	6
C	1	—	—	—	—	—	—	1
D	—	1	—	—	—	—	—	1
E	—	1	1	—	—	—	—	2
F	—	3	—	—	—	—	—	3
G	—	1	—	—	—	—	—	1
H	—	1	—	—	—	—	—	1
I	—	1	—	—	—	—	—	1
J	—	—	1	1	—	—	—	2
K	—	—	—	—	—	—	1	1
Total	33	26	4	6	15	12	23	119

Table S6 Polymorphic nucleotide positions for 11 haplotypes of *Podocnemis lewyana*

Haplotype	Nucleotide position (alignment of 691 bp)										
	92	177	204	221	433	452	474	490	506	527	568
A	A	A	G	C	G	G	A	T	A	G	G
B	A
C	T	.	.
D	.	.	A
E	A
F	G
G	G
H	.	G	A	.
I	A	.	.	.
J	A
K	.	.	.	T

Table S7 Using control region sequence data, mismatch distribution models, Tajima's D and Fu's F_S detect population expansion in populations of *Podocnemis lewyana*. The model of population expansion is significantly supported by a goodness-of-fit test (Rogers and Harpending 1992; Schneider and Excoffier 1999), Tajima's D (Tajima 1989), and Fu's F_S values (Fu 1997)

	I – Upper Magdalena	II – Lower Magdalena	III – Lower Cauca	IV – San Jorge	(V + VI + VII) – Sinú	ALL
Model parameters						
N	32	26	4	6	50	119
S	2	7	2	1	1	11
τ	0.471 (0.059-1.033)	0.721 (0.189-1.391)	1.273 (0-3.354)	0.445 (0-1.617)	3 (0.463-3)	3 (0.336-3.754)
θ_0	0 (0-0.181)	0 (0-0.083)	0 (0-2.528)	0 (0-0.004)	0 (0-0.002)	0 (0-0.011)
θ_1	99999 (7.564-99999)	99999 (4.996-99999)	99999 (1729-99999)	99999 (99869-99999)	0.043 (0-99999)	0.425 (0-99999)
Goodness-of-fit test						
SSD	0.007	0.002	0.113	0.003	0.00000152	0.00336
P	0.374*	0.652*	0.391*	0.920*	0.885*	0.553*
Tajima's D	-0.484	-1.937	-0.709	-0.933	-1.103	-2.137
P	0.332	0.008*	0.286	0.261	0.044*	0.001*
Fu's F_S	-0.437	-4.555	-0.887	-0.003	-1.636	-13.041
P	0.313	0.000001*	0.096	0.272	0.024*	0.00001*

N = sample size; S = number of segregating sites. Parameters of the model of population expansion: τ = age of expansion, θ_0 = population size before expansion and θ_1 = population size after expansion. When SSD values in the goodness-of-fit test for the mismatch distribution are non-significant ($P > 0.05$), the data do not deviate from the expectation of population expansion. Negative significant D and F_S values are expected when population expansion occurs. Non-significant SSD values and significant D and F_S values asterisked. The number of bootstrap replicates in the mismatch test was 1000