

% divergence (p-dist) within populations

	MAX	MIN	# haplotypes
EMI	-	-	1
API	0.2	-	2
CAK	3.6	0.2	6
KAI	10.3	0.2	5
TIG	0.8	0.2	4
BAR	1.3	0.3	4
SHN	1.8	0.2	4
TNTB	-	-	1
CAS	4.9	0.3	9
TNT1	10.3	0.2	11
TNT2	10.5	0.2	10
CAW	0.2	-	2
SVA	2.3	0.2	5
VEI	1.1	0.2	5
INI	2.3	-	2

Table S1. Intra-specific genetic diversity of *C. terranovus*: % of maximum and minimum p-distance values calculated among haplotypes from each population.

	EMI	API	CAK	KAI	TIG	BAR	SHN	TNTB	CAS	TNT1	TNT2	CAW	SVA	VEI	INI
EMI	-														
API	66.50	-													
CAK	11.17	66.17	-												
KAI	71.00	18.10	70.40	-											
TIG	68.00	9.50	67.67	17.70	-										
BAR	65.75	10.00	65.42	18.00	5.50	-									
SHN	88.75	58.50	87.08	51.10	60.62	61.12	-								
TNTB	74.00	43.50	74.83	48.80	46.00	44.75	65.50	-							
CAS	89.00	59.28	87.35	51.33	61.67	61.94	11.42	63.89	-						
TNT1	84.54	55.14	83.35	50.96	57.59	57.57	26.09	45.00	26.89	-					
TNT2	83.10	53.60	82.23	50.94	56.25	56.05	32.45	39.20	32.96	31.91	-				
CAW	64.50	4.00	64.17	17.30	10.00	8.87	60.50	43.50	60.83	56.41	54.60	-			
SVA	89.60	60.90	88.07	52.44	63.50	63.40	9.90	61.20	11.89	22.93	28.58	62.10	-		
VEI	89.90	59.90	88.33	50.24	62.60	62.00	10.30	62.20	9.93	24.93	30.26	60.30	8.04	-	
INI	91.50	59.50	89.83	52.50	63.00	63.50	12.00	62.20	12.22	26.00	31.50	61.50	11.70	9.80	-

Table S2. Matrix of average nucleotide differences among populations. Abbreviation used in the text as in Table I.

Haplotypes	# of haplotype sequences
Cluster 1 B, D, E, F, H, L, M, N, P, Q, V, W, X, Y, Z, AI, AJ, AT, AS, AU, AV, AW, AY, AZ, BB, BC, BL, BM, BN and BO	56
Cluster 2 AK, AL, AM, AN, AO, AP, AQ, AR, BH, BI, BJ, BK, BD, BE, BF and BG	49
Cluster 3 AA, AB, AC, AD, AE, AF and AG	20
Cluster 4 C, G, O, AH, AX and BA	13
Cluster 5 A, I, J, K, R, S, T and U	26
	total 164

Table S3. List of haplotypes observed in the *C. terranovus* populations grouped according to the Bayesian clustering method.