

Population	marker	sequences	polymorphisms	haplotypes	π	θ from π	Tajima's D	Tajima's D p-value	ANNUAL MEAN TEMP (°C)	generations/a	average distance to ancestral haplotype
MF	COI	185	12	13	0.00083	0.00083	-2.10749	< 0.05	11.01	9.07	0.0007148
MG	COI	104	8	11	0.00174	0.00174	-1.5315	ns	9.74	7.85	0.00087831
NB2	COI	6	0	1	0	0	na	na	9.91	7.44	0
NG	COI	10	1	2	0.00036	0.00036	-1.11173	ns	8.50	6.43	0.00017575
NMF	COI	50	5	6	0.00069	0.00069	-1.73932	ns	9.87	7.70	0.00040175
SB	COI	31	0	1	0	0	na	na	10.19	8.91	0
SBKP	COI	11	1	2	0.00093	0.00093	-1.1285	ns	8.80	7.30	0.00078466
SI	COI	33	0	1	0	0	na	na	12.06	10.57	0.00014569
SP160	COI	27	5	5	0.00297	0.00298	0.32451	ns	14.73	12.66	0.00369836
SP164	COI	19	5	5	0.00285	0.00286	0.50054	ns	13.72	11.40	0.0041355
SP194b	COI	21	7	7	0.00474	0.00477	0.18576	ns	13.30	10.80	0.00422067
SP235	COI	30	7	6	0.00295	0.00296	-0.22533	ns	13.72	11.40	0.00385777
SP71	COI	34	5	6	0.00245	0.00246	0.32752	ns	15.77	14.15	0.00250389
SP75	COI	35	5	5	0.00218	0.00219	-0.1323	ns	15.41	13.61	0.00282366
SP8A	COI	31	7	7	0.00311	0.000312	0.03321	ns	14.72	12.65	0.00275525
SSA	COI	63	9	10	0.00137	0.00138	-1.66641	ns	16.59	15.02	0.00137703
SSB	COI	88	8	8	0.00168	0.00169	-1.40147	ns	16.47	14.86	0.00108912
STC	COI	19	0	1	0	0	na	na	9.48	7.99	0

statistics of COI data

Ordinary Least Squares Regression: A-B

Slope a: 0.00 Std. error a: 0.00010789
Intercept b: -0.0016548 Std. error b: 0.0013843

95% bootstrapped confidence intervals (N=1999):
Slope a: (7.1295E-05, 0.00038657)
Intercept b: (-0.0033187, 0.00031898)

Correlation:
r: 0.51491
r2: 0.26513
t: 2.3263
p (uncorr.): 0.034425
Permutation p: 0.0359

Population	marker	sequences	polymorphisms	haplotypes	π	θ from π	Tajima's D	Tajima's D p-value	ANNUAL MEAN TEMP (°C)	generations/a	average distance to ancestral haplotype
MF	L44	348	17	25	0.00254	0.00255	-1.2708	ns	11.01	9.07	0.00165484
MG	L44	44	10	13	0.00311	0.00312	-1.11771	ns	9.74	7.85	0.00181465
NB2	L44	12	7	6	0.00439	0.00442	0.00035	ns	9.91	7.44	0.00
NG	L44	16	3	5	0.00241	0.00242	1.13586	ns	8.50	6.43	0.00173813
NMF	L44	110	8	7	0.00105	0.00105	-1.69836	ns	9.87	7.70	0.00181418
SB	L44	64	0	1	0	0	na	na	10.19	8.91	0.00027844
SI	L44	38	9	18	0.00653	0.00659	1.0259	ns	12.06	10.57	0.00398105
SSA	L44	92	10	13	0.00423	0.00425	0.26756	ns	16.59	15.02	0.00338913
SSB	L44	160	15	18	0.00345	0.00347	-1.1137	ns	16.47	14.86	0.00347038
SP194b	L44	78	3	5	0.00181	0.00182	1.07954	ns	13.30	10.80	0.00099
STC	L44	20	0	1	0	0	na	na	9.48	7.99	0.000198

statistics of L44 data

Ordinary Least Squares Regression: D-E

Slope a: 0.00027731 Std. error a: 0.00021922
Intercept b: -0.00050536 Std. error b: 0.0025991

Correlation:
r: 0.38854
r2: 0.15096
t: 1.265
p (uncorr.): 0.23764
Permutation p: 0.2474

Population	marker	sequences	polymorphisms	haplotypes	π	θ from π	Tajima's D	Tajima's D p-value	ANNUAL MEAN TEMP (°C)	generations/a	average distance to ancestral haplotype
MF	PMCA3-E4	44	3	4	0.00196	0.00197	-1.64246	ns	11.01	9.07	0.00207905
MG	PMCA3-E4	40	10	11	0.00228	0.00229	-0.70539	ns	9.74	7.85	0.00358099
NB2	PMCA3-E4	12	3	4	0.00247	0.00247	-0.12836	ns	9.91	7.44	0.00292065
NG	PMCA3-E4	14	2	3	0.0009	0.0009	-1.45138	ns	8.50	6.43	0.00306777
NMF	PMCA3-E4	38	5	7	0.00247	0.00248	-0.9273	ns	9.87	7.70	0.00313993
SB	PMCA3-E4	48	1	2	0.00202	0.00202	1.33417	ns	10.19	8.91	0.00221336
SSA	PMCA3-E4	44	6	7	0.00224	0.00225	-0.62046	ns	16.59	15.02	0.00433546
SSB	PMCA3-E4	48	2	4	0.00309	0.0031	1.50191	ns	16.47	14.86	0.00504609
SP194b	PMCA3-E4	70	9	9	0.00099	0.00099	-1.57174	ns	13.30	10.80	0.00627161

statistics of PMCA3-E4 data

Ordinary Least Squares Regression: B-C

Slope a: 8.35E-05 Std. error a: 8.31E-05

Intercept b: 0.0010724 Std. error b: 0.0010031

Correlation:

r: 0.35511

r2: 0.1261

t: 1.005

p (uncorr.): 0.34835

Permutation ρ : 0.3449

ns - not significant na - not available

calculated in DnaSP v5.10.01

(Librado, P. & Rozas, J. 2009 DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. Bioinformatics 25: 1451-1452)