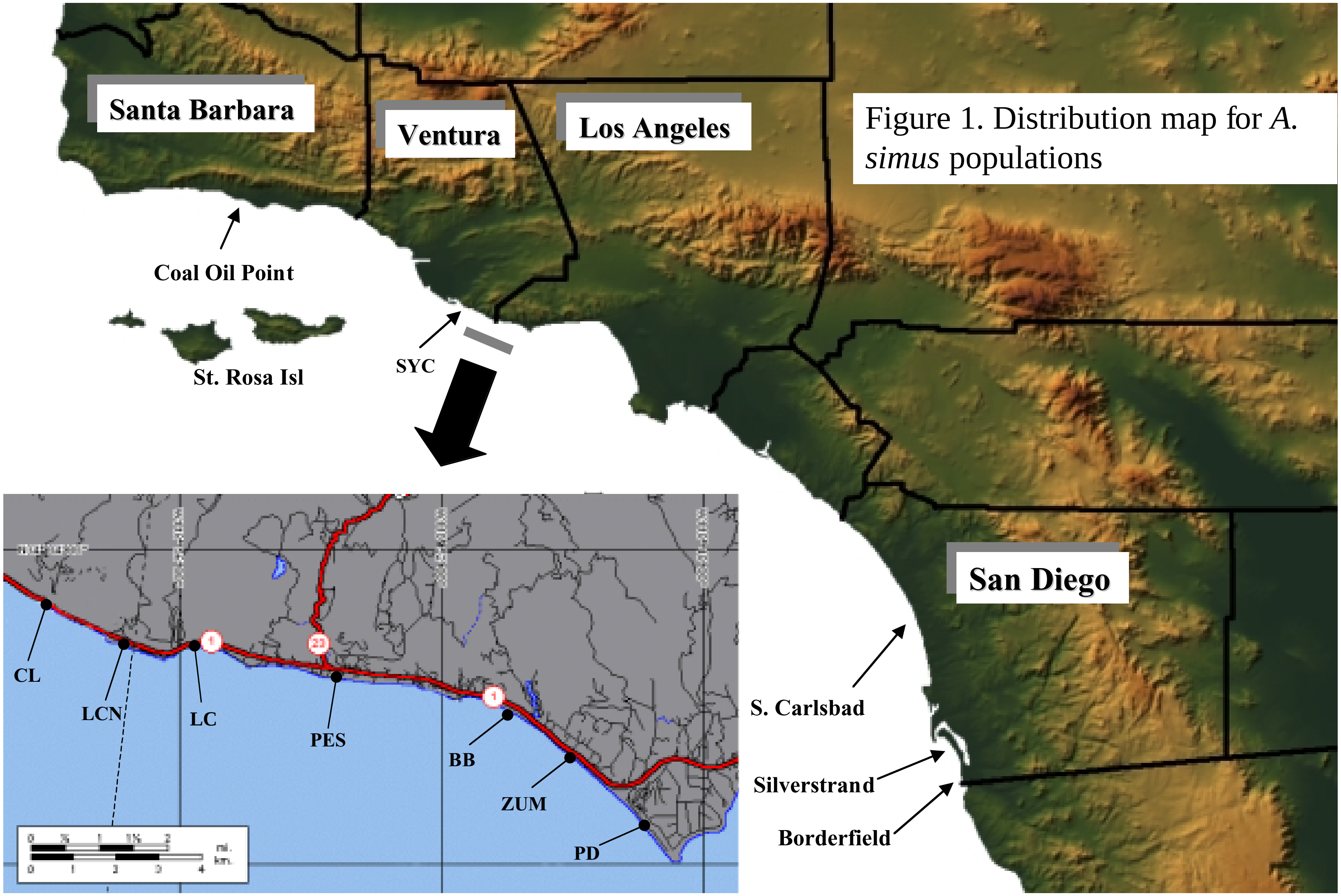

Figure 1. Distribution map for *A. simus* populations

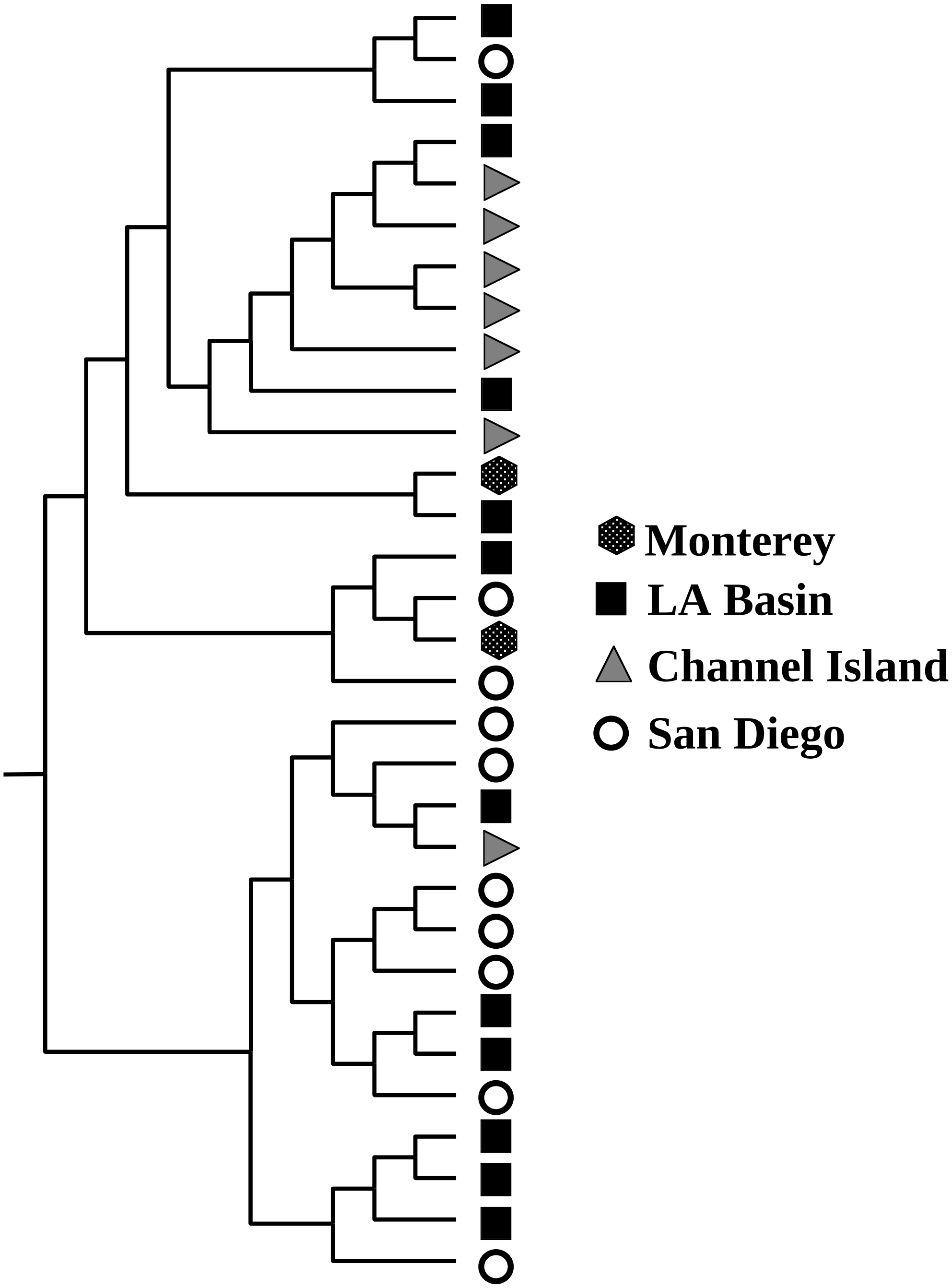

Figure 2. Dendogram of individuals sampled from each colineal haplotype array evaluated on the basis of a UPGMA cluster analysis using 12 morphological features.

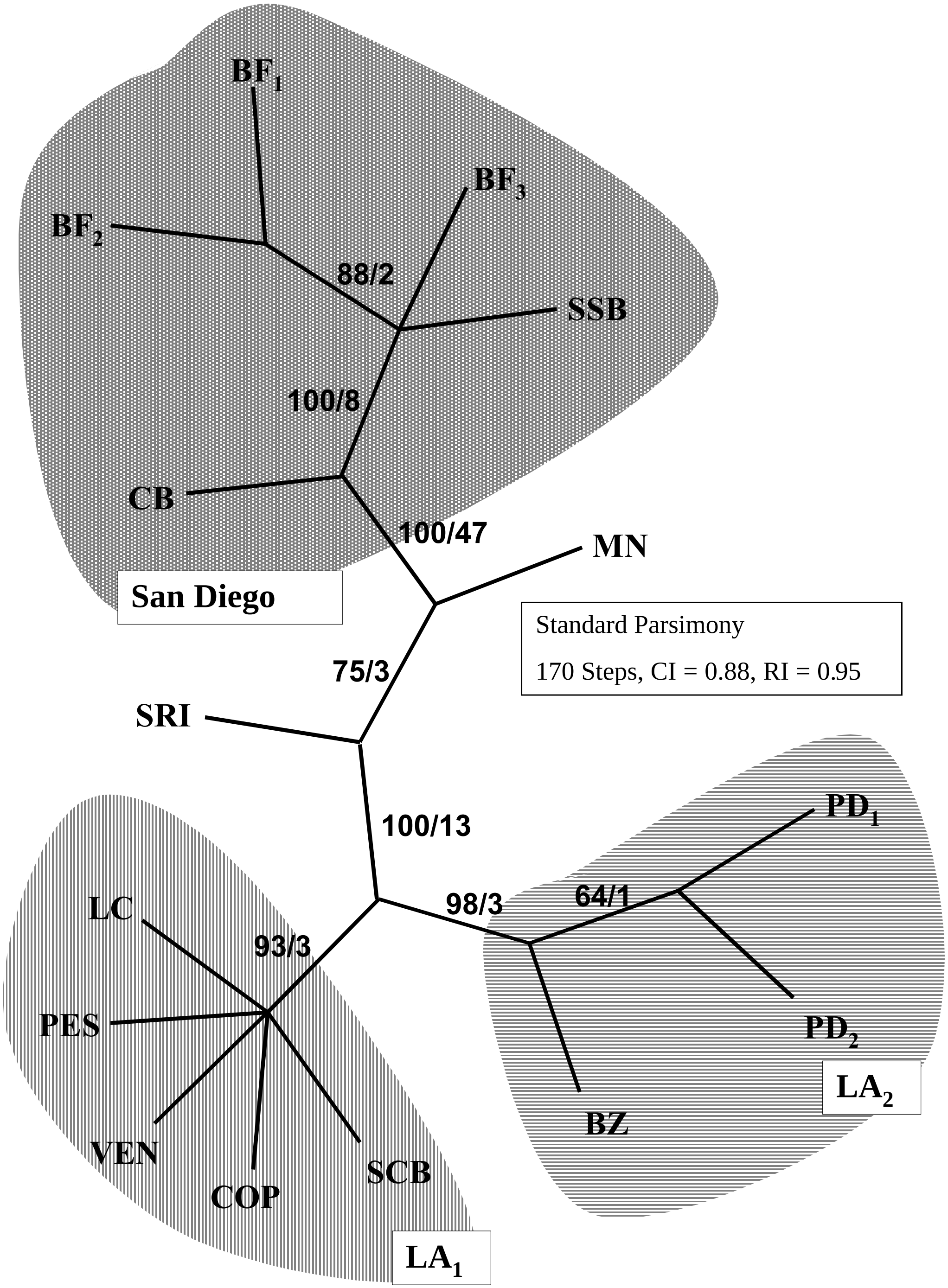

Figure 3. Unrooted strict consensus tree from maximum parsimony analysis of 765 bp of 16S rRNA. Bootstrap and decay values are indicated at each node (bootstrap/decay).

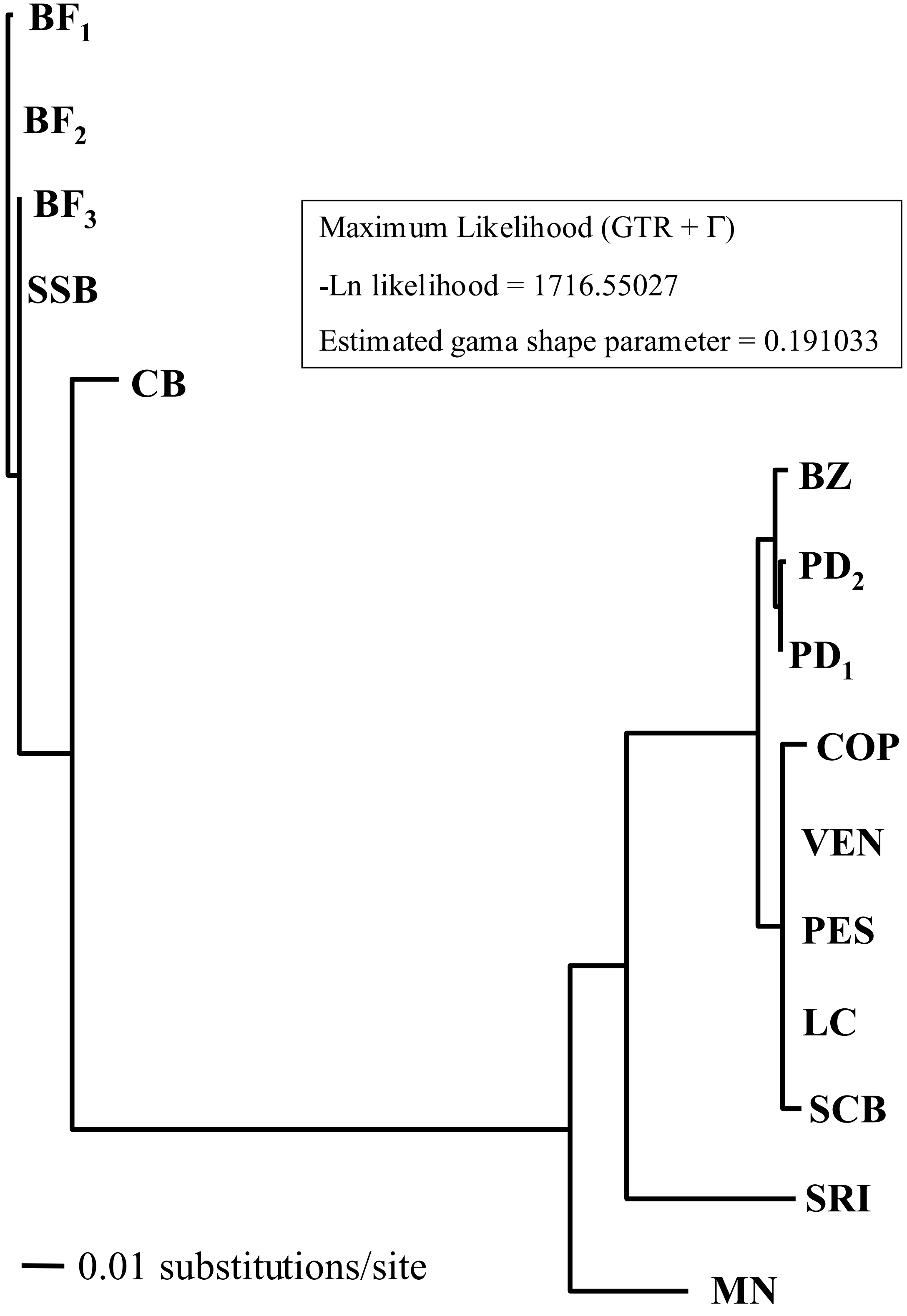

Figure 4. Maximum likelihood phylogeny estimate base on a general time reversible model of nucleotide substitution.

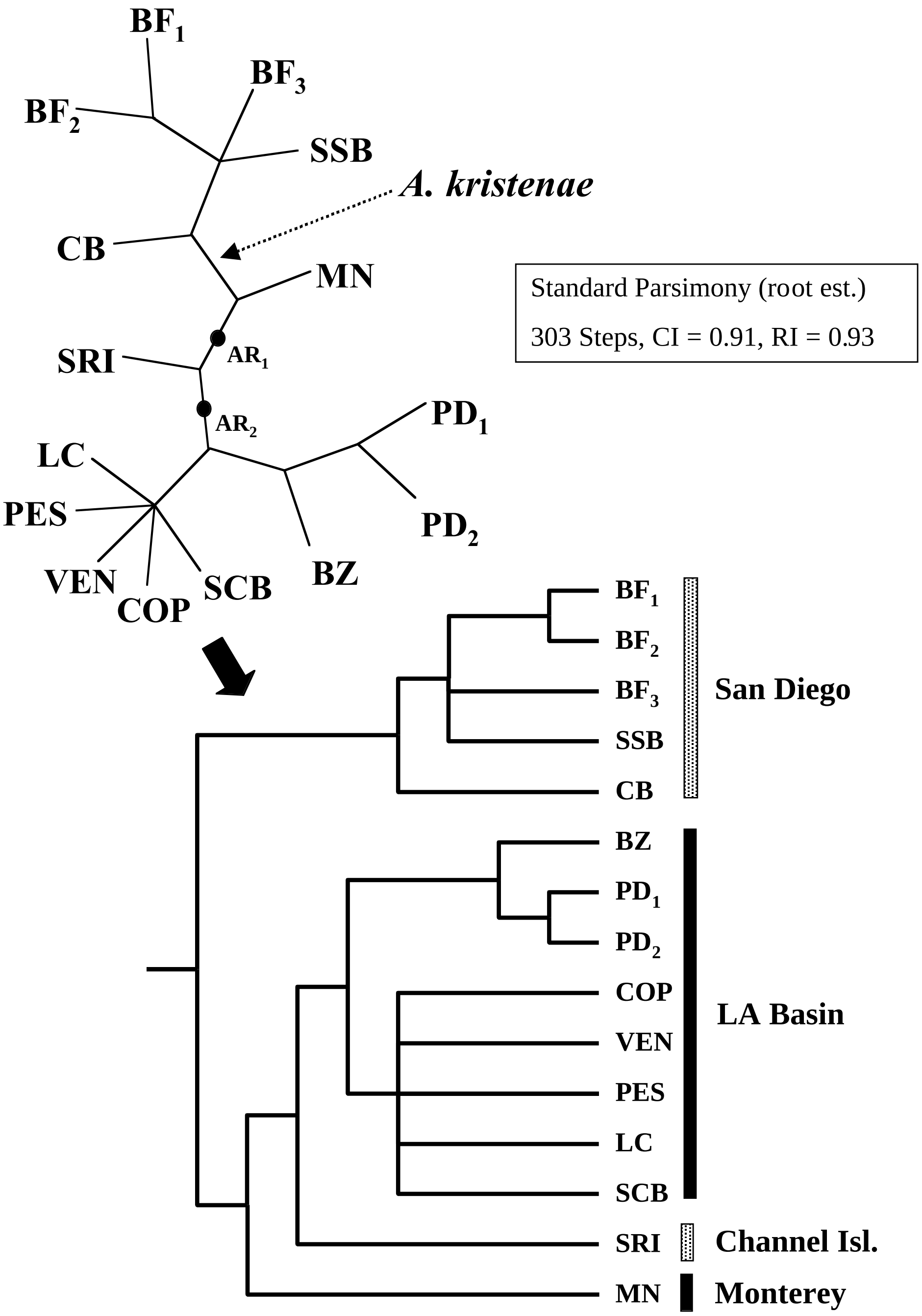

Figure 5. Estimation of *Aptostichus simus* population haplotype network root, top inset shows alternative root placement considerations (see Tbl. 5).

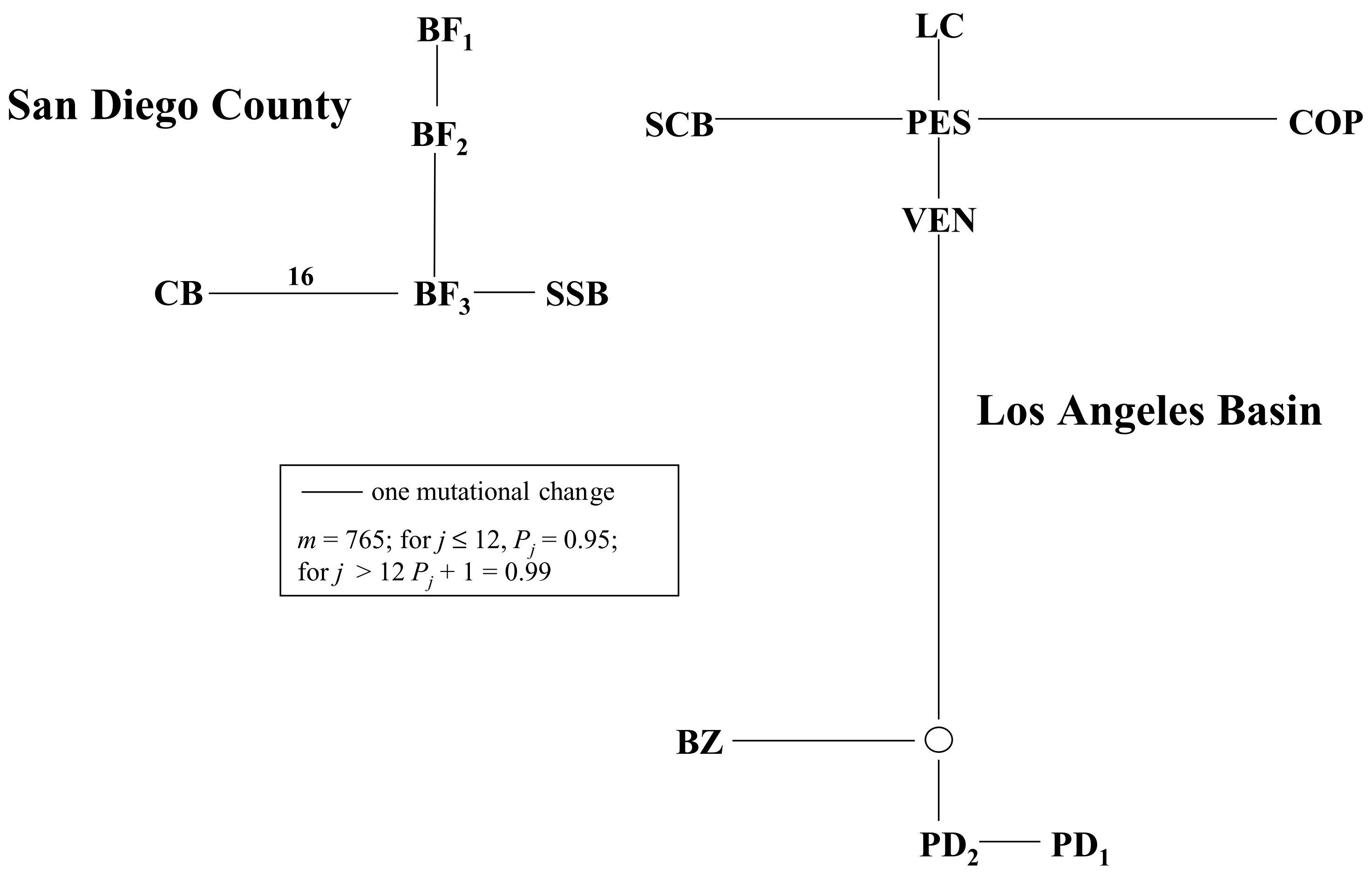

Figure 6. TCS algorithm estimation of haplotype relationships within the San Diego County and LA Basin areas.

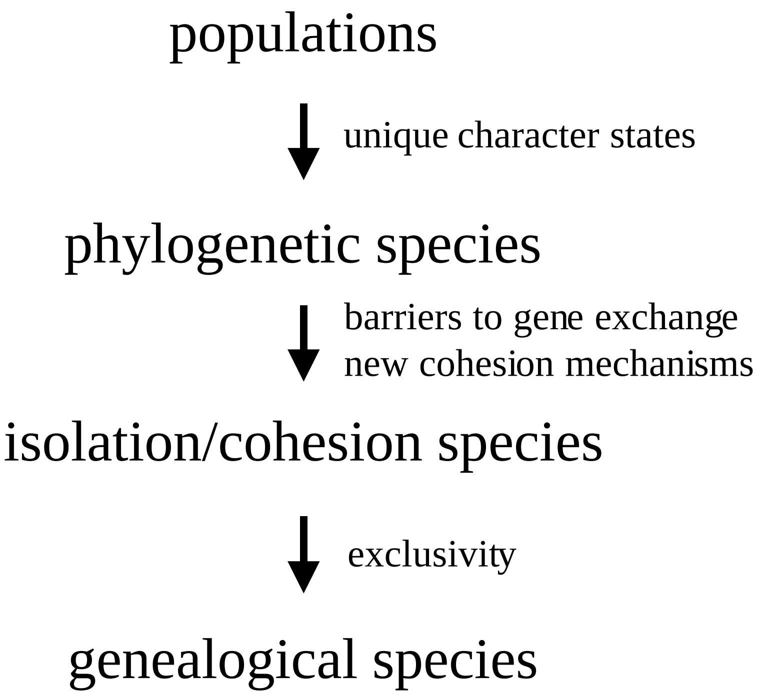

Figure 7. Speciation life history diagram from Harrison (1998)

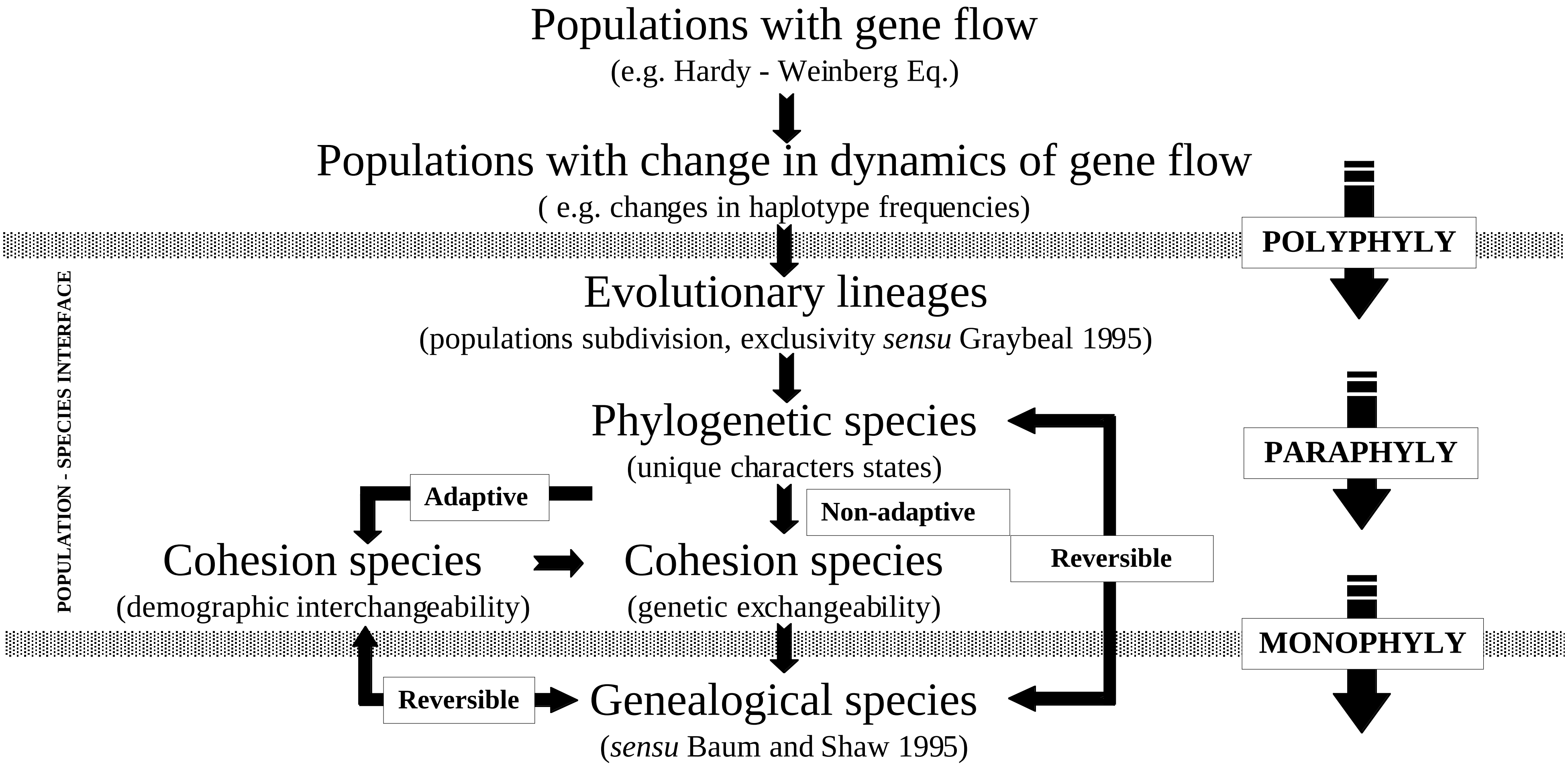

Figure 8. Species life history diagram modified to include the components of the Templeton's Cohesion Species Concept.

Table 1. List of sample acronyms, haplotypes, localities, and Genebank Accession numbers for all of the populations sampled in this study.

Acronym (N) Haplotype*	**Locality**	**Latitude Longitude**	**Genebank Accession #**
Northern			
MLB (4) MN	CA: Monterey County: Moss Landing State Beach	N 36° 48.52' W 121° 47.31'	
SRB (4) MN	CA: Monterey County: Salinas River State Beach	N 36° 47.435' W 121° 47.48'	
Los Angeles Basin			
COP (7)	CA: Santa Barbara County: Coal Oil Point Preserve, UC Santa Barbara	N 34° 24.51' W 119° 52.76'	
SCB (5)	CA: Ventura County: Sycamore Cove Beach	N 34° 4.23' W 119° 0.91'	
CLB (5) VEN	CA: Ventura County: County Line Beach	N 34° 3.14' W 118° 57.8'	
LCN (5) VEN	CA: Ventura County: Staircase Beach	N 34° 2.76' W 118° 56.74'	
LC (5)	CA: Los Angeles County: Leo Carrillo State Beach	N 34° 2.63' W 118° 56.32'	
PES (5)	CA: Los Angeles County: El Pescador State Beach	N 34° 2.38' W 118° 53.71'	
BB (5) VEN & BZ	CA: Los Angeles County: Broad Beach	N 34° 1.99' W 118° 50.95'	
ZUM (5) BZ	CA: Los Angeles County: Zuma Beach County Park	N 34° 1.32' W 118° 49.9'	
PD (5)	CA: Los Angeles County: Point Dume State Beach	N 34° 0.57' W 118° 48.96'	
Island			
SRI (5)	CA: Santa Barbara County: Santa Rosa Island	N 34° 0.23' W 120° 14.14'	
Southern			
CB (3)	CA: San Diego County: South Carlsbad State Beach	N 33° 6.23' W 117° 19.16'	
SSB (3)	CA: San Diego County: Silverstrand Stand State Beach	N 32° 37.33' W 117° 8.23'	
BF (3)	CA: San Diego County: Borderfield State Beach	N 32° 32.46' W 117° 7.50'	

*Haplotype given only if haplotype designation different than locality designation, see Table () for additional details.

Table 2. Morphometric values, means and standard errors, for each of the *Aptostichus simus* haplotypes. CARw = carapace width, CEPHw = cephalic region width, STERNl, w = sternum length and width, LABl, w = labium length and width. All ratio values are multiplied by 100.

Haplotype (N)	**Carapace len. (mm)**	**CARw/ CEPHw**	**STERNl/ STERNw**	**SIG/ STERNw**	**LABl/ LABw**	**Leg I len. (mm)**	**Labial cuspules**	**Endite cuspules**	**Rastellar spines**	**Cheliceral dentition**	**Patella III spines**	**Tibia III spines**
Channel Island (7)	6.30 ±0.35	149.08 ±0.96	83.96 ±0.79	23.67 ±1.20	69.31 ±1.29	43.66 ±0.60	0.14 ±0.14	~200 ±0	11.28 ±0.36	4.43 ±0.20	17.57 ±0.43	6.43 ±0.61
LA Basin (12)	6.59 ±0.25	148.71 ±1.07	88.00 ±0.97	22.48 ±1.17	70.86 ±1.49	43.43 ±0.49	0	~200 ±0	11.25 ±0.35	4.08 ±0.08	22.17 ±1.17	6.00 ±0.39
Monterey (2)	5.69 - 6.25	148.00 - 152.81	91.00 - 91.01	20.37 - 27.47	66.67 - 76.39	41.83 - 48.18	0	~200 ±0	10 - 11	4	15 - 16	2 - 3
San Diego (10)	7.81 ±0.24	147.26 ±0.94	89.04 ±1.38	16.84 ±1.05	67.51 ±1.28	45.20 ±1.28	0	~200 ±0	13.18 ±0.42	4.27 ±0.14	22.18 ±1.02	5.36 ±0.58

Table 3. *Aptostichus simus* haplotype pairwise distances based on 16S rRNA sequences. Uncorrected proportional differences above the diagonal, absolute number of nucleotide differences below.

Hap*	BFB$_1$	BFB$_2$	BFB$_3$	SSB	CB	BZ	COP	VEN	PES	LC	MN	PD$_1$	PD$_1$	SRI	SCB
BFB$_1$	--	0.001	0.004	0.005	0.025	0.117	0.122	0.115	0.116	0.118	0.110	0.115	0.113	0.126	0.118
BFB$_2$	1	--	0.003	0.004	0.024	0.116	0.120	0.113	0.115	0.116	0.108	0.113	0.112	0.125	0.116
BFB$_3$	3	2	--	0.001	0.021	0.115	0.118	0.111	0.112	0.114	0.106	0.112	0.111	0.122	0.114
SSB	4	3	1	--	0.023	0.116	0.119	0.112	0.114	0.112	0.107	0.113	0.112	0.121	0.115
CB	19	18	16	17	--	0.117	0.120	0.113	0.115	0.116	0.104	0.115	0.113	0.119	0.116
BZ[1]	88	87	86	87	88	--	0.020	0.013	0.015	0.016	0.059	0.005	0.004	0.065	0.019
COP	91	90	88	89	90	15	--	0.007	0.005	0.007	0.065	0.020	0.019	0.067	0.009
VEN[1]	86	85	83	84	85	10	5	--	0.001	0.003	0.061	0.013	0.012	0.065	0.005
PES	87	86	84	85	86	11	4	1	--	0.001	0.060	0.015	0.013	0.064	0.004
LC	88	87	85	84	87	12	5	2	1	--	0.061	0.016	0.015	0.063	0.005
MN[3]	82	81	79	80	78	44	49	46	45	46	--	0.061	0.060	0.061	0.064
PD$_1$	86	85	84	85	86	4	15	10	11	12	46	--	0.001	0.063	0.019
PD$_2$	85	84	83	84	85	3	14	9	10	11	45	1	--	0.064	0.017
SRI	94	83	91	90	89	49	50	49	48	47	46	47	48	--	0.065
SCB	88	87	85	86	87	14	7	4	3	4	48	14	13	49	--

*****Haplotype; [1]BZ = BB$_1$ and ZUM; [2]VEN (Ventura County) = BB$_2$, LCN and CLB; [3]MN (Monterey County) = MLB and SRB

Table 4. Maximum likelihood and likelihood ratio test values are given for each of the models of molecular evolution examined by Modeltest (Posada and Crandall *in press*). Likelihood ratio test values that test a molecular clock hypothesis are also reported here.

Substitution Model	**d.f.**	**H_O Model -Ln**	**H_A Model -Ln**	**Lrt Probability**
Equal base frequencies	3	Jukes Cantor 1969 (JC) 1921.449	Felsenstein 1981 (F81) 1800.750	$P < 0.000001$
Equal ti/tv	1	F81	Hasegawa et al. 1985 (HKY) 1760.319	$P < 0.000001$
Equal ti, equal tv	4	HKY	General Time Reversible* (GTR) 1738.735	$P < 0.000001$
Equal rates	1	GTR	GTR + Γ (gamma distribution) 1716.474	$P < 0.000001$
Invariant sites	1	GTR + Γ	GTR + Γ + I (invariant sites) 1716.334	n.s.**
Molecular Clock	13	M_{CLOCK} 1728.629	$M_{NO\text{-}CLOCK}$ 1716.550	n.s.***

*Rodríguez et al 1996

**not significant, $P > 0.50$

***not significant, $P > 0.02$

Table 5. Templeton Wilcoxon Rank - Sum (TWR) and Kishino - Hasegawa (KH) tests used to statistically examine alternative root assignments (Fig. 4)

Root	**Tree Score: MP** **ML**	**N**	**Statistic: TWR** **KH**	**P value: TWR** **KH**
Optimal	303 steps	--	--	--
	-Ln = 2156.40504			
AR_1	310 steps	11	T = 12	0.017
			T = 2.1157	0.017
	-Ln = 2308.78764		T = 9.1664	< 0.00005
AR_2	314 steps	17	T = 27	0.0038
			T = 2.6795	0.0037
	-Ln = 2340.43453		T = 9.2820	< 0.00005

Table 6. Summary of some recent intra and interspecific molecular phylogenetic studies in arthropods.

Citation	**Taxonomic Level**	**MtDNA gene(s)**	**Taxon**	**Range of Divergence**
Aubert *et al.* 1999	Interspecifc	16SrRNA & ND1	Papilionidae: Lepidoptera	0.5 - 8.0%
Taylor *et al.* 1998	Intraspecific (North America)	16S rRNA	*Daphnia laevis*	5 - 8%
Hedin 1997	Intra & interspecific	ND1	*Nesticus* (Nesticidae: Araneae)	Intra: ≤ 7% Inter: 8.2 - 13%
Chiba 1999	Intra & interspecific	16S rRNA	*Mandarina* (Land Snails)	Intra: 0 - 10% Inter: 5.8 - 16.5%
Wilcox *et al.* (1997)	Intraspecific	COI	*Cordylocherncs scorpioindes* (Pseudoscorpiones)	2.6 - 13.8%
Juan *et al.* 1995	Interspecfic	COI	*Pimelia* (Tenebrionidae: Coleoptera)	2.2 - 21.2%
Schneider - Broussard *et al.* (1998)	Intraspecific	16S rRNA	*Menippe* (Stone Crabs)	0 - 1.7%
Baric & Sturmbauer (1999)	Intraspecific	16s rRNA	*Opiothrix* (Echinodermata: Ophiuroidea)	9.0 - 12%
Han & McPheron 1997	Interspecific	16S rRNA	Tephritidae (Insecta: Diptera)	3 - 18%

Table 7. Pairwise geographical distances (terrestrial) between all populations in the LA Basin haplotype network.

LOCALE	SCB	CL	LCN	LC	PES	BB	ZUM	PD	COP
SCB	--	5.21	7.05	8.47	11.88	15.95	17.74	19.75	88.09
CL		--	1.81	3.31	6.79	10.71	12.71	14.52	93.30
LCN			--	1.58	5.06	9.03	10.94	12.64	95.14
LC				--	3.39	7.46	9.42	11.24	96.56
PES					--	4.04	5.97	7.91	99.97
BB						--	3.12	4.12	104.4
ZUM							--	2.06	105.83
PD								--	107.84
COP									--