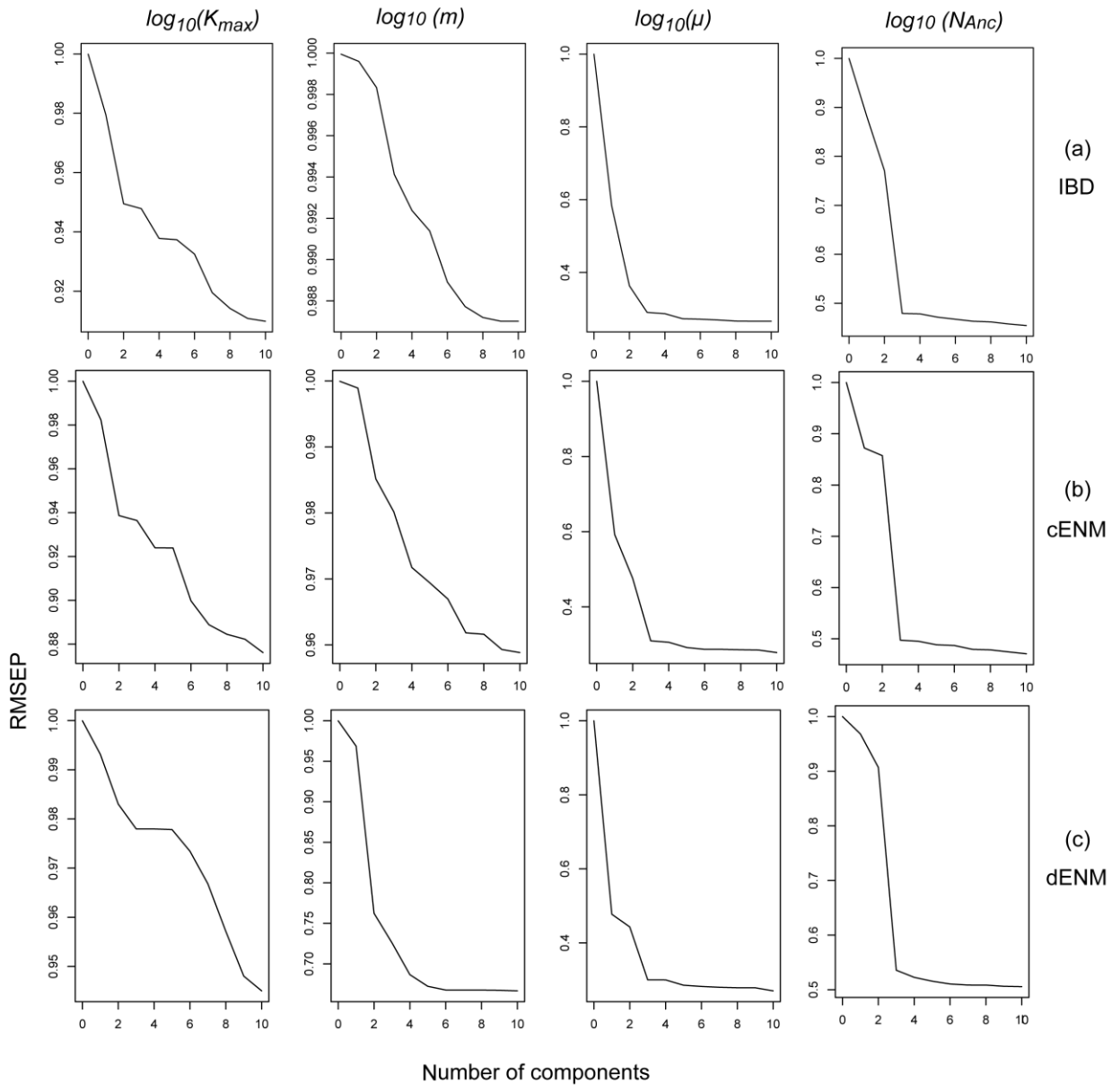
Supplemental Materials:



Supplemental Figure 1. Root Mean Square Error (RMSE) of parameter estimation against number of PLSs included under four demographic models: a) IBD, b) cENM, and c) dENM.

Supplemental Table 1. Geographic locations of sampled individuals and their assigned population (see Fig. 1 for distributional details).

ID#	LAT	LONG	POP
LL40	-21.7833	114.1833	CB
LL90	-21.8833	114.0167	CB
LL118	-22.4025	113.8433	CB
LL19	-22.6833	114.05	CB
LL21	-22.6833	114.05	CB
LL69	-22.6833	113.9833	CB
LL151	-23.1466	113.7764	CB
LL150	-23.1477	113.7761	CB
LL15	-23.8833	113.4833	C
LL135	-24.1383	113.4458	C
LL34	-24.1383	113.4458	C
LL49	-24.1383	113.4458	C
LL128	-24.1833	113.45	C
LL134	-24.1833	113.45	C
LL137	-24.1833	113.45	C
LL133	-24.193	113.4553	C
LL38	-24.193	113.4553	C
LL48	-24.223	113.4914	C
LL50	-24.223	113.4914	C
LL142	-25.1155	113.7292	C
LL64	-25.1155	113.7292	C
LL65	-25.1155	113.7292	C
LL35	-25.1258	113.8228	C
LL63	-25.1258	113.8228	C
LL141	-25.1316	113.7681	C
LL25	-25.1316	113.7681	C
LL36	-25.1316	113.7681	C
LL62	-25.1341	113.8056	C
LL43	-25.8205	113.5392	P
LL32	-25.8388	113.6064	P
LL33	-25.8388	113.6064	P
LL98	-25.8541	113.8625	P
LL148	-25.85417	113.8625	P
LL37	-25.8752	113.5503	P
LL149	-25.97538	113.57049	P
LL71	-25.9833	113.6	P
LL143	-26.25	113.8	P
LL144	-26.25	113.8	P
LL145	-26.26667	113.78333	P
LL146	-26.26667	113.78333	P
LL12	-26.4333	114.0667	P
LL39	-26.4333	114.0667	P
LL45	-26.4894	114.0556	P
LL47	-26.4894	114.0556	P
LL52	-26.5225	114.0025	P

LL53	-26.5225	114.0025	P
LL44	-26.5463	113.9633	P
LL54	-26.5463	113.9633	P
LL72	-26.5666	114	P
LL70	-25.9333	113.1667	SB
LL126	-26	113.2	SB
LL05	-26.0333	113.2	SB
LL06	-26.0333	113.2	SB
LL07	-26.0333	113.2	SB
LL87	-26.3333	113.3833	SB
LL76	-26.3833	113.3167	SB
LL77	-26.3833	113.3167	SB
LL78	-26.3833	113.3167	SB
LL79	-26.3833	113.3167	SB
LL89	-26.3833	113.3167	SB
LL74	-26.4666	113.4667	SB
LL75	-26.4666	113.4667	SB
LL107	-26.7	113.6667	SB
LL73	-27.0116	114.4	ZU
LL28	-27.2591	114.0675	ZU
LL29	-27.2591	114.0675	ZU
LL30	-27.2591	114.0675	ZU
LL31	-27.2591	114.0675	ZU
LL46	-27.2591	114.0675	ZU
LL60	-27.7	114.1667	ZU
LL61	-27.7	114.1667	ZU
LL08	-27.85	114.1667	ZU
LL41	-27.8977	114.1669	ZU
LL42	-27.8977	114.1669	ZU
LL66	-28.3	113.5833	ZU
LL67	-28.3	113.5833	ZU
LL22	-28.6166	114.6	SM
LL23	-28.6166	114.6	SM
LL10	-28.7333	115	SM
LL03	-28.7666	114.6167	SM
LL04	-28.7666	114.6167	SM
LL14	-28.7666	114.6167	SM
LL82	-28.7666	114.6167	SM
LL83	-28.7666	114.6167	SM
LL84	-28.7666	114.6167	SM
LL85	-28.7666	114.6167	SM
LL86	-28.7666	114.6167	SM
LL13	-28.8666	114.6333	SM
LL100	-29.2866	114.9244	SM

Supplemental Table 2. List of nuclear loci sequenced in this study. Primers used for amplification and the PCR conditions (i.e., annealing temperature, T_A (C), and magnesium chloride concentrations, $MgCl_2$ (mM)) are provided along with the type of marker; anonymous nuclear loci developed from this study are listed as anonymous and PCRs using touchdown amplification are marked as TD (see Edwards 2007).

Locus	Type	Forward Primer (5' - 3')	Reverse Primer (5' - 3')	Reference	T_A (C)	$MgCl_2$ (mM)
ATP	intron	CGTGAGGGHAAYGATTTHTACCATGAGATG	TCTGTCCATAAACTAGCG	(Jarman et al. 2002)	59	2
BACH1	exon	GATTTGAHCCYTTRCTTCAGTTTGC	ACCTCACATTCYTGTTCYCTRGC	(Townsend et al. 2008)	(see Townsend et al. 2008)	
GAPD	intron	ACCTTTAATGCGGGTGCTGGCATTGC	CATCAAGTCCACAACACGGTTGCTGTA	(Dolman and Phillips 2004)	63	2
L17	anonymous	TGTCCCCGTCRGTCAATAAA	AAGGAGAGCCAAGACCTGAAC	This study	65	2
L25	anonymous	GCTCTGGAATTAGCATTATCWCTTG	GGTGGGAAACATTTCTTTGTTG	This study	65	2
L37	anonymous	GTGTGCSAAGAAGAAAGGAGGM	TTTGCGAGTGCGACAGWTT	This study	65	2
L74	anonymous	GTGGATGGGGGTTATGTTTG	TGGTCAGCATTTGCMCTCAC	This study	65	2
L101	anonymous	GGCACACACAGCACATTTTT	AGAAGAAGAARAAAYCCCAAGGT	This study	65	2
L110	anonymous	TTGTGTGGGGATGCTGACT	KGCGGAGAGGAAAAATGG	This study	65	2
L115	anonymous	GGGGAACCTGTCTATCCTACAA	AGCGGAACCACTGCAAAA	This study	65	2
L145	anonymous	YRAGGACCARCAAATCATCAAC	GCCAGCAAGGGCTAYMAA	This study	65	2
L169	anonymous	CAAAGAAAAAGACAAGGGGAGA	AGGTGACTGAAAGGCTGAGAAG	This study	65	2
L218	anonymous	GCAAACCCAGAATGTCCTAATC	TGCAAGCAAGGGTACAAGG	This study	65	2
L269	anonymous	CACCCAGCCCAAGAAATG	TTCATCAGACACAACAGAAGTGG	This study	TD	2.5
L272	anonymous	GAAAGACCCCCAAGAAAGAMAG	GACACACCAAGAGAAGGCATAAA	This study	65	2
L308	anonymous	TTGTGGTGTCCAGTGMGGAA	TGGGTGAAGGGAGGAATG	This study	63	2.5
L323	anonymous	CAGCAYAGAGGACACAAAGGT	AAYGWACRGAGGGAACTAACAAG	This study	65	2
L426	anonymous	TCAACTGCCTTCCAAAATAACC	TCTTCCATACAATCCTACCCATCT	This study	65	2
L907	anonymous	CAGATGATAGCCAGAAATAAGCAC	TCACAGAAATCCAAACCTACCT	This study	59	2.5
L926	anonymous	ACCCCTTTCCTTCTCACCTT	CCACCTTTGCTTSCTTCCTC	This study	63	0.8
L1088	anonymous	CAAAAGGTTYGTGAGGCAAGA	GCCAGAGGATTGGAGGATAG	This study	65	2
NTF	exon	ATGTCCATCTTGTTTTATGTGATATTT	ACRAGTTTRTTGTTYTCTGAAGTC	(Townsend et al. 2008)	(see Townsend et al. 2008)	
PRLR	exon	GACARYGARGACCAGCAACTRATGCC	GACYTTGTGRACTTCYACRTAATCCAT	(Townsend et al. 2008)	(see Townsend et al. 2008)	
PTPN	exon	AGTTGCCTTGTWGAAGGRGATGC	CTRGCAATKGACATYGGYAATAC	(Townsend et al. 2008)	(see Townsend et al. 2008)	

Supplemental Table 3. Settings for NGen sequence assembler (DNASTAR) used for the 454 dataset in the discovery of polymorphic loci.

Categories	Parameters	Settings
Repeat	Max Mer Gap	10
Repeat	Match Size	17
Repeat	Min End Flag Len	25
Repeat	Min Flag Length	50
Repeat	Min Mer Match	2
Quality	End Region	5
Quality	Maximum uncalled bases	2
Quality	Minimum Average High Quality	22
Quality	Minimum Average Low Quality	20
Quality	Minimum End Basepair Quality	15
Quality	NTrimWinLength	7
Quality	Window Length	30
Alignment	Fixed Coverage	20
Alignment	Default Quality	15
Alignment	Gap Penalty	75
Alignment	Genome Length	10000000
Alignment	HaploidSNP	FALSE
Alignment	HaploidThreshold	0
Alignment	LowCoverageThreshold	0
Alignment	Match Score	10
Alignment	Match Window Length	50
Alignment	Match Repeat Percent	150
Alignment	Max Gap	15
Alignment	Max Usable Count	25
Alignment	Match Size	19
Alignment	Match Spacing	20
Alignment	Minimum Match Percent	85
Alignment	Mismatch Penalty	15
Alignment	Skip Realign	FALSE
Alignment	SNP Match Percentage	90
Alignment	SNP Passes	2
Alignment	Split False Joins	FALSE
Alignment	Split Template Contigs	FALSE
Alignment	Template Default Quality	500
Alignment	Use Repeat Handling	TRUE

Supplemental Table 4. Length of each locus and sampling per populations for each locus.

		Populations							
Gene	**Length**	**CB**	**C**	**P**	**SB**	**ZU**	**SM**	**Total**	**Genbank Accession No.**
ATP	490	16	40	40	28	24	26	174	KC545970 - KC546143
BACH1	1218	16	40	32	24	18	22	152	KC546144 - KC546295
GAPD	630	12	30	22	19	12	20	115	KC546296 - KC546411
L17	178	16	40	40	28	24	26	174	KC546412 - KC546585
L25	276	16	38	40	28	26	26	174	KC546586 - KC546759
L37	234	14	28	16	16	24	22	120	KC546760 - KC546879
L74	265	14	34	34	24	22	26	154	KC546880 - KC547035
L101	367	6	12	12	14	8	22	74	KC547036 - KC547109
L110	378	14	24	18	14	16	16	102	KC547110 - KC547211
L115	543	14	38	40	26	22	24	164	KC547212 - KC547375
L145	259	14	26	20	24	14	14	112	KC547376 - KC547487
L169	587	14	36	36	18	14	18	136	KC547488 - KC547623
L218	180	6	20	18	6	18	26	94	KC547624 - KC547717
L269	302	14	36	26	20	22	20	138	KC547718 - KC547855
L272	212	12	38	42	28	20	16	156	KC547856 - KC548011
L308	369	14	34	28	22	22	22	142	KC548012 - KC548153
L323	341	16	36	38	26	18	26	160	KC548154 - KC548313
L426	154	16	34	28	26	24	26	154	KC548314 - KC548467
L907	222	16	40	40	24	18	24	162	KC548468 - KC548629
L926	169	16	38	36	28	26	26	170	KC548630 - KC548799
L1088	179	16	40	42	28	26	26	178	KC548800 - KC548977
NTF3	656	14	30	32	20	20	20	136	KC548978 - KC549113
PRLR	557	14	38	34	28	22	26	162	KC549114 - KC549275
PTPN12	865	16	40	34	26	22	26	164	KC549276 - KC549439

Supplemental Table 5. Soil properties used in the construction of soil layers for the PCA analyses (for detailed description see McKenzie et al. (2000).

Variable	Type	Description
Aclay50	integer	median A horizon clay %
Bclay50	integer	median B horizon clay %
Athick50	numeric	median A horizon thickness (m)
Bthick50	numeric	median B horizon thickness (m)
Solumthick50	numeric	median solum thickness (m)
Astruct50	integer	median A horizon grade of pedality
Bstruct50	integer	median B horizon grade of pedality
A Ks	integer	A horizon $\log_{10}$ (saturated hydraulic conductivity mm/hr) - 50th percentile
AKserror	integer	$\log_{10}$(A Ks) error
B Ks	integer	B horizon $\log_{10}$ (saturated hydraulic conductivity mm/hr) - 50th percentile
BKserror	integer	$\log_{10}$(B Ks) error
Calcrete	Boolean	absence (0) or presence (1) of calcrete in or below the profile
Nutrients	integer	nutrient status low (1), moderate (2) and high (3)

Supplemental Table 6. Molecular indices calculated per locus and presented for each population separately (see Fig.1 for distributional information), as well as across all populations, including heterozygozity (*H*) and the standard deviation (*H_sd*), the number of segregating sites (*S*), the number of haplotypes (*K*) and nucleotide diversity (π).

				K							***π***						
Gene	***H***	***H_sd***	***S***	**CB**	**C**	**P**	**SB**	**ZU**	**SM**	**species**	**CB**	**C**	**P**	**SB**	**ZU**	**SM**	**species**
ATP	0.955	0.065	49	9	15	21	17	24	13	55	0.009	0.010	0.015	0.011	0.009	0.005	0.100
BACH1	0.762	0.017	40	7	10	7	8	4	5	35	0.001	0.002	0.001	0.001	0.001	0.001	0.033
GAPD	0.914	0.057	60	6	9	10	9	6	6	40	0.018	0.008	0.017	0.005	0.008	0.002	0.095
L101	0.956	0.101	28	4	7	8	6	6	5	29	0.012	0.020	0.017	0.009	0.012	0.010	0.076
L1088	0.500	0.042	3	3	3	3	5	5	8	3	0.007	0.005	0.004	0.004	0.002	0.007	0.017
L110	0.961	0.102	32	5	8	11	4	6	6	34	0.009	0.016	0.016	0.004	0.017	0.010	0.085
L115	0.730	0.033	5	5	6	5	4	6	3	7	0.003	0.003	0.003	0.002	0.003	0.002	0.009
L145	0.944	0.110	32	4	11	11	8	2	5	34	0.004	0.026	0.025	0.020	0.010	0.018	0.124
L169	0.975	0.043	29	6	9	14	10	8	10	49	0.003	0.005	0.007	0.013	0.010	0.006	0.049
L17	0.404	0.017	5	6	4	5	4	2	1	7	0.003	0.004	0.003	0.002	0.001	0.000	0.028
L218	0.625	0.043	20	6	4	3	2	5	3	13	0.055	0.005	0.004	0.003	0.006	0.002	0.111
L25	0.744	0.059	24	8	10	15	2	10	5	31	0.060	0.012	0.027	0.000	0.013	0.004	0.087
L269	0.944	0.080	20	1	14	14	13	8	4	38	0.000	0.018	0.014	0.009	0.014	0.004	0.066
L272	0.652	0.040	6	6	3	5	3	6	4	9	0.007	0.005	0.004	0.004	0.004	0.003	0.028
L308	0.954	0.050	22	5	6	11	8	6	9	39	0.004	0.003	0.003	0.006	0.027	0.029	0.060
L323	0.627	0.022	12	3	4	8	9	6	2	21	0.001	0.001	0.004	0.005	0.002	0.000	0.035
L37	0.938	0.087	22	8	15	4	5	3	6	35	0.041	0.021	0.004	0.020	0.004	0.011	0.094
L426	0.615	0.040	7	3	4	4	4	5	2	8	0.003	0.004	0.002	0.005	0.005	0.001	0.045
L74	0.767	0.030	10	3	7	5	3	2	5	17	0.003	0.009	0.010	0.004	0.001	0.005	0.038
L907	0.749	0.033	11	12	12	23	16	16	17	16	0.003	0.014	0.002	0.006	0.008	0.004	0.050
L926	0.741	0.111	6	12	7	5	5	9	3	12	0.082	0.055	0.024	0.052	0.032	0.001	0.036
NTF3	0.816	0.024	26	3	7	10	10	6	2	22	0.002	0.003	0.003	0.004	0.002	0.001	0.040
PRLR	0.932	0.033	48	5	7	17	9	18	11	52	0.002	0.002	0.005	0.005	0.006	0.003	0.086
PTPN12	0.951	0.023	40	7	10	18	8	15	8	59	0.002	0.004	0.004	0.002	0.002	0.002	0.046
Total	1.000	0.055	520	28	25	24	42	40	16	175	0.003	0.006	0.004	0.005	0.005	0.003	0.061

Supplemental Table 7. List of summary statistics used in ABC analyses.

Summary Statistics	**Description**	**Number**
S_{TOT}	segregating sites in the species	1
S	segregating sites in each population	6
PrS	private segregating sites	6
π	pairwise genetic differences within each population	6
F_{ST}	pairwise F_{ST}–values among populations	15
total		34

Supplemental Table 8. Pairwise F_{st} of the six populations ordered from north to south (lower triangle) and the significance (upper triangle). Haplotype distances between individuals are calculated using Tajima and Nei's correction. Significance of each F_{st} is assessed with 1023 permutations. +, significant ($P < 0.05$); -, non-significant. Note that Fst between P and SB is the only non-significant one.

	CB	C	P	SB	ZU	SM
CB		+	+	+	+	+
C	0.298		+	+	+	+
P	0.247	0.095		-	+	+
SB	0.291	0.097	0.020		+	+
ZU	0.425	0.262	0.178	0.237		+
SM	0.550	0.392	0.355	0.421	0.219	

Supplemental methods:

Conditions used for simulation under each of the models tested with ABC:

(i) IBD model: simulations are started from the current distribution. Migration and population growth are allowed each generation, but there is no suitability differences among demes (i.e., the carrying capacity remains the same across grid cells). In other words, the population densities and the number of emigrants from a specific deme that migrated into the surrounding cells were uniform across surrounding cells (i.e., they did not differ according to cell-specific suitabilities).

(ii) cENM model: expansion of populations start at current distributions as with the IBD model. However, the suitability of each cell follows the current ENM. Consequently, the local carrying capacity of a cell is proportional to its suitability score, as is the number of emigrants.

(iii) dENM model: populations start expansion at the LGM refugia areas (i.e., areas with highest suitability) predicted from ENM based on paleoclimatic data from the LGM 21thousand years ago. Maps of population carrying capacities change overtime (see Brown and Knowles 2012), with the demographic simulations informed during the first and last 1/3 of the generations from the ENM from the past and present, respectively, and a composite map (i.e., the average habitat suitabilities from the past and present ENMs) informing the demographic simulations for the intervening generations.

Given that the species lives in coastal sand plain or dunes, it is very unlikely for the species to migrate to majority of the inland area. Thus, we coded areas with predicted suitability less than 0.01 to be inhabitable in all models. The number of generations for expansion and migrations in the models were as follows: 7000 years before the present for the IBD, cENM, and the last third of the dENM. The dENM model was run for a total of 21,000 years before the present to account for the shifting distributions associated with the last glacial maximum (as detailed above). We used one generation per 10 years as a

generation time to reduce the length of the time forward simulations (i.e., the demographic simulations conducted in SPLATCHE2; Currat et al. 2004). The maximum coalescent time (a parameter in the program Splatch2 that specifies when gene lineage coalescence across patches must occur) was set to be much greater than 4N for all models to avoid the forced coalescence to a single common ancestor.

We note that any biological interpretation of absolute parameter values of the mutation rate and migration rate would therefore need to be scaled according to realistic generational times for *L. lineopuntulata*, although this has not been studied empirically.

References:

Brown, J. L., and L. L. Knowles. 2012. Spatially explicit models of dynamic histories: examination of the genetic consequences of Pleistocene glaciation and recent climate change on the American Pika. Molecular Ecology 21:3757-3775.

Currat, M., N. Ray, and L. Excoffier. 2004. SPLATCHE: a program to simulate genetic diversity taking into account environmental heterogeneity. Molecular Ecology Notes 4:139-142.

Dolman, G., and B. Phillips. 2004. Single copy nuclear DNA markers characterized for comparative phylogeography in Australian wet tropics rainforest skinks. Molecular Ecology Notes 4:185-187.

Edwards, D. L. 2007. Biogeography and speciation of a direct developing frog from the coastal arid zone of Western Australia. Molecular Phylogenetics and Evolution 45:494-505.

Jarman, S. N., R. D. Ward, and N. G. Elliott. 2002. Oligonucleotide primers for PCR amplification of coelomate introns. Marine Biotechnology 4:347-355.

McKenzie, N. J., D. W. Jacquier, L. J. Ashton, and H. P. Cresswell. 2000. Estimation of soil properties using the Atlas of Australian Soils. Technical Report 11/00, CSIRO Land and Water, Canberra.

Townsend, T. M., R. E. Alegre, S. T. Kelley, J. J. Wiens, and T. W. Reeder. 2008. Rapid development of multiple nuclear loci for phylogenetic analysis using genomic resources: An example from squamate reptiles. Molecular Phylogenetics and Evolution 47:129-142.