

1 ONLINE SUPPLEMENTARY MATERIALS

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3 **Online Table 1.** Primer pairs used to generate the 534 repeatable, polymorphic AFLP loci used in
4 our analyses. The number of loci yielded by each primer pair is also provided.

Primer	(Sequence 5' – 3')	Number of loci
Preselective		
Eco + C	GACTGCGTACCAATTCC	
Mse + C	GATGAGTCCTGAGTAAC	
Selective		
Eco + CTC	GACTGCGTACCAATTCCTC	
Eco + CAG	GACTGCGTACCAATTCCAG	
Mse + CTG	GATGAGTCCTGAGTAACTG	
Mse + CGA	GATGAGTCCTGAGTAACGA	
Mse + CAA	GATGAGTCCTGAGTAACAA	
Mse + CCT	GATGAGTCCTGAGTAACCT	
Primer Combinations		
D	Eco + CTC / Mse + CGA	105
E	Eco + CTC / Mse + CAA	62
F	Eco + CTC / Mse + CCT	70
G	Eco + CTC / Mse + CTG	66
I	Eco + CAG / Mse + CGA	49
J	Eco + CAG / Mse + CAA	52
K	Eco + CAG / Mse + CCT	58
L	Eco + CTC / Mse + CGC	72

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1 **Online Table 2.** Baseline information about population variability. For AFLPs, the mean (s.e.)
 2 within-population expected heterozygosity (i.e., Nei's gene diversity within populations) is
 3 provided, as estimated in AFLP-SURV following the methods of Lynch and Milligan (1994). For
 4 mtDNA, within-population pairwise sequence divergence is provided, as estimated in MEGA v. 3.1
 5 (Kumar et al. 2004) and corrected for multiple hits using the Kimura 2-parameter model (Kimura
 6 1980). Also reported is host-plant patch size estimated from aerial photographs as in Sandoval
 7 (1994a) and Nosil et al. (2003). Host-plant patch size is correlated with insect population size
 8 (Sandoval 1994a).

Pop.	AFLPs expected heterozygosity (s.e.)	mtDNA sequence divergence (s.e.)	Host-plant patch size m ²
1.PRC	0.117 (0.007)	0.023 (0.006)	68,181
2. VPC	0.107 (0.006)	0.023 (0.006)	100,000
3. HVC	0.120 (0.007)	0.018 (0.005)	1,048
4. HVA	0.113 (0.007)	0.019 (0.005)	2,141
5. LA	0.132 (0.007)	0.019 (0.005)	35,857
6. R23A	0.132 (0.006)	0.027 (0.005)	23,478

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Online Table 3. Detailed summary of behavior for all 78 loci detected as outliers at the 95% quantile level. ‘X’s denote particular population pairs in which a locus was observed to be an outlier. Also shown is which loci were outliers in the ‘global analysis’ where individuals were pooled into groups corresponding to the two hosts (see text for details). The detailed information in this table was used to assemble the outlier classification scheme reported in Table 3. The number of each population pair corresponds to the numbered comparisons listed in Table 2 and Figure 2 of the main text.

Locus	Different-host Pairs									Same-host Pairs						Global
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
G39														X		
D50, E14, G40, G43, I7, K100, K85, K													X			
G55, G60									X							
D74, F129, F81									X					X	X	X
G23, J53, L42, L71								X								
G17, J105								X					X			
G24, I12, J18							X									
G56							X						X			
D43							X	X							X	X
D102, G22, I19						X										
F139						X									X	X
G37, L80						X			X							X
D86, F74, G36						X			X					X	X	X
D47						X	X	X	X							X
G19, G29					X											
D67				X												
I15				X			X									
D23				X			X							X		
D30				X			X						X			
D93				X			X						X	X		
D125				X		X	X		X				X			
D59, D98, G14, G20, G78, I35, J132, L37												X				X
K31									X			X				
G							X					X				
L70						X						X				
I20, I					X							X				

Online Table 4. Results of simple and partial mantel tests examining how F_{ST} , estimated using all AFLP loci within a class, is related to indices of adaptive divergence and to geographic distance. All distance matrices were log-transformed. Results are also shown for mtDNA divergence, where the only significantly positive associations were detected (in bold). The simple mantel test of genetic distance against geographic distance is the same for each index of adaptive divergence. AD = Adaptive Divergence. GeoD = Geographic Distance. Analogous analyses using raw distance matrices are presented in the main text.

	Class of AFLP loci								mtDNA	
	Total Loci		Neutral Loci		Other Outlier		DH-Specific Outliers		r	p
	r	p	r	p	r	p	r	p		
GeoD simple										
All indices	0.33	0.16	0.35	0.15	0.28	0.15	-0.01	0.50	0.73	0.02
GeoD partial										
Host Preference	0.30	0.10	0.33	0.11	0.24	0.18	-0.12	0.36	0.50	0.04
Ecomorphology	0.32	0.19	0.33	0.17	0.31	0.15	-0.08	0.40	0.71	0.03
% <i>Ceanothus</i>	0.34	0.17	0.33	0.19	0.34	0.12	-0.05	0.42	0.67	0.04
AD simple										
Host Preference	0.16	0.31	0.16	0.32	0.15	0.27	0.13	0.33	0.72	<0.01
Ecomorphology	0.05	0.39	0.14	0.30	-0.08	0.46	0.25	0.20	0.40	0.08
% <i>Ceanothus</i>	0.04	0.41	0.12	0.34	-0.09	0.44	0.10	0.30	0.58	<0.01
AD partial										
Host Preference	-0.07	0.43	-0.10	0.35	-0.04	0.51	0.17	0.27	0.46	0.06
Ecomorphology	-0.03	0.52	0.06	0.38	-0.17	0.33	0.26	0.20	0.31	0.14
% <i>Ceanothus</i>	-0.10	0.42	-0.02	0.51	-0.22	0.24	0.12	0.29	0.46	0.05

GeoD simple = simple mantel of F_{ST} vs. geographic distance

GeoD partial = partial mantel of F_{ST} vs. geographic divergence, controlling for adaptive divergence

AD simple = simple mantel of F_{ST} vs. adaptive divergence

AD partial = partial mantel of F_{ST} vs. adaptive divergence, controlling for geographic distance

Online Table 5. Summary of the distribution of mantel correlation coefficients from analyses of F_{ST} at individual loci against adaptive divergence and geographic distance ($n = 206$, of which 155 were non-outliers in the genome scan). Distance matrices were log-transformed prior to analysis (three loci were excluded due to negative distance in all comparisons). Binomial tests examine whether significant associations were positive more often than expected by chance. One-sample t-tests examine whether the mean of a distribution differs from zero (d.f. = 1 minus the sample size). Significant results are in bold. The simple mantel test of genetic distance against geographic distance is the same for each index of adaptive divergence. AD = Adaptive Divergence. GeoD = Geographic Distance. No. sig. + = number of loci exhibiting a significant positive relationships at $p < 0.05$; in parentheses are the number of loci with significant positive associations that were outliers in the Dfdist analyses. No. sig. - = number of loci exhibiting a significant negative relationship at $p < 0.05$. Analogous analyses using raw distance matrices are presented in the main text.

	No. sig. +	No. sig. -	Binomial p	Significant Loci Only			All Loci		
				Mean	t-test	p	Mean	t-test	p
GeoD simple									
All indices	27 (5)	11	0.014	0.35	4.70	<0.001	0.11	4.57	<0.001
GeoD partial									
Host Preference	29 (7)	5	<0.001	0.44	6.76	<0.001	0.07	3.35	0.001
Ecomorphology	27 (5)	7	0.001	0.43	5.50	<0.001	0.10	4.10	<0.001
% <i>Ceanothus</i>	26 (5)	10	0.011	0.35	4.23	<0.001	0.09	3.64	<0.001
AD simple									
Host Preference	16 (3)	3	0.004	0.47	5.06	<0.001	0.09	4.54	<0.001
Ecomorphology	14 (1)	7	0.189	0.26	2.53	0.020	0.04	2.43	0.016
% <i>Ceanothus</i>	12 (1)	6	0.238	0.19	1.85	0.081	0.06	3.36	0.001
AD partial									
Host Preference	14 (4)	6	0.115	0.25	2.20	0.040	0.02	1.40	0.163
Ecomorphology	18 (2)	9	0.122	0.26	2.57	0.016	0.01	0.24	0.814
% <i>Ceanothus</i>	18 (2)	7	0.043	0.23	2.45	0.022	0.01	0.22	0.830

GeoD simple = simple mantel of F_{ST} vs. geographic distance

GeoD partial = partial mantel of F_{ST} vs. geographic divergence, controlling for adaptive divergence

AD simple = simple mantel of F_{ST} vs. adaptive divergence

AD partial = partial mantel of F_{ST} vs. adaptive divergence, controlling for geographic distance