Table S1. Summary statistics from weighted, grouped logistic regressions of SNP frequency against latitude.

Gene	**SNP number**	**β_0 (± S. E.), $\beta_{1\#}$ (± S. E.)**	**q-value***	**pseudo-R^2**
BRh opsin	6	0.133 (0.046)	0.008	0.624
	39	0.139 (0.060)	0.028	0.479
	41	0.147 (0.049)	0.006	0.663
	152	0.193 (0.049)	0.0008	0.851
	172	0.210 (0.047)	7.35E-05	0.923
	186	0.035 (0.094)	NS	0.015
	189	-0.063 (0.043)	NS	0.188

β_0: linear regression coefficient; $\beta_{1\#}$: quadratic regression coefficient, #: β_1 only shown where relevant
* FDR-adjusted q-values associated with regression coefficients, NS: not significant at $q<0.05$ threshold

Table S1. Contd.

Gene	SNP number	β_0 (± S. E.), $\beta_{1\#}$ (± S. E.)	q-value	pseudo-R^2
BRh opsin	375	1.573 (0.604), -0.021 (0.008) #	0.016, 0.011	0.861
	405	-0.045 (0.048)	NS	0.081
	543	-0.034 (0.036)	NS	0.085
	553	0.196 (0.052)	0.001	0.833
	564	-0.082 (0.042)	NS	0.297
	570	-0.022 (0.037)	NS	0.035
	606	0.033 (0.043)	NS	0.055

Table S1. Contd.

Gene	SNP number	β_0 (± S. E.), $\beta_{1\#}$ (± S. E.)	q-value	pseudo-R^2
BRh opsin	615	0.013 (0.035)	NS	0.013
	647	0.451 (0.097)	4.00E-0.5	0.971
	846	0.140 (0.051)	0.012	0.587
	901	0.262 (0.056)	4.00E-0.5	0.950
	930	-0.049 (0.035)	NS	0.174
	942	-0.070 (0.042)	NS	0.262
	948	-1.885 (0.834), 0.025 (0.011) #	0.033, 0.027	0.658

Table S1. Contd.

Gene	SNP number	β_0 (± S. E.), $\beta_{1\#}$ (± S. E.)	q-value	pseudo-R^2
BRh opsin	972	2.821 (1.052), -0.038 (0.014) #	0.013, 0.010	0.770
LWRh opsin	328	14.372 (4.545), -0.166 (0.054) #	0.005, 0.005	0.999
	330	14.372 (4.545), -0.166 (0.054) #	0.005, 0.005	0.999
	334	14.546 (4.550), -0.168 (0.054) #	0.005, 0.005	0.999
	429	14.546 (4.551), -0.168 (0.054) #	0.005, 0.005	0.999
	435	14.546 (4.550), -0.168 (0.054) #	0.005, 0.005	0.999
	489	12.654 (3.876), -0.146 (0.046) #	0.005, 0.005	0.999

Table S1. Contd.

Gene	SNP number	β_0 (± S. E.), $\beta_{1\#}$ (± S. E.)	q-value	pseudo-R^2
LWRh opsin	510	14.114 (4.545), -0.163 (0.054) #	0.005, 0.006	0.999
	528	15.024 (4.385), -0.174 (0.052) #	0.005, 0.005	0.999
	582	0.050 (0.040)	NS	0.156
	726	-0.010 (0.033)	NS	0.009
	933	14.309 (4.568), -0.165 (0.054) #	0.005, 0.005	0.999
UVRh opsin	189	-0.437 (0.061)	2.24E-11	0.999
	660	-0.391 (0.040)	7.20E-06	0.981

Table S1. Contd.

Gene	**SNP number**	**β_0 (± S. E.), $\beta_{1\#}$ (± S. E.)**	**q-value**	**pseudo-R^2**
UVRh opsin	699	-0.537 (0.055)	1.18E-14	1
wingless	42	-0.016 (0.067)	NS	0.006
	150	-0.109 (0.108)	NS	0.117
	219	-0.032 (0.041)	NS	0.064
	240	-0.047 (0.076)	NS	0.041
	327	-0.061 (0.073)	NS	0.075
EF-1 alpha	274	-0.087 (0.036)	0.024	0.475

Table S1. Contd.

Gene	SNP number	β_0 (± S. E.), $\beta_{1\#}$ (± S. E.)	q-value	pseudo-R^2
EF-1 alpha	286	-0.087 (0.036)	0.025	0.469
	421	0.107 (0.083)	NS	0.180
	649	-0.087 (0.036)	0.024	0.475
	721	-0.084 (0.036)	0.028	0.449
	934	0.101 (0.040)	0.018	0.514
	949	-0.125 (0.042)	0.007	0.560
	967	0.010 (0.031)	NS	0.009

Table S2. A list of the white admiral butterfly (*Limenitis arthemis*) populations which were sampled for an AFLP genome scan analysis through two parts of the hybrid zone (*L. a. arthemis* x *L. a. astyanax*).

Transect	Site	Code	Locality	Latitude	Longitude	Wing pattern	Subspecies	*N*	F_{ST}
East	1	NB	Holtville, New Brunswick, Canada	46.5653°	-66.4619°	white-banded	*arthemis*	19	0.43
	2	ON	Algonquin, Ontario, Canada	44.7037°	-75.6695°	white-banded	*arthemis*	16	0.45
	3	ME	Hancock Co., Maine, USA	44.5770°	-68.3567°	white-banded	*arthemis*	14	0.64
	4	VT	Addison Co., Vermont, USA	44.0495°	-72.9600°	white-banded	*arthemis*	24	0.34
	5	FL	Finger Lakes National Forest, NY, USA	42.4987°	-76.8133°	intergrades	*arthemis-astyanax*	11	0.21
	6	AF	Allegheny National Forest, PA, USA	42.0483°	-78.8751°	intergrades	*arthemis-astyanax*	19	0.26
	7	RG	Ricketts Glen, Columbia Co., PA, USA	41.3788°	-76.2662°	intergrades	*arthemis-astyanax*	24	0.27
	8	PO	Poconos, Luzerne Co., PA, USA	41.1022°	-75.6864°	intergrades	*arthemis-astyanax*	24	0.37
	9	BM	Blue Mtns, Carbon Co., PA, USA	40.7658°	-75.7338°	intergrades	*arthemis-astyanax*	24	0.40
	10	VA	Shenandoah Co., Virginia, USA	38.8800°	-78.4303°	red-spotted purple	*astyanax*	24	0.51
	11	GA	Putnam Co., Georgia, USA	33.3066°	-83.4816°	red-spotted purple	*astyanax*	24	0.43
West	A	TB	Thunder Bay, Ontario, Canada	48.4068°	-89.2455°	white-banded	*arthemis*	16	0.55
	B	HO	Houghton County, Michigan, USA	47.0500°	-88.6148°	white-banded	*arthemis*	24	0.52
	C	BA	Bayfield County, Wisconsin, USA	46.6651°	-91.1222°	white-banded	*arthemis*	24	0.49
	D	TA	Taylor County, Wisconsin, USA	45.2231°	-90.5299°	intergrades	*arthemis-astyanax*	24	0.66
	E	JU	Juneau County, Wisconsin, USA	43.8673°	-90.0747°	intergrades	*arthemis-astyanax*	24	0.75
	F	JO	Jo Daviess County, Illinois, USA	42.3149°	-90.2245°	intergrades	*arthemis-astyanax*	24	0.36
	G	MA	Mason County, Illinois, USA	40.2271°	-89.9253°	red-spotted purple	*astyanax*	24	0.40
	H	KY	Jefferson Co., Kentucky, USA	38.1938°	-85.6435°	red-spotted purple	*astyanax*	19	0.58
	I	MS	Calhoun Co., Mississippi, USA	33.8839°	-89.3227°	red-spotted purple	*astyanax*	15	0.41

These study samples correspond to Fig. S6, where each population is identified by a site label in the map. General collection locality information, along with the wing pattern characterizations and sample sizes are listed for each sampled region. Butterflies characterized as red-spotted purples (*L. a. astyanax*) are known Batesian mimics of the chemically-defended pipevine swallowtail, *Battus philenor*.

Table S3. Primer combinations (showing only the selective nucleotides) used to isolate AFLP loci during the final selective amplification of DNA from *Limenitis arthemis,* and the number of the resulting monomorphic and polymorphic bands generated from each combination ($N = 417$ individuals).

***Eco*RI**	***Mse*I**	**Loci**	**Polymorphic Loci**
ACT	CTC	307	59
	CTG	157	31
ACA	CTC	249	36
	CTG	258	28
AAC	CAA	174	35
	CAT	236	47
	CTA	274	50
	CTT	273	48
AT	CTG	115	13
AGG	CAC	267	48
AG	CC	263	61
TT	CC	150	34

In total there were 2723 loci, of which 490 were variable across the populations. Of the 490 variable AFLP loci, 424 were estimated as neutral and 66 were detected as outliers potentially under the influence of selection. Estimates of population differentiation for all 490 variable AFLP markers ($F_{ST} = 0.21$) was driven by inclusion of outlier loci. After analyzing the data separately, $F_{ST} = 0.09$ for the 424 neutral loci, and $F_{ST} = 0.51$ for the 66 outlier loci.

Table S4. Pairwise population F_{ST} calculated for 424 neutral and 66 outlier loci, below and above diagonal, respectively.

		1	2	3	4	5	6	7	8	9	10	11	A	B	C	D	E	F	G	H	I
		NB	ON	ME	VT	FL	AF	RG	PO	BM	VA	GA	TB	HO	BA	TA	JU	JO	MA	KY	MS
1	NB	—	0.12	0.13	0.70	0.09	0.29	0.65	0.68	0.68	0.10	0.12	0.04	0.71	0.61	0.69	0.55	0.03	0.03	0.10	0.01
2	ON	0.04	—	0.02	0.63	0.17	0.14	0.57	0.60	0.60	0.18	0.15	0.05	0.64	0.51	0.61	0.42	0.12	0.12	0.09	0.11
3	ME	0.06	0.05	—	0.62	0.19	0.09	0.56	0.60	0.60	0.17	0.11	0.09	0.64	0.50	0.61	0.39	0.21	0.14	0.12	0.21
4	VT	0.18	0.17	0.18	—	0.67	0.65	0.07	0.06	0.08	0.70	0.67	0.65	0.02	0.18	0.18	0.43	0.71	0.67	0.68	0.70
5	FL	0.07	0.10	0.10	0.16	—	0.25	0.63	0.66	0.65	0.09	0.06	0.04	0.69	0.58	0.67	0.54	0.13	0.05	0.16	0.08
6	AF	0.10	0.08	0.07	0.17	0.04	—	0.60	0.63	0.62	0.30	0.27	0.17	0.67	0.54	0.65	0.49	0.34	0.31	0.21	0.32
7	RG	0.14	0.14	0.15	0.03	0.12	0.13	—	0.02	0.07	0.66	0.62	0.60	0.08	0.21	0.04	0.29	0.67	0.62	0.63	0.65
8	PO	0.16	0.15	0.15	0.04	0.16	0.15	0.02	—	0.03	0.68	0.65	0.63	0.07	0.21	0.07	0.36	0.69	0.65	0.65	0.68
9	BM	0.16	0.15	0.14	0.06	0.16	0.16	0.04	0.02	—	0.68	0.64	0.63	0.13	0.22	0.15	0.36	0.69	0.65	0.65	0.68
10	VA	0.11	0.10	0.09	0.17	0.12	0.09	0.12	0.12	0.11	—	0.04	0.10	0.72	0.62	0.70	0.58	0.09	0.08	0.09	0.07
11	GA	0.24	0.27	0.29	0.32	0.18	0.26	0.29	0.33	0.33	0.29	—	0.10	0.68	0.57	0.66	0.50	0.13	0.06	0.11	0.12
A	TB	0.08	0.06	0.09	0.20	0.11	0.13	0.18	0.19	0.18	0.12	0.29	—	0.66	0.55	0.64	0.50	0.10	0.08	0.11	0.08
B	HO	0.10	0.11	0.12	0.10	0.12	0.14	0.09	0.11	0.10	0.14	0.26	0.13	—	0.25	0.15	0.44	0.72	0.68	0.69	0.71
C	BA	0.16	0.18	0.20	0.17	0.11	0.18	0.16	0.20	0.20	0.21	0.20	0.18	0.09	—	0.33	0.33	0.63	0.58	0.59	0.62
D	TA	0.13	0.14	0.17	0.15	0.10	0.16	0.12	0.16	0.16	0.19	0.21	0.15	0.05	0.04	—	0.32	0.70	0.66	0.67	0.69
E	JU	0.10	0.10	0.13	0.15	0.10	0.13	0.11	0.15	0.14	0.15	0.22	0.14	0.05	0.08	0.04	—	0.59	0.51	0.53	0.57
F	JO	0.06	0.04	0.06	0.17	0.08	0.07	0.13	0.14	0.13	0.06	0.24	0.07	0.09	0.15	0.13	0.09	—	0.06	0.10	0.01
G	MA	0.10	0.10	0.12	0.18	0.08	0.12	0.15	0.17	0.16	0.10	0.25	0.11	0.10	0.10	0.08	0.07	0.05	—	0.10	0.02
H	KY	0.06	0.04	0.07	0.17	0.08	0.08	0.12	0.12	0.11	0.05	0.23	0.07	0.10	0.14	0.11	0.09	0.03	0.06	—	0.06
I	MS	0.11	0.13	0.16	0.25	0.11	0.17	0.20	0.23	0.21	0.16	0.27	0.14	0.17	0.15	0.14	0.15	0.12	0.11	0.08	—

Values derived using pre-defined F_{IS} for both neutral (0.69) and outlier (0.72) datasets. Refer to Table S2 for population numbers and locations.

Table S5. Analysis of molecular variance (AMOVA) using pairwise genetic distances (F_{ST}) for five gene datasets (*BRh*, *LWRh*, *UVRh*, *wingless*, and *EF-1 alpha*) and ten populations of *Limenitis arthemis*.

Gene	Source of variation	Variance component	Percentage variation	Fixation Index	Sum of squares
BRh	Among groups (F_{CT})	0.5	2.5	0.02	1340.8
	Among populations within groups (F_{SC})	10.0	46.2	0.47	7969.1
	Within populations (F_{ST})	11.1	51.3	0.49	10961.0
LWRh	Among groups (F_{CT})	0.2	9.7	0.10	125.7
	Among populations within groups (F_{SC})	0.2	8.0	0.09	159.5
	Within populations (F_{ST})	2.0	82.4	0.18	1882.4
UVRh	Among groups (F_{CT})	0.1	21.4	0.21	92.5
	Among populations within groups (F_{SC})	0.0	5.0	0.06	24.6
	Within populations (F_{ST})	0.5	73.6	0.26	452.0
wingless	Among groups (F_{CT})	0.0	0.1	0.00	3.1
	Among populations within groups (F_{SC})	0.0	1.9	0.02	10.0
	Within populations (F_{ST})	0.5	98.0	0.02	479.2
EF-1 alpha	Among groups (F_{CT})	0.0	0.6	0.01	16.5
	Among populations within groups (F_{SC})	0.0	1.6	0.02	32.0
	Within populations (F_{ST})	1.8	97.9	0.02	1759.0

Populations were grouped to maximize the among group variance component (F_{CT}), which would indicate whether there is spatial genetic structure across the sampled populations. With noteworthy exceptions in the three opsin genes, the genetic variance is largely attributable to genetic diversity within populations but F_{ST} values are quite low ($F_{ST} = 0.02$), suggesting little evidence for population

structure. The high F_{ST} estimates for the three opsin genes suggest significant population genetic variation, and it is regionally distributed among populations within geographic clusters. All AMOVA results are highly significant for $\alpha = 0.05$.

Table S6. Comparisons of population pairwise genetic distances (F_{ST}) for the five gene datasets, *BRh*, *LWRh*, *UVRh*, *wingless*, and *EF-1 alpha*.

BRh	WB	NH	VT	MA	RG	PO	BM	WAI	VA	GA
WB		+	+	+	+	+	+	+	+	+
NH	0.141		+	+	+	+	+	+	+	+
VT	0.448	0.345		+	+	+	+	+	+	+
MA	0.624	0.541	0.332		+	+	+	+	+	+
RG	0.417	0.355	0.105	0.249		+	+	+	+	-
PO	0.504	0.421	0.146	0.310	0.044		+	+	+	+
BM	0.501	0.474	0.285	0.175	0.197	0.263		+	+	+
WAI	0.835	0.753	0.659	0.898	0.710	0.771	0.825		+	+
VA	0.553	0.464	0.175	0.233	0.073	0.061	0.216	0.837		+
GA	0.444	0.402	0.156	0.146	0.050	0.085	0.131	0.784	0.032	

LWRh	WB	NH	VT	MA	RG	PO	BM	WAI	VA	GA
WB		-	-	-	-	-	+	+	+	+
NH	0.000		+	-	-	-	+	+	+	+
VT	0.002	0.017		-	-	+	+	+	+	+
MA	0.007	-0.003	0.041		-	-	+	+	+	+
RG	-0.007	-0.003	0.002	0.005		-	+	+	+	+
PO	0.024	0.006	0.059	-0.008	0.016		+	+	+	+
BM	0.187	0.128	0.247	0.100	0.173	0.076		-	+	+
WAI	0.208	0.142	0.260	0.123	0.191	0.095	0.005		+	+
VA	0.365	0.272	0.428	0.273	0.356	0.232	0.053	0.054		-
GA	0.346	0.256	0.403	0.262	0.336	0.224	0.065	0.053	0.015	

UVRh	WB	NH	VT	MA	RG	PO	BM	WAI	VA	GA
WB		+	+	+	+	+	+	+	+	+
NH	0.034		-	+	+	+	+	+	+	+
VT	0.022	0.003		+	+	+	+	+	+	+
MA	0.061	0.164	0.133		-	-	-	+	+	+
RG	0.025	0.113	0.089	-0.005		+	-	+	+	+
PO	0.164	0.294	0.253	0.035	0.064		-	-	+	+
BM	0.102	0.231	0.192	0.017	0.030	0.002		+	+	+
WAI	0.233	0.360	0.315	0.065	0.111	0.013	0.045		-	+
VA	0.295	0.416	0.376	0.118	0.168	0.024	0.073	0.007		+
GA	0.524	0.594	0.566	0.378	0.415	0.221	0.292	0.225	0.118	

wingless	WB	NH	VT	MA	RG	PO	BM	WAI	VA	GA
WB		+	+	+	-	+	-	-	+	+
NH	0.040		+	+	-	-	+	+	-	+
VT	0.031	0.016		+	+	-	+	+	+	+
MA	0.024	0.019	0.022		-	-	-	-	+	-
RG	0.010	0.006	0.018	0.003		-	-	-	-	-
PO	0.029	0.003	0.002	0.007	0.002		+	-	-	-
BM	0.009	0.046	0.030	0.014	0.013	0.024		-	+	-
WAI	0.006	0.033	0.021	0.005	0.007	0.011	-0.004		+	-
VA	0.053	0.003	0.024	0.020	0.022	0.012	0.056	0.040		+
GA	0.029	0.015	0.022	0.008	0.000	0.004	0.015	0.011	0.029	

EF-1 alpha	WB	NH	VT	MA	RG	PO	BM	WAI	VA	GA
WB		-	+	-	+	+	-	+	-	+
NH	-0.003		-	-	-	-	-	+	+	+
VT	0.019	0.010		+	-	-	-	+	-	-
MA	-0.001	0.003	0.030		+	+	+	+	+	+
RG	0.012	0.006	0.000	0.024		-	-	+	-	-
PO	0.016	0.010	0.002	0.032	0.002		-	+	-	-
BM	0.011	0.008	0.005	0.027	0.001	0.000		+	-	-
WAI	0.100	0.081	0.038	0.125	0.043	0.038	0.035		+	+
VA	0.009	0.009	0.012	0.026	0.007	0.006	0.001	0.057		+
GA	0.041	0.031	0.008	0.065	0.009	0.002	0.007	0.019	0.017	

Significance of pairwise comparisons ($P < 0.05$) is indicated (+) above the diagonal. Population labels correspond to localities in Figure 1, and are in order of decreasing latitude from WB to GA.

Table S7. List of outlier loci detected by the hierarchical island model (Excoffier et al. 2009).

Gene	SNP (bp)	H_o	F_{ST}	*P*-value	Threshold	Pattern
BRh	**6**	0.274	0.038	1.00E-07	***	<
1028 bp	**39**	0.178	0.032	1.00E-07	***	<
	41	0.254	0.041	1.00E-07	***	<
	141	0.004	0.002	2.80E-02	*	<
	152	0.311	0.074	1.00E-07	***	<
	172	0.350	0.085	1.00E-07	***	<
	186	0.051	0.018	1.00E-02	*	<
	189	0.189	0.010	1.00E-07	***	<
	216	0.051	0.030	3.00E-02	*	<
	375	0.472	0.050	1.00E-07	***	<
	405	0.152	0.043	1.00E-07	***	<
	468	0.059	0.022	6.00E-03	**	<
	474	0.004	0.002	2.80E-02	*	<
	519	0.004	0.002	2.80E-02	*	<
	543	0.289	0.017	1.00E-07	***	<
	549	0.070	0.042	1.10E-02	*	<
	553	0.278	0.067	1.00E-07	***	<
	564	0.178	0.016	1.00E-07	***	<
	570	0.289	0.016	1.00E-07	***	<
	606	0.219	0.016	1.00E-07	***	<
	615	0.360	0.004	1.00E-07	***	<
	647	0.184	0.081	1.00E-07	***	<
	735	0.521	0.772	8.00E-03	**	>
	736	0.521	0.772	8.00E-03	**	>
	737	0.521	0.772	8.00E-03	**	>
	738	0.521	0.772	8.00E-03	**	>
	739	0.520	0.783	7.00E-03	**	>
	740	0.520	0.783	7.00E-03	**	>
	741	0.520	0.783	7.00E-03	**	>
	742	0.520	0.783	7.00E-03	**	>
	743	0.520	0.783	7.00E-03	**	>
	744	0.520	0.783	7.00E-03	**	>
	745	0.520	0.783	7.00E-03	**	>
	746	0.520	0.783	7.00E-03	**	>
	748	0.517	0.767	1.00E-02	*	>
	749	0.517	0.767	1.00E-02	*	>
	750	0.517	0.767	1.00E-02	*	>
	751	0.517	0.767	1.00E-02	*	>
	811	0.070	0.054	2.20E-02	*	<
	846	0.243	0.035	2.40E-05	***	<

	901	0.289	0.095	4.08E-03	***	<
	930	0.310	0.005	1.62E-04	***	<
	942	0.296	0.036	1.19E-05	***	<
	948	0.280	0.028	1.00E-07	***	<
	966	0.066	0.029	4.53E-03	***	<
	972	0.172	0.042	3.63E-04	***	<
	987	0.092	0.045	2.07E-03	***	<
	4.6%	*0.305*	*0.287*			
LWRh	355	0.004	0.002	2.20E-02	*	<
800 bp	**582**	0.345	0.008	3.40E-06	***	<
	621	0.017	0.004	5.00E-02	ms	<
	726	0.447	0.019	4.00E-03	**	<
	0.5%	*0.203*	*0.008*			
UVRh	**189**	0.377	0.154	2.61E-01	ns	<
241 bp	**660**	0.232	0.089	7.89E-02	ns	<
	699	0.519	0.338	1.09E-01	ns	<
	1.2%	*0.376*	*0.194*			
wingless	143	0.004	0.017	3.50E-02	ms	<
402 bp	162	0.025	0.057	2.70E-02	ms	>
	198	0.004	0.002	3.50E-02	ms	<
	0.7%	*0.011*	*0.025*			
EF-1 alpha	145	0.004	0.002	4.30E-02	ms	<
1066 bp	349	0.004	0.002	4.30E-02	ms	<
	376	0.004	0.002	4.30E-02	ms	<
	421	0.085	0.002	4.00E-02	ms	<
	457	0.012	0.002	4.94E-02	ms	<
	718	0.020	0.063	1.75E-02	*	>
	778	0.004	0.002	4.34E-02	ms	<
	808	0.004	0.002	4.30E-02	ms	<
	967	0.422	0.003	3.78E-02	ms	<
	1048	0.004	0.002	4.34E-02	ms	<
	0.9%	*0.056*	*0.008*			

For the five gene datasets, each SNP is identified in base pair position, observed heterozygosity (H_O), observed F_{ST}, *P*-value, significance threshold (non-significant – ns, marginally significant – ms, and asterisks indicate the threshold: $P < 0.05$ *, $P < 0.01$ **, and $P < 0.001$ ***), and pattern of outlier detection (observed F_{ST} < expected, or observed F_{ST} > expected). Also listed for each gene dataset are the percent outlier loci, and average observed H_O and F_{ST}. SNP loci in bold typeface correspond to the markers identified in Figure 2.