Supplemental Information for *The American Naturalist* article

Dispersal predicts hybrid zone widths across animal diversity: Implications for species

borders under incomplete reproductive isolation

Jay P. McEntee[1], J. Gordon Burleigh[1], Sonal Singhal[2*]

[1]Department of Biology, University of Florida, Gainesville, FL, USA 32611

[2]Department of Biology, California State University, Dominguez Hills, Carson, CA, USA 90747

*corresponding author e-mail: sonal.singhal1@gmail.com

SUPPLEMENTARY TABLES

Table S1: Hybrid zones for which geographic clines were estimated in the literature but were not included in our global analysis because of missing data. Several iconic hybrid zones are neither listed here nor included in our final dataset because geographic clines were not measured. Some bird hybrid zones where dispersal data were lacking were included in bird-only analyses where a morphological proxy (hand-wing index) for dispersal was used as a predictor of cline width instead.

Taxon 1	Taxon 2	reason excluded	representative citation
Albinaria hippolyti, lineage 1	*Albinaria hippolyti*, lineage 2	no mtDNA data	Schilthuizen and Lombaerts (1995) *Biol J of Linn Soc* 54: 111 - 138.
Allonemobius fasciatus	*Allonemobius socius*	cline widths not reported as point estimates	Howard (1986) *Evolution* 40: 34 - 43.
Aponomma hydrosauri	*Aponomma libatum*	cline widths not reported as point estimates	Bull and Burzacott (2001) *Mol Ecol* 10: 639 - 49.
Apis mellifera	*Apis mellifera*	cline estimates mostly wider than transects. Most fitted data appear non-clinal	Chavez-Galarza et al. (2015) *Mol Ecol* 24: 2973–2992
Barytettix humphreysii humphreysii	*Barytettix hymphreysii cochisei*	cline data not given in terms of geographic distance	Knowles *et al.* (2016) *J Orthoptera Research* 25: 75 - 82.
Caledia captiva "Moreton" lineage	*Caledia captiva* "Torresian" lineage	no mtDNA data	Shaw and Wilkinson (1980) *Chromosoma* 80: 1 - 31.
Chorthippus albomarginatus	*Chorthippus oschei*	cline data not formalized	Vedenina (2011) *Biol J of Linn Soc* 102: 275 - 291.
Cottus gobio E lineage	*Cottus gobio* W lineage	cline widths not reported as point estimates	Kontula and Vainola (2004) *Biol J of Linn Soc* 81: 535-552.
Crocodylus acutus	*Crocodylus moreletti*	Cline widths larger than transect, cline centers outside transect	Pacheco-Sierra *et al.* (2016) *Mol Ecol* 25: 3484 -3498.
Eopsaltria australis North	*Eopsaltria australis* South	mtDNA data cannot be assigned to taxa	Morales *et al.* (2017) *J Biogeography* 44: 522 – 536.
Gasterosteus aculeatus, marine population	*Gasterosteus aculeatus*, freshwater population	no mtDNA data	Pederson *et al.* (2017) *BMC Evol Bio* 17: 130.
Gasterosteus	*Gasterosteus*	no mtDNA data	Vines *et al.* (2016)

aculeatus, stream population	*aculeatus,* anadramous population		*Evolution* 70: 1023 – 1038.
Geomys breviceps	*Geomys bursarius*	cline widths not reported as point estimates	Cothran and Zimmerman (1985) *J Mammology* 66: 489 – 497.
Jacana spinosa	*Jacana jacana*	no dispersal data; included in bird only analysis	Miller *et al.* (2014) *BMC Evol Bio* 14: 227.
Manacus vitellinus	*Manacus candei*	no dispersal data; included in bird only analysis	Brumfield *et al.* (2001) *Evolution* 55: 2070 – 2087.
Nectarinia moreaui	*Nectarinia fuelleborni*	no dispersal data; included in bird only analysis	McEntee et al. (2016) Evolution 70: 1307 – 1321.
Paratya australiensis, Kilcoy Ck	*Paratya australiensis,* Branch Ck	cline widths not reported	Wilson, Schmidt and Hughes (2016) *J Heredity* 107: 413 – 422.
Patella ulyssiponensis	*Patella rustica*	cline center reported only	Sa-Pinto *et al* (2012) *PLOS One* 7: e50330.
Plethodon jordani	*Plethodon glutinosus*	cline data not formalized	Hairston *et al.* (1992) *Evolution* 46:930 – 938.
Podisma pedestris XO	*Podisma pedestrix XY*	mtDNA data from GenBank cannot be assigned to taxa	Barton and Hewitt (1981) *Evolution* 35: 1008 – 1018.
Poephila acuticauda, yellow-beaked	*Poephila acuticauda,* red-beaked	mtDNA data from GenBank cannot be assigned to taxa	Griffith and Hooper (2016) *Emu* 2: 141 – 150.
Quiscalus quiscula versicolor	*Quiscalus quiscula quiscula*	no formal cline analysis	Yang and Selander (1968) *Systematic Biology* 17: 107 – 143.
Ranitomeya imitator banded	*Ranitomeya imitator* striped	no mtDNA data	Twomey *et al.* (2015) *Am Nat* 187: 205 – 224.
Ranitomeya imitator spotted	*Ranitomeya imitator* striped	no mtDNA data	Twomey *et al.* (2015) *Am Nat* 187: 205 – 224.
Ranitomeya imitator striped	*Ranitomeya imitator* vardero	no mtDNA data	Twomey *et al.* (2015) *Am Nat* 187: 205 – 224.
Sorex araneus – Novosibirsk	*Sorex araneus* – Tomsk	no mtDNA data	Polyakov *et al.* (2011) *J Evol Bio* 24: 1393 – 1402.
Xiphophorus birchmanni	*Xiphophorus malinche*	cline widths not reported as point estimates	Culumber *et al.* (2011) *Mol Ecol* 20: 342 – 356.
Zosterops borbonicus, grey-headed	*Zosterops borbonicus,* brown-naped	no mtDNA data	Delahie *et al.* (2017) *J Evol Bio* 30: 2132 – 2145.
Zosterops pallidus	*Zosterops virens capensis*	no dispersal data; included in bird only analysis	Oatley *et al.* (2017) *Biol J Linn Soc* 121: 670 – 684.

Table S2: Summary of sensitivity analyses done using two approaches. The first used mtDNA distance only as a predictor ("mtDNA only") and the other used both nDNA and mtDNA distances as predictors ("nDNA + mtDNA"). Detailed results presented in Tables S3 – S22. For the most part, results across sensitivity analyses mirror results found in the full analysis (shown in blue at bottom).

potential issue	how addressed	"mtDNA only"			"nDNA + mtDNA"		
		n	best-fitting model	adj. r^2	n	best-fitting model	adj. r^2
Outlier loci might be biasing cline estimates	only included cline widths estimated from molecular hybrid indices	87	~ log(dispersal)	0.35	55	~ log(dispersal)	0.34
hybrid-zone independent measures of dispersal were sometimes less relevant to the given taxa than hybrid-zone dependent measures	repeated analysis using the most relevant measure of dispersal per taxon pair ("best dispersal"), which resulted in a mix of dependent- and independent dispersal measures	127	~ log(best dispersal)	0.34	73	~ log(best dispersal) + log(mtDNA dist) + log(nDNA dist) + log(mtDNA dist) × log(best dispersal) + log(nDNA dist) × log(best dispersal)	0.46
genetic divergence and cline width could be autocorrelated if introgression is common	use maximum pairwise genetic distances as proxies for selection against hybrids instead of mean distances	115	~ log(dispersal)	0.34	69	~ log(dispersal) + log(max nDNA dist) + log(max nDNA dist) × log(dispersal)	0.35
Hybrid zone widths were measured using a diversity of cline types	only included cline widths estimated from mtDNA	74	~ log(dispersal) + taxonomic group + log(dispersal) × taxonomic group	0.49	45	~ log(dispersal) + log(mtDNA dist) + log(nDNA dist) + log(dispersal) × taxonomic group + log(nDNA dist) × taxonomic group	0.74
our proxies of dispersal and selection against hybrids are possibly inaccurate	built models for birds, in which we have an alternate proxy for dispersal (hand-wing index; HWI)	37	~ log(HWI)	0.067			
our proxies of dispersal and selection against hybrids are possibly inaccurate	built models for birds, in which we have an alternate proxy for selection (phylogenetic distance)	18	~ log(dispersal) + log(phy dist) + log(dispersal) × log(phy dist)	0.438			
full model		125	~ log(dispersal)	0.34	73	~ log(dispersal) + log(mtDNA dist) + log(nDNA dist) + log(mtDNA dist) × log(dispersal)	0.40

Table S3: Model fitting for data set filtered to include clines estimated for molecular hybrid indices only (n = 87 hybrid zones). We fit linear models that predicted the log of cline width, with the log of dispersal, log of mtDNA distance, taxonomic group, and all two-way interactions as predictors. All variables were scaled and centered prior to modelling. Shown are the five models with the highest AICc weight.

Model	AICc	weights	adj. r^2
~ 1 + log(dispersal)	213.8	0.453	0.349
~ 1 + log(dispersal) + log(mtDNA dist)	215.3	0.212	0.347
~ 1 + log(dispersal) + log(mtDNA dist) + log(mtDNA dist)×log(dispersal)	216	0.146	0.35
~ 1 + log(dispersal) + taxonomic group	216.6	0.109	0.384
~ 1 + log(dispersal) + log(mtDNA dist) + taxonomic group	218.5	0.043	0.382

Table S4: Model-averaged coefficient estimates for the top three predictor variables for hybrid index models (shown in Table S3) as measured by relative importance. Coefficients not shown for taxonomic group because these are estimated for each of seven taxa.

Predictor	Coefficient	relative importance
log(dispersal)	0.6±0.21	1
log(mtDNA dist)	-0.04±0.14	0.44
taxonomic group		0.19

Table S6: Model fitting for data set filtered to include clines estimated for molecular hybrid indices only (n = 55 hybrid zones). We fit linear models that predicted the log of cline width, with the log of dispersal, log of mtDNA distance, log of nDNA distance, taxonomic group, and two-way interactions as predictors. All variables were scaled and centered prior to modelling. Shown are the five models with the highest AICc weight.

Model	AICc	weights	adj. r^2
~ 1 + log(dispersal)	137.5	0.234	0.341
~ 1 + log(dispersal) + log(mtDNA dist) + log(mtDNA dist)×log(dispersal)	138.1	0.181	0.366
~ 1 + log(dispersal) + log(mtDNA dist) + log(nDNA dist)+ log(mtDNA dist)×log(dispersal)	138.4	0.155	0.379
~ 1 + log(dispersal) + log(nDNA dist)	139.7	0.081	0.331
~ 1 + log(dispersal) + log(mtDNA dist)	139.8	0.075	0.33

Table S7: Model-averaged coefficient estimates for predictor variables for the top three predictor variables for hybrid index models (shown in Table S6) as measured by relative importance.

Predictor	Coefficient	relative importance
log(dispersal)	0.55±0.27	1
log(mtDNA dist)	-0.03±0.19	0.64
log(dispersal)×log(mtDNA dist)	0.16±0.37	0.51

Table S7: Model fitting for data set using the most relevant estimate of dispersal available ("best available" dispersal estimates; n = 127 hybrid zones). Some of these dispersal estimates are dependent on hybrid zone width estimates. We fit linear models that predicted the log of cline width, with the log of dispersal, log of mtDNA distance, taxonomic group, and two-way interactions as predictors. All variables were scaled and centered prior to modelling. Shown are the five models with the highest AICc weights.

Model	AICc	weights	adj. r^2
~ 1 + log(best dispersal)	312.4	0.519	0.337
~ 1 + log(best dispersal) + log(mtDNA dist)	314	0.24	0.334
~ 1 + log(best dispersal) + log(mtDNA dist) + log(mtDNA dist)×log(best dispersal)	314.7	0.172	0.337
~ 1 + log(best dispersal) + taxonomic group	318.9	0.021	0.34
~ 1 + log(best dispersal) + taxonomic group + taxonomic group×log(best dispersal)	319.3	0.017	0.379

Table S8: Model averaging results for the data set using the "best available" dispersal estimates (shown in Table S7). Only the top three predictors (as measured by relative importance) are shown.

Predictor	Coefficient	relative importance
log(best dispersal)	0.56±0.18	1
log(mtDNA dist)	-0.03±0.11	0.44
log(best dispersal)×log(mtDNA dist)	0.02±0.07	0.19

Table S9: Model fitting for data set using the best available dispersal estimate (n = 73 hybrid zones). Some of these dispersal estimates are dependent on hybrid zone width estimates. We fit linear models that predicted the log of cline width, with the log of dispersal, log of mtDNA distance, log of nDNA distance, taxonomic group, and two-way interactions as predictors. All variables were scaled and centered prior to modelling. Shown are the five models with the highest AICc weights.

Model	AICc	weights	adj. r^2
~ 1 + log(best dispersal) + log(mtDNA dist) + log(nDNA dist)+ log(mtDNA dist)×log(best dispersal) + log(nDNA dist)×log(best dispersal)	172	0.29	0.457
~ 1 + log(best dispersal) + log(mtDNA dist) + log(nDNA dist)+ log(mtDNA dist)×log(best dispersal)	172.5	0.228	0.443
~ 1 + log(best dispersal) + log(mtDNA dist) + log(nDNA dist)+ log(mtDNA dist)×log(best dispersal) + log(nDNA dist)×log(best dispersal) + log(nDNA dist)×log(mtDNA dist)	173.2	0.156	0.459
~ 1 + log(best dispersal) + log(nDNA dist)+ log(nDNA dist)×log(best dispersal)	174.1	0.103	0.421
~ 1 + log(best dispersal) + log(mtDNA dist) + log(nDNA dist)+ log(mtDNA dist)×log(best dispersal) + log(nDNA dist)×log(mtDNA dist)	174.9	0.067	0.435

Table S10: Model averaging results for the data set using the "best available" dispersal estimates (shown in Table S9). Only the top three predictors (as measured by relative importance) are shown.

Predictor	Coefficient	relative importance
log(best dispersal)	0.66±0.22	1
log(nDNA dist)	-0.25±0.23	0.95
log(mtDNA dist)	0.05±0.18	0.86

Table S11: Model fitting for data set using maximum mtDNA distance instead of mean mtDNA distance (n = 115 hybrid zones). We fit linear models that predicted the log of cline width, with the log of dispersal, log of maximum mtDNA distance, taxonomic group, and two-way interactions as predictors. All variables were scaled and centered prior to modelling. Shown are the five models with the highest AICc weights.

Model	AICc	weights	adj. r^2
~ 1 + log(dispersal)	283	0.635	0.339
~ 1 + log(dispersal) + log(max mtDNA dist)	285.1	0.221	0.333
~ 1 + log(dispersal) + log(max mtDNA dist) + log(max mtDNA dist)×log(dispersal)	286.7	0.099	0.331
~ 1 + log(dispersal) + taxonomic group	289.3	0.027	0.344
~ 1 + log(dispersal) + log(max mtDNA dist) + taxonomic group	291.7	0.008	0.338

Table S12: Model averaging results for the dataset using maximum mtDNA distance instead of mean mtDNA distance (shown in Table S11) as measured by relative importance. Only the top three predictors (as measured by relative importance) are shown.

Predictor	Coefficient	relative importance
log(dispersal)	0.57±0.17	1
log(mtDNA dist)	-0.02±0.1	0.42
log(dispersal)×log(mtDNA dist)	0.02±0.07	0.18

Table S13: Model fitting for data set using maximum genetic distance instead of mean distances (n = 73 hybrid zones). We fit linear models that predicted the log of cline width, with the log of dispersal, log of maximum mtDNA distance, log of maximum nDNA distance, taxonomic group, and two-way interactions as predictors. All variables were scaled and centered prior to modelling. Shown are the five models with the highest AICc weights.

Model	AICc	weights	adj. r^2
~ 1 + log(dispersal) + log(max nDNA dist) + log(max nDNA dist)×log(dispersal)	163	0.193	0.354
~ 1 + log(dispersal)	163.7	0.134	0.32
~ 1 + log(dispersal) + log(max mtDNA dist) + log(max nDNA dist) + log(max nDNA dist)×log(dispersal)	164.2	0.106	0.355
~ 1 + log(dispersal) + log(max mtDNA dist)	164.5	0.089	0.325
~ 1 + log(dispersal) + log(max mtDNA dist) + log(max nDNA dist) + log(max mtDNA dist)×log(dispersal)	164.8	0.08	0.35

Table S14: Model averaging results for the dataset using maximum genetic distances instead of mean distances (shown in Table S13) as measured by relative importance. Only the top three predictors (as measured by relative importance) are shown.

Predictor	Coefficient	relative importance
log(dispersal)	0.61±0.24	1
log(max nDNA dist)	-0.11±0.25	0.72
log(max mtDNA dist)	0.07±0.2	0.59

Table S15: Model fitting for data set filtered to include only mitochondrial DNA clines (n = 74 hybrid zones). We fit linear models that predicted the log of cline width, with the log of dispersal, log of mtDNA distance, taxonomic group, and two-way interactions as predictors. All variables were scaled and centered prior to modelling. Shown are the five models with the highest AICc weights.

Model	AICc	weights	adj. r^2
~ 1 + log(dispersal) + taxonomic group + taxonomic group×log(dispersal)	180.7	0.427	0.492
~ 1 + log(dispersal)	181.9	0.235	0.354
~ 1 + log(dispersal) + log(mtDNA dist) + taxonomic group + taxonomic group×log(dispersal)	183.4	0.115	0.487
~ 1 + log(dispersal) + log(mtDNA dist) + log(mtDNA dist)×log(dispersal)	183.9	0.089	0.359
~ 1 + log(dispersal) + log(mtDNA dist)	184.1	0.079	0.346

Table S16: Model averaging results for the data set that only includes mtDNA clines (models shown in Table S15), including coefficients and relative importance. Only the top three predictors (as measured by relative importance) are shown. Coefficients not reported for predictors including taxonomic group because these are calculated for each one of the seven taxonomic groups.

Predictor	Coefficient	relative importance
log(dispersal)	0.73±0.54	1
taxonomic group		0.6
log(mtDNA dist)	-0.02±0.1	0.33

Table S17: Model fitting for data set filtered to include only mitochondrial DNA clines (n = 45

hybrid zones). We fit linear models that predicted the log of cline width, with the log of dispersal,

log of mtDNA distance, log of nDNA distance, taxonomic group, and two-way interactions as

predictors. All variables were scaled and centered prior to modelling. Shown are the five models

with the highest AICc weights.

Model	AICc	weights	adj. r^2
~ 1 + log(dispersal) + log(mtDNA dist) + log(nDNA dist)+ taxonomic group + taxonomic group×log(dispersal) + taxonomic group×log(nDNA dist)	112.3	0.166	0.741
~ 1 + log(dispersal) + log(mtDNA dist) + log(nDNA dist)+ log(mtDNA dist)×log(dispersal)	112.4	0.154	0.416
~ 1 + log(dispersal) + taxonomic group + taxonomic group×log(dispersal)	112.6	0.143	0.579
~ 1 + log(dispersal) + log(nDNA dist)+ taxonomic group + taxonomic group×log(dispersal) + taxonomic group×log(nDNA dist)	112.9	0.121	0.71
~ 1 + log(dispersal)	115.1	0.041	0.317

Table S18: Model averaging results for the data set that only includes mtDNA clines (models

shown in Table S17), including coefficients and relative importance. Only the top three

predictors (as measured by relative importance) are shown. Coefficients not reported for

predictors including taxonomic group because these are calculated for each one of the seven

taxonomic groups.

Predictor	Coefficient	relative importance
log(dispersal)	1.41±1.84	0.98
log(nDNA dist)	-0.45±0.97	0.68
taxonomic group		0.6

Table S19: Model fitting for data set filtered to only include avian hybridizing pairs (n = 37 hybrid zones). Models predicting the log of the geometric mean of cline width were fit using a linear model. Predictors were the log of mtDNA distance and hand-wing index (HWI), a proxy for dispersal, and their interaction. All variables were scaled and centered prior to modelling. Shown are the five models with the highest AICc weights.

Model	AICc	weights	adj. r^2
~ 1 + log(HWI)	107.1	0.379	0.067
~ 1 + log(HWI) + log(mtDNA dist)	108.1	0.238	0.08
~ 1	108.3	0.206	0
~ 1 + log(mtDNA dist)	109.5	0.114	0.004
~ 1 + log(HWI) + log(mtDNA dist) + log(mtDNA dist)×log(HWI)	110.7	0.062	0.052

Table S20: Model averaging results for the dataset limited to avian hybridizing pairs, using hand-wing index (HWI) as a proxy for dispersal (shown in Table S19), including coefficients and relative importance. Only the top three predictors (as measured by relative importance) are shown.

| Predictor	Coefficient	relative importance
log(HWI)	0.21±0.4	0.68
log(mtDNA dist)	0.08±0.26	0.41
log(HWI)×log(mtDNA dist)	0±0.03	0.06

Table S21: Model fitting for data set filtered to only include avian hybridizing pairs (n = 18 hybrid zones; the outlier *Sula* boobies was removed). Models predicting the log of the geometric mean of cline width were fit using a linear model. Predictors were the log of phylogenetic divergence time (TMRCA), log of dispersal, and their interaction. All variables were scaled and centered prior to modelling. Shown are the five models with the highest AICc weight.

Model	AICc	weights	adj. r^2
~ 1 + log(dispersal) + log(phy div time) + log(phy div time)×log(dispersal)	49.9	0.705	0.438
~ 1	52.6	0.179	0
~ 1 + log(dispersal)	54.8	0.059	-0.02
~ 1 + log(phy div time)	55.3	0.047	-0.048
~ 1 + log(dispersal) + log(phy div time)	58.2	0.011	-0.086

Table S22: Model averaging results for the dataset limited to avian hybridizing pairs, using phylogenetic divergence time (TMRCA) as a proxy for selection against hybrids (shown in Table S21), including coefficients and relative importance. Only the top three predictors (as measured by relative importance) are shown.

| Predictor	Coefficient	relative importance
log(dispersal)	0.37±0.7	0.77
log(phy div time)	-0.24±0.5	0.76
log(dispersal)×log(phy div time)	0.82±1.22	0.71

SUPPLEMENTARY FIGURES
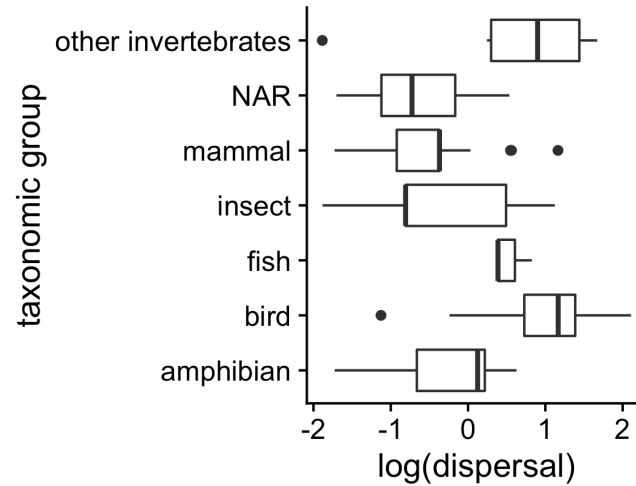
Figure S1: Log dispersal rate estimates across taxonomic groups (*n*=127); log dispersal is both scaled and centered. Dispersal varies more than four orders of magnitude. Taxonomic group is a significant predictor of variation in dispersal rates ($F_{6, 120}$ = 17.75; p-val = 1.2e-14; adj. r^2 = 0.44)
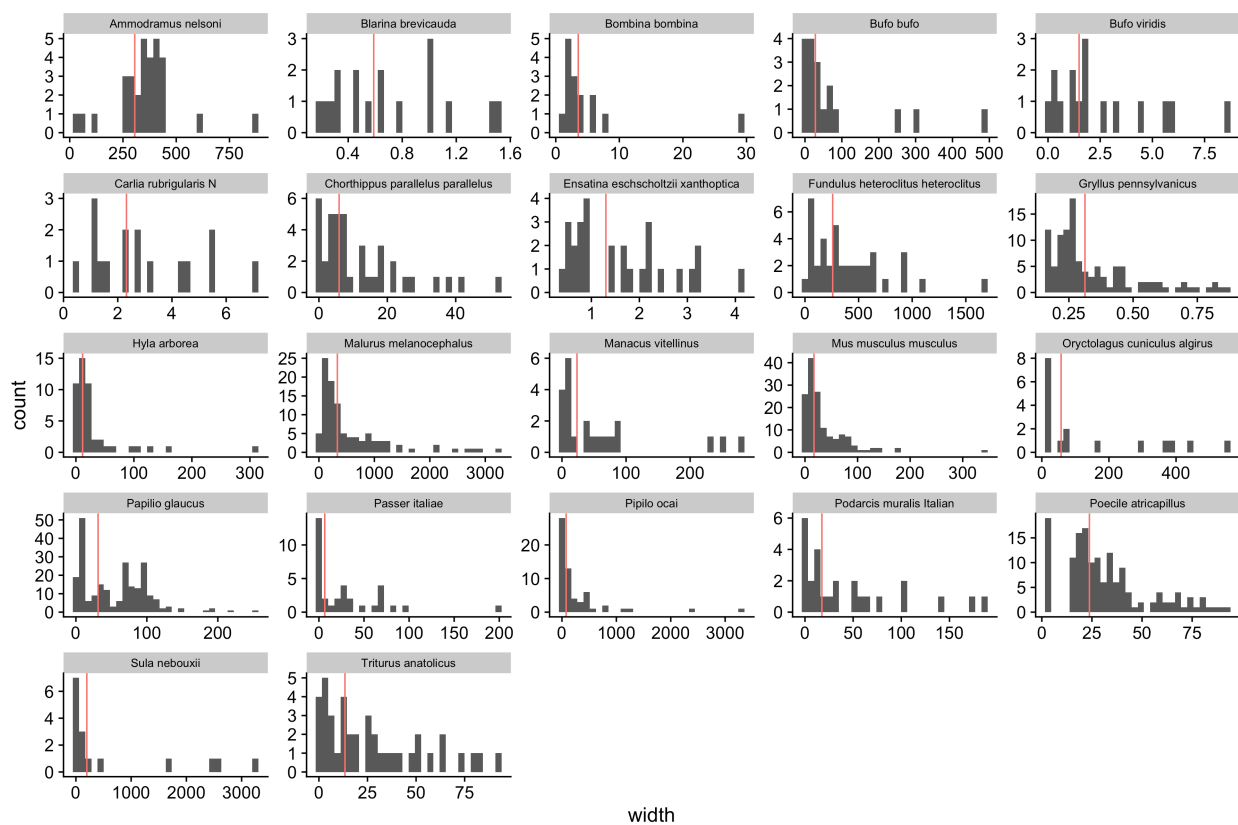
Figure S2: Distribution of cline widths (in kilometers) across hybrid zones for which 15 or more clines were inferred. The red vertical line depicts the geometric mean of cline widths. Variation among cline widths has both methodological and biological sources – e.g., using non-diagnostic markers or due to variable introgression across loci and traits. For most zones, the geometric mean of widths summarizes this variation well to capture the central tendency of cline widths.
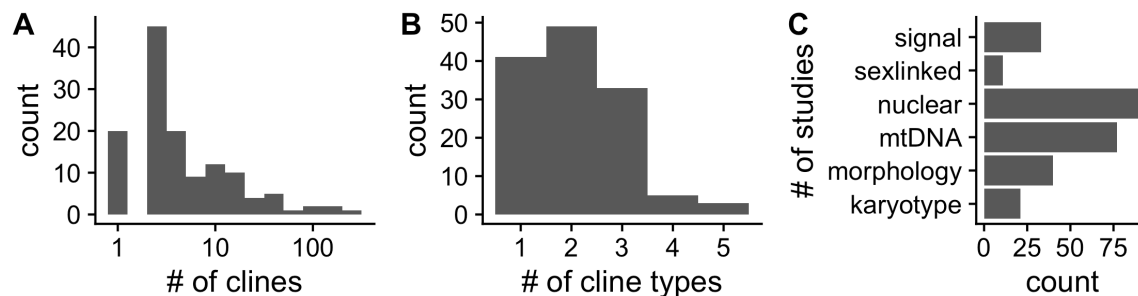
Figure S3: Clines summarized across hybrid zones. (A) The number of clines estimated per hybrid zone. A median of 4 clines were estimated per hybrid zone. (B) The number of cline types estimated per hybrid zone. A median of 2 types of clines were estimated per hybrid zone. (B) The number of hybrid zone studies that estimated each type of cline (signal-related traits like song, sex-linked genetic markers, nuclear genetic markers, mtDNA genetic markers, morphological measures, and karyotypes).
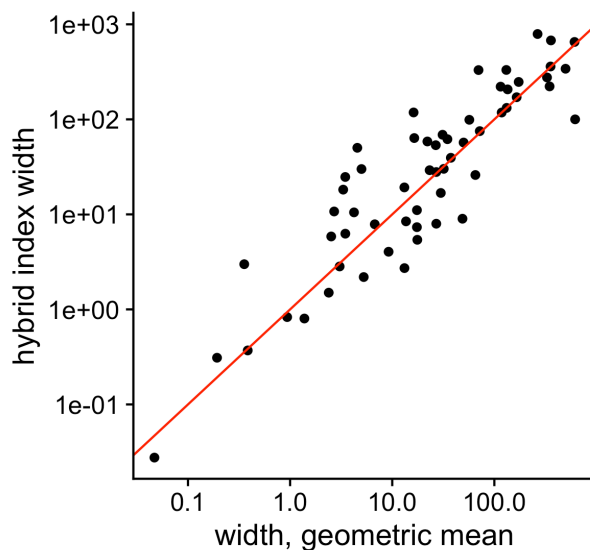
Figure S4: Correlation of cline widths estimated from molecular indices of hybrid index and the geometric mean of cline widths inferred from biallelic loci. These two estimates of cline width are significantly correlated (Spearman's r = 0.87; p < 2.2 x 10^{-16}; n = 58) and estimates tend to fall near the line of unity (shown in red). Because hybrid indices are inherently polygenic, they are likely to capture the central tendency of hybrid zones. These results suggest our geometric mean cline width estimates also accurately reflect the central tendency of hybrid zones and are not upwardly biased by outlier loci.
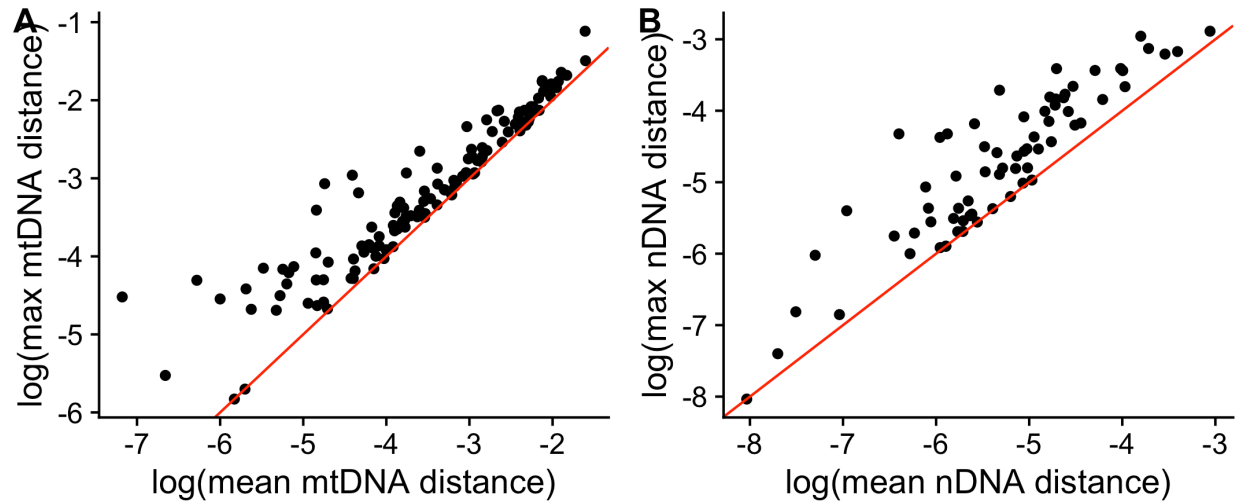
Figure S5: Mean versus maximum (A) mtDNA and (B) nDNA genetic distances for hybridizing taxon pairs. Mean vs. maximum genetic distances are significantly correlated (mtDNA: Pearson's r = 0.93; $p < 2.2 \times 10^{-16}$; n = 121; nDNA: Pearson's r = 0.90; $p < 2.2 \times 10^{-16}$; n = 70). Line of unity is shown in red. These results suggest that introgression across hybridizing pairs affects few of our genetic distance estimates.
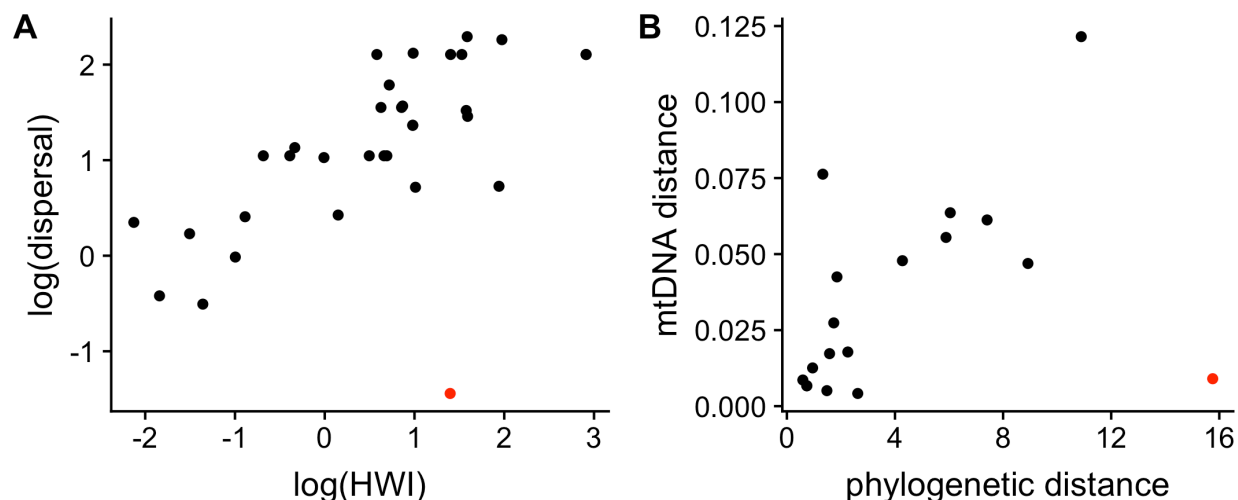
Figure S6: Correlations between alternative proxies for dispersal and selection against hybrids, for bird hybrid zones only. (A) Correlation between our literature-based estimates of dispersal rate and a common morphological proxy for dispersal capacity, hand-wing index (HWI), with both on the natural log scale. All variables were scaled and centered prior to analysis. Pearson's r = 0.50 (p = 0.0003; n = 33). The taxon pair *Sula nebouxii & S. variegata* is an outlier (shown in red). Excluding this pair returns a Pearson's r = 0.67 (p = 2 x 10^{-5}; n = 32). Log HWI also predicts log dispersal when phylogeny is taken into account using phylogenetic generalized linear modeling, with Ornstein-Uhlenbeck (OU) errors (slope = 0.37±0.13SE, t = 2.96, p = .007; p-value is conditional on α_{OU} = 0.006; calculated using function `phylolm` with option `OUrandomRoot`). (B) Correlation between mtDNA distance and phylogenetic distance between hybridizing pairs based on a global phylogeny of birds (Burleigh *et al*. 2015). Pearson's r = 0.41 (p = 0.08; n = 18). The taxon pair *Baeolophus atricristatus & B. bicolor* is an outlier (shown in red). Excluding this pair returns a Pearson's r = 0.78 (p = .0002; n = 17). These results suggest our estimates of dispersal rate and divergence are robust to the use of alternate predictors as proxies for hybrid zone dispersal and selection against hybrids. However, the mtDNA data used to estimate divergence in our study and the data used in the global phylogeny overlap, so a correlation is expected.
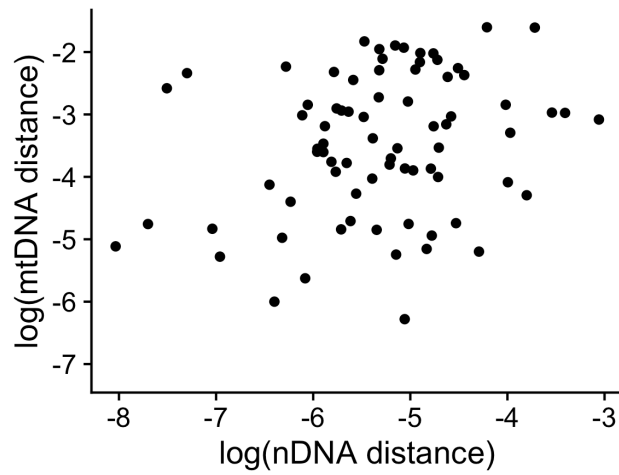
Figure S7: Correlation of genetic distances estimated from mtDNA vs. nDNA for hybridizing taxon pairs. These two estimates are weakly but significantly correlated (Pearson's r = 0.26; p = 0.021; n = 77).