

Appendix from J. P. McEntee et al., “Dispersal Predicts Hybrid Zone Widths across Animal Diversity: Implications for Species Borders under Incomplete Reproductive Isolation” (Am. Nat., vol. 196, no. 1, p. 000)

Table A1: Key metadata collected for each cline included in this study

Metadata	Details	Notes
Type	The type of phenotypic or molecular trait for which the cline was estimated	Summarized as morphological traits, traits involved in mating (e.g., pheromones or bird song), mitochondrial DNA markers, nuclear DNA markers, karyotypic markers, or sex-linked DNA markers (see fig. S2C)
No. markers	For molecular clines, the number of loci used to infer the cline	...
Biallelic or quantitative	Whether the cline-fitting analysis treats characters as biallelic or quantitative	Molecular cline estimates based on more than one locus were coded quantitative; all morphological data were coded quantitative
Width	Point estimate for cline width	...
Center	Point estimate for cline center	...
Difference between tails	The difference in trait values at the extreme tails of each hybridizing species	For biallelic traits, this reflected differences in allele frequency; for quantitative traits, this reflected standardized differences in phenotypes
Program used	The program used to estimate cline parameters	...

Table A2: Key metadata collected for each hybridizing pair included in this study

Metadata	Details	Notes
Taxa	The scientific names of the hybridizing taxa	Some hybrid zones occur between taxa not currently recognized as species; in these cases, we followed the naming convention used by the study’s authors
Moving or not?	Whether authors provided or referred to evidence that the hybrid zone is moving in position over time	Many studies did not provide this information
Anthropogenic?	Whether the hybrid zone arose as a result of anthropogenic disturbance and/or is being affected by anthropogenic effects	Many studies did not provide this information
Genetic distance	Estimates of genetic distance (reported in units of substitution) between the taxa for both mitochondrial DNA and nuclear DNA; both mean and maximum distance were calculated	We calculated most estimates using GenBank data, while other estimates were taken from the literature; for all estimates, we noted the marker and model of molecular evolution used
Dispersal estimate	Estimates of dispersal (and their units) for the taxa or closely related taxa	
Dispersal type	The methodology used to estimate dispersal	Many ecological and genetic approaches were used to estimate dispersal, including mark-recapture studies and approaches based on isolation by distance
Dispersal independent of hybrid zone	Whether the estimate of dispersal used estimates of cline width	Cline width, in conjunction with estimates of linkage disequilibrium in the hybrid zone center, is often used to estimate dispersal; including such dispersal estimates creates nonindependence among data sets
Generation time	Estimated generation time for the taxa	...
Taxonomic group	Broadly categorized into amphibian, bird, fish, insect, mammal, nonavian reptile, and other invertebrates	...
Geographic location	Broadly geographic regions	...
Citation	All articles from which cline and hybrid zone data were mined	...