

Supporting Information

SI Materials and Methods

Sampling and Taxonomy. Our species sampling was determined by the species for which datasets were currently available or under construction in our labs. We restricted sampling to the mainland New World because New World birds are much better represented in existing genetic resources collections and genetic datasets than Old World species, which are particularly poorly sampled in tropical areas (1). In only a few cases (*Anas strepera*, *Calidris ptilocnemis*, *Corvus corax*, *Hirundo rustica*, and *Pinicola enucleator*) do study species contain Old World populations, which were not sampled for our analyses. Several of these species (the *Anas*, *Calidris*, and *Pinicola*) are important as the only or one of few representatives of their clade with phylogeographic data available. The phylogenetic dataset used to estimate speciation rates was worldwide in coverage. This strategy allowed us to maintain consistency between datasets – both the population genetic datasets (with the five exceptions above) and the phylogenetic dataset included all subtending lineages rather than a potentially biased subset of daughter lineages. Including all species in the phylogeny, combined with an analytical correction for taxa lacking genetic data, allowed us to estimate absolute speciation rates from each lineage for direct comparison with population differentiation rates.

Population Differentiation Rate Estimation. Mitochondrial gene trees were time-calibrated using an uncorrelated relaxed substitution rate based on published avian mitochondrial rates of 0.0125 substitutions/site/My for ND2 and ATPA6, 7, & 8 (2) and 0.0105 s/s/My for CytB (3). For the gene COI we used the same rate as CytB because the loci mutate at similar rates (2). For the clock rate parameter we specified a lognormal distribution on the prior with the mean set to the above-mentioned substitution rates and a standard deviation of 0.1. We note that these substitution rates may differ from the rates represented in the phylogenetic data. Because substitution rates differ between short and long timescales (4), however, using rates that have been widely applied and tested on intraspecific timescales is the best option in this case. We expect any bias in crown and stem ages from the population-level data relative to branching times from the phylogenetic data to be minimal and have minimal impact on population differentiation rate estimates. Moreover, because we apply the same calibrations for all study species, this bias would be equivalent across species and therefore would not impact correlations between population differentiation and speciation rates.

We estimated time-calibrated gene trees in BEAST using a coalescent-constant-size tree prior and the best-fit nucleotide substitution model as determined in MEGA6 (5). We ran each analysis for 50 million generations sampling every 2,500 generations, performed multiple independent runs for validation, and assessed Markov chain Monte Carlo (MCMC) convergence and determined burn-in by examining ESS values and likelihood plots in Tracer v.1.5 (6). For some datasets that did not achieve high ESS values after 50 million generations, we included additional generations until the results were stable. Maximum clade credibility (MCC) trees were estimated from the posterior distribution of trees for each species using TreeAnnotator (7).

bGMYC determines the number of genetic species by estimating the number of clusters within which splits in the gene tree fit a coalescent model rather than a model of interspecific diversification (Yule model) in a Bayesian framework. We ran the program for 250,000

46 generations using the single.phy function and discarded the first 15,000 generations as burn-in.
47 We ran each analysis multiple times for validation, and assessed MCMC diagnostics by
48 examining likelihood plots in Tracer. Units delimited using the GMYC model are typically
49 regarded as species. In birds, however, more stringent criteria, involving metrics of reproductive
50 isolation or phenotypic divergence, are typically applied for species delimitation (8, 9). Non-
51 interbreeding populations failing to meet this criteria, such as many of the units delimited in this
52 study, are often assigned subspecies status. Many of the units in this study may even fail to meet
53 some researchers' criteria for subspecies status, indeed many have not been elevated to
54 subspecies despite prior publications based on the same genetic data examined here. As a result,
55 GMYC units in birds are perhaps better treated as genetically differentiated populations, and we
56 follow this philosophy here. A similar perspective, treating delimited groups as populations, has
57 recently been advocated for the multispecies coalescent more generally (10). Regardless of their
58 taxonomic status, however, GMYC clusters represent more finely resolved and more recently
59 diverged groups relative to the terminal taxa in the avian phylogeny we examined, and thus are
60 appropriate for comparing divergence rates between recent and deep timescales, the fundamental
61 goal of this study. An alternate method for identifying geographic variants would have been to
62 use named subspecies, a strategy we examine below.

63 We corrected for differences in the age of species by calculating the rate at which bGMYC
64 clusters formed since the species' crown age. All rates were calculated using a starting diversity
65 of one despite the use of crown age. Crown age in our study corresponds to the first divergence
66 between mitochondrial haplotypes rather than the first divergence between bGMYC clusters, and
67 thus represents a time point when only one bGMYC cluster was present. The area across which a
68 species is distributed might also predict its level of differentiation, but we found area was not
69 strongly correlated with the number of differentiated populations ($R^2 = 0.029$, $P = 0.025$),
70 certainly much less so than age ($R^2 = 0.285$, $P < 0.001$). This suggests that population
71 differentiation has similar evolutionary potential regardless of the size of the area across which it
72 occurs, and we therefore do not control for area in any subsequent analyses.

73 Because we examined differentiation at shallow time scales, we might assume that extinction
74 is infrequent and pure-birth (Yule) models provide reasonable estimates of differentiation rate,
75 and these were used for primary analyses. Jointly estimating speciation and extinction is possible
76 using birth-death models and taking advantage of branch length information in population
77 phylogenies. However, the majority of our population trees contained so few tips that the
78 likelihood surface for parameter estimation was flat and confidence intervals were very large (T.
79 J. Stadler, pers. comm.). Instead, we examined models that estimated speciation provided
80 different fixed extinction rates. We examined differentiation rates using models with moderate
81 ($\epsilon = 0.45$) and high ($\epsilon = 0.9$) constant rates of extinction, in addition to the pure-birth
82 model.

83
84 **Speciation Rate Estimation.** The software program BAMM uses reversible-jump MCMC to
85 examine models differing in the number of time-varying diversification processes present across
86 the phylogeny. Each process includes a time-varying speciation term and a time-invariant
87 extinction rate. In the BAMM run using the primary taxonomy, multiple tips from within the
88 same species were collapsed so as to avoid overlap in the data used for estimation of speciation
89 and population differentiation rates. We ran BAMM using a model allowing for variable rates for
90 at least 350 million generations in both the split and primary analyses, completing multiple runs
91 with the same settings for validation. We sampled every 200,000 generations and discarded 10%

92 of the sample as burn-in. Marginal distributions of speciation rates at the tips of the tree represent
93 estimates of present-day speciation rates for those taxa.

94
95 **Comparative Analyses.** We first used STRAPP, which computes the correlation between
96 character states at the tips of the tree and their corresponding diversification rates, and assesses
97 significance by permuting speciation rates among regimes estimated in BAMM. Parametric
98 uncertainty in diversification rates is accommodated by conducting tests across the posterior
99 distribution of rates inferred using BAMM. The permutation test is used to control for the
100 covariance among species from the same macroevolutionary rate regime, thereby explicitly
101 incorporating covariance among replicates with shared history and macroevolutionary dynamics.
102 All tests presented are two-tailed tests, examining the alternative hypothesis that there is a
103 correlation between population differentiation and speciation rates. One-tailed tests, in which the
104 alternative hypothesis is the presence of a positive correlation between population differentiation
105 and speciation rates, resulted in greater significance values than the two-tailed tests presented.
106 The primary two-tailed test presented in the main text, for example, resulted in a significance
107 level of $P = 0.018$, whereas the equivalent one-tailed test resulted in a level of $P = 0.010$. We
108 used the two-tailed test as a more conservative index of trait-dependent diversification.

109 We also conducted comparative analyses of the number of splits summary statistic of
110 speciation rate using phylogenetic generalized least squares (PGLS) in the caper package (11) in
111 R. PGLS analysis using the number of splits summary statistic produced similar results to
112 STRAPP overall. We log-transformed rate values to reduce heteroscedasticity in the residuals of
113 PGLS models. In addition to the results presented in the main text, PGLS analysis using the split
114 taxonomy (PGLS slope = 0.239, $P < 0.001$) and time threshold (PGLS slope = 0.141, $P = 0.021$)
115 resulted in a correlation similar to that using the primary taxonomy. The relationship with PGLS
116 was also robust to the use of lower (0.7; PGLS slope = 0.217, $P < 0.001$) and higher (0.9; PGLS
117 slope = 0.227, $P < 0.001$) posterior probability thresholds for assigning individuals to population
118 clusters, to whether the population differentiation rate was measured using the stem age rather
119 than crown age of a species (PGLS slope = 0.349, $P < 0.001$), to the random removal of 20%
120 (PGLS slope = 0.211, $P < 0.001$) and 40% (PGLS slope = 0.209, $P < 0.001$) of samples from the
121 dataset, to the removal of populations containing a single individual (PGLS slope = 0.210, $P <$
122 0.001), and to models of population differentiation incorporating moderate ($eps = 0.45$; PGLS
123 slope = 0.182, $P < 0.001$) or high ($eps = 0.9$; PGLS slope = 0.134, $P = 0.002$) extinction rates.

124 Multivariate analyses were conducted to evaluate whether predictors aside from population
125 differentiation might better explain speciation rate variation. Although STRAPP does not
126 accommodate multi-predictor tests, multivariate tests can be easily accomplished in a PGLS
127 framework. We therefore conducted multivariate tests using the DR statistic and PGLS models.
128 We gathered data on a set of alternative predictor variables that have been hypothesized to
129 impact avian diversification rates (see Main Text). We gathered range information for each
130 species from existing digital range maps (12). We estimated range size and midpoint latitude,
131 and calculated migratory distance as the distance between the breeding and wintering latitudinal
132 midpoints for migratory species (for non-migratory species, migratory distance was zero). We
133 gathered georeferenced observational data from the eBird database (May 2013 release)(13). We
134 filtered erroneous records based on the digital distributional maps and selected 1000 records
135 from unique localities 1 km or more apart. We extracted elevation and 19 current climatic
136 variables at a spatial resolution of 2.5 arc seconds from the WorldClim database (14) and also
137 measured the per-cell difference between the 19 current climate variables and the corresponding

138 paleoclimate layers from the last glacial maximum (MIROC: Model for Interdisciplinary
139 Research on Climate) in ArcGIS (ESRI Inc., Redlands, CA) as a metric for climate stability
140 through time. We reduced the dimensionality of the current climate, elevation, and climate
141 stability variables ($n = 39$ total) using principal components analysis and selected PC1 (explained
142 49.2% of variable variance) and PC2 (explained 18.1% of variance) for further analysis. We used
143 museum specimens of each species to measure tarsus length (a common proxy for body size in
144 birds) and a morphological metric of dispersal ability called Kipp's index that represents a ratio
145 of wing length to breadth (15,16). We measured at least five male specimens in adult plumage
146 per species. Spectral information on sexual dichromatism is available for only a subset (37%) of
147 our study species (17), which was insufficient for use in multi-predictor PGLS models. We
148 therefore scored simple presence/absence of dichromatism in each species based on visual
149 inspection of museum specimens. We log-transformed positive right-skewed variables (DR
150 statistic, population differentiation rate, environmental PC1, range size, tarsus length, and Kipp's
151 index) to reduce residual heteroscedasticity and ran multi-predictor PGLS models containing all
152 nine variables (all as additive predictors), including population differentiation. We then removed
153 each variable one-by-one and evaluated the resulting models. We compared the full model and
154 the nine models with a variable removed using the sequential sums of squares with the
155 `anova.pgls` function in `caper` (11) and performed AIC model comparison.

156 We evaluated the robustness of the difference between tropical and temperate species in the
157 strength of the association between population differentiation and speciation rates. The larger
158 sample size of the tropical species may underlie the more significant result in that group, but
159 resampling the tropical dataset 1000 times to the same sample size as the temperate group
160 consistently produced stronger correlations (results in Main Text) in analysis using the BMM
161 speciation rates, albeit not with the DR speciation rates. We also evaluated the possibility of a
162 null hypothesis in which species were randomly assigned to two groups the same size as the
163 temperate and tropical positions. Again, this permutation test suggested that the correlations were
164 more different than expected in when using BMM speciation rates ($P = 0.026$), but was not
165 significant for the DR speciation rates ($P = 0.283$). Overall, these results suggest the stronger
166 correlation in tropical relative to temperate species reflects real differences among the species in
167 the two regions. $P = 0.026$, $P = 0.283$.

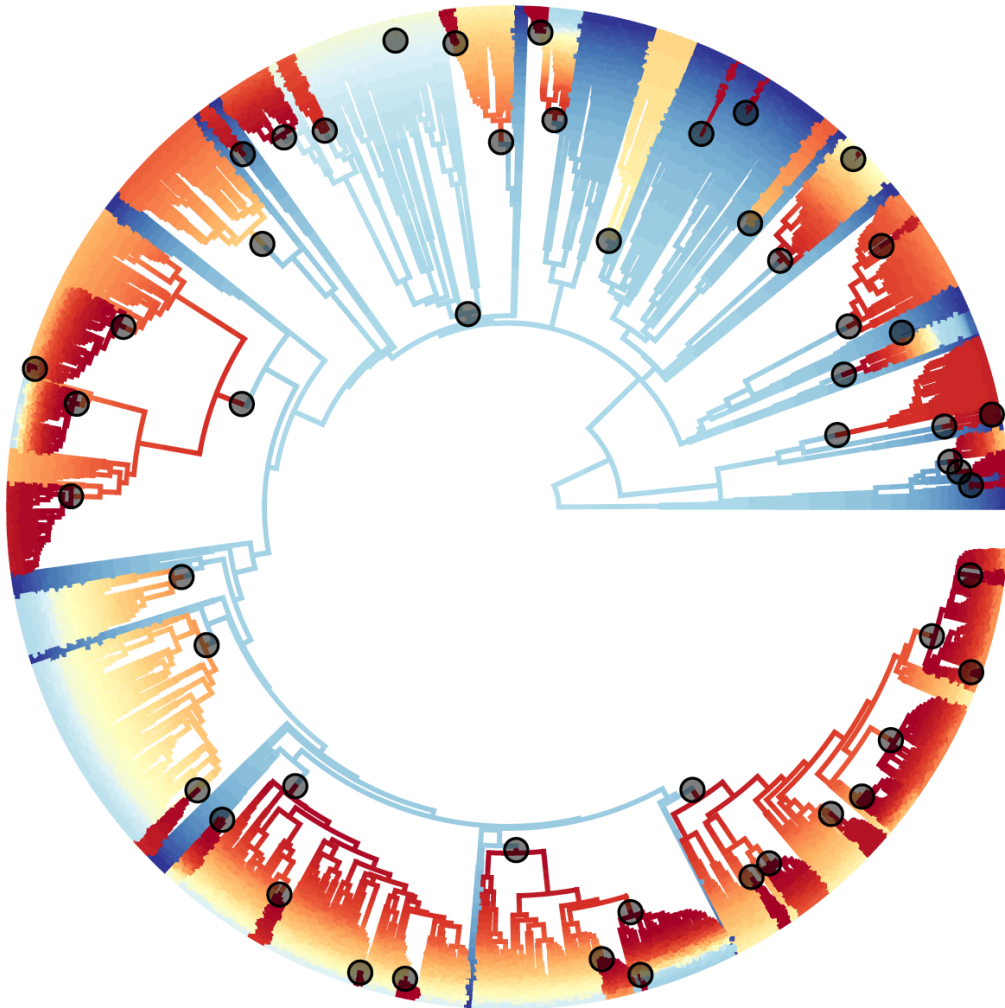
168
169 **Comparison to Analysis of Taxonomic Subspecies.** Prior studies of the association between
170 intraspecific diversity and species diversification have relied on the number of taxonomic
171 subspecies within a species as a proxy of intraspecific diversity (see Main Text). Taxonomic
172 subspecies in birds typically correspond to morphologically distinguishable groups that are
173 geographically separated, but criteria for subspecies status have been variably applied and there
174 is limited intersection between currently recognized subspecies and intraspecific diversity based
175 on genetic data (18). The use of genetic structure within species may sufficiently reduce
176 subjectivity and improve comparability in estimates of intraspecific diversity, such that the
177 reflect a quantity that more accurately predicts the diversification potential of a lineage. It also
178 provides explicit timing information on the crown age of populations and population splitting
179 events for estimation of rates of population differentiation. We compared our estimates of
180 genetic differentiation in our study species to currently recognized subspecies diversity based on
181 the Clements/eBird taxonomy (19) because the AOS taxonomies do not treat subspecies.
182 Subspecies richness was correlated with number of genetically differentiated populations ($R^2 =$
183 0.228 , $P < 0.001$), but we found no association between speciation rate and either the number of

184 taxonomic subspecies within a species (BAMM $r = 0.021$, $P = 0.716$) or the rate of formation of
185 subspecies since the crown age of a species (BAMM $r = 0.148$, $P = 0.210$). These results suggest
186 metrics of genetic differentiation capture intraspecific diversity that better reflects diversification
187 dynamics in evolutionary lineages than taxonomic proxies.

188

189 SI Figures

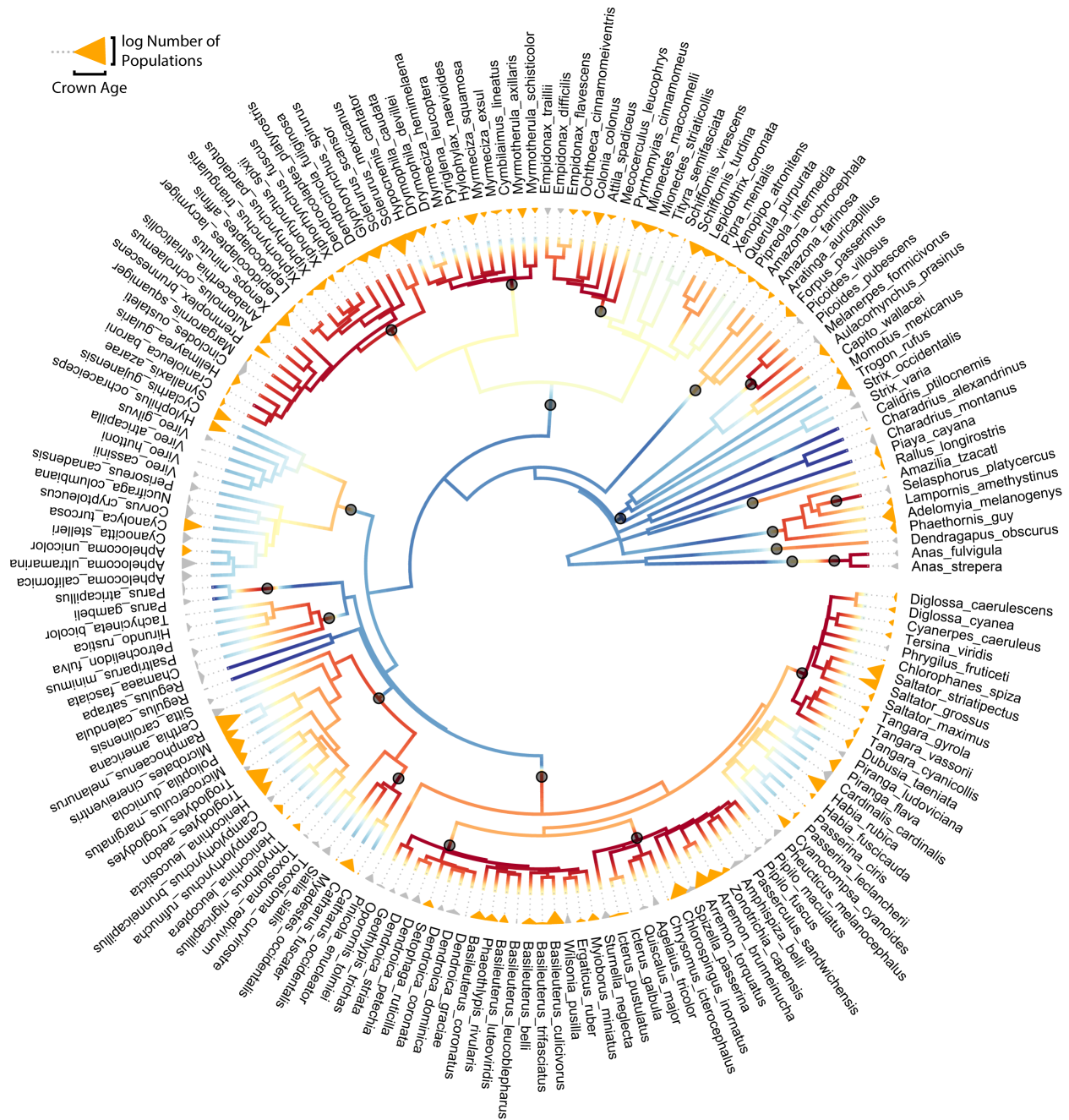
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191 **Fig. S1.** A phylorate plot showing speciation rates and macroevolutionary regime shifts (black
192 circles) from the maximum shift credibility sample from the BAMM posterior. The tree contains
193 all 6,617 species from the phylogeny with genetic data (after collapsing species from the original
194 phylogeny that were in the same species in our primary taxonomy).

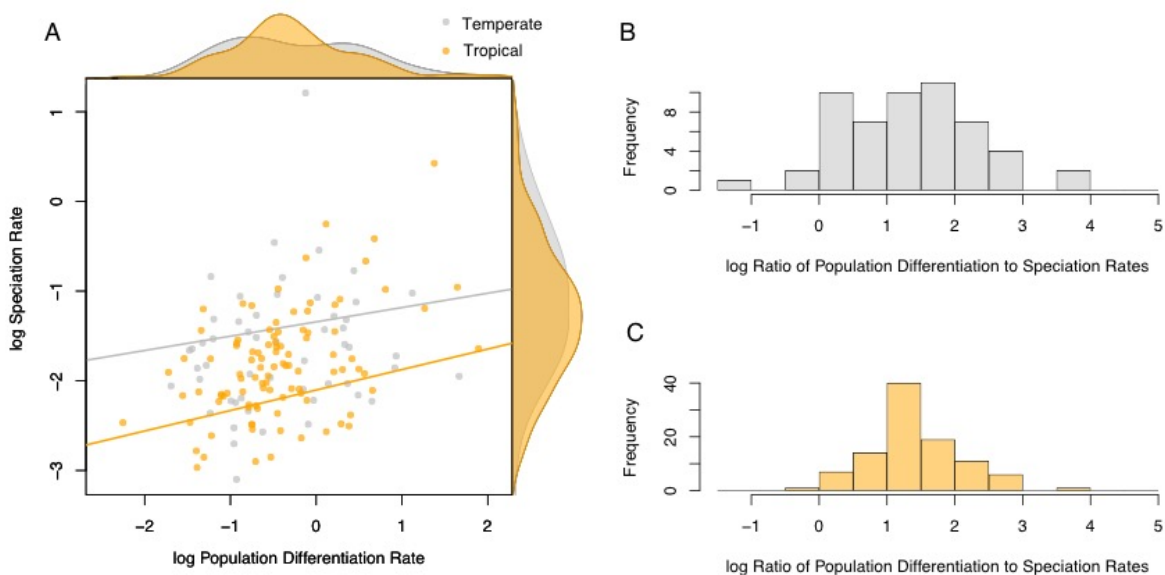
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197
 198 **Fig. S2.** A phylorate plot of the study species similar to that from Fig. 2 in the main text. Colors
 199 on the phylogeny in the center indicate mean posterior speciation rates along branches. The black
 200 circles represent rate regime shifts in the maximum shift credibility sample from the posterior.
 201 Triangles encircling the phylogeny depict population differentiation rates and are colored
 202 according to whether a species is tropical (orange) or temperate (gray). Species names are listed
 203 adjacent to the circle representing their differentiation rate. For species containing multiple AOS
 204 species names, the name shown was selected randomly from the name set.

205
 206
 207
 208



209
 210 **Fig. S3.** Plots showing differences in relative population differentiation and speciation rates
 211 between temperate and tropical species using the DR statistic. (A) Tropical species show a
 212 relationship between population differentiation rates and speciation rates (0.229 , $P < 0.001$),
 213 whereas temperate species do not (PGLS slope = 0.160 , $P = 0.086$). Kernel density plots showing
 214 the relative distributions of rates between tropical and temperate species are plotted opposite the
 215 axis of the rate to which they correspond and show that neither differentiation or speciation rates
 216 differ noticeably between temperate and tropical species. The ratio of population differentiation
 217 rate to speciation rate, however, is more variable in temperate species (B) than tropical species
 218 (C).
 219

220 **SI Table**

221
 222 **Table S1.** Change in AICc weights in multivariate PGLS models of speciation rate variation.
 223

Variable	ΔAICc^*
Population differentiation rate	5.536
Range size	-0.223
Range midpoint latitude	-2.050
Migratory distance	2.202
Environmental PC1	-1.929
Environmental PC2	0.752
Tarsus length (body size proxy)	3.164
Kipp's Index (dispersal ability proxy)	-1.917
Sexual dichromatism	-2.019

* difference between model with variable removed and full model

SI Appendix: Study species

Species	AOS Species	Locus	References
1	<i>Adelomyia melanogenys</i>	CR-ATP8-ATP6	21, 22
2	<i>Agelaius phoeniceus</i>	ND2	23
	<i>Agelaius tricolor</i>		
3	<i>Amazilia tzacatl</i>	ND2	24
4	<i>Amazona farinosa</i>	CytB	25
5	<i>Amazona ochrocephala</i>	ND2	26, 27
	<i>Amazona aestiva</i>		
6	<i>Anabacerthia striaticollis</i>	ND2	28
7	<i>Anas fulvigula</i>	CR	29
8	<i>Anas strepera</i>	CR	30
9	<i>Aphelocoma caerulescens</i>	ND2	31
	<i>Aphelocoma californica</i>		
	<i>Aphelocoma insularis</i>		
10	<i>Aphelocoma ultramarina</i>	ND2	31, 32
	<i>Aphelocoma wollweberi</i>		
11	<i>Aphelocoma unicolor</i>	ND2	31, 32
12	<i>Aratinga solstitialis</i>	CytB	33
	<i>Aratinga jandaya</i>		
	<i>Aratinga auricapillus</i>		
13	<i>Arremon brunneinucha</i>	COII	34
14	<i>Arremon torquatus</i>	ND2	28, 35
	<i>Arremon assimilis</i>		
	<i>Arremon atricapillus</i>		
	<i>Arremon basilicus</i>		
	<i>Arremon costaricensis</i>		
	<i>Arremon perijanus</i>		
	<i>Arremon phaeopleurus</i>		
<i>Arremon phygas</i>			
15	<i>Artemisiospiza belli</i>	CytB	36
	<i>Artemisiospiza nevadensis</i>		
16	<i>Attila spadiceus</i>	CytB	37
17	<i>Aulacorhynchus prasinus</i>	ND2	38
18	<i>Automolus ochrolaemus</i>	CytB	37
19	<i>Basileuterus belli</i>	ND2	39
20	<i>Basileuterus culicivorus</i>	CytB	40
21	<i>Basileuterus tristriatus</i>	ND2	41
	<i>Basileuterus trifasciatus</i>		

Species	AOS Species	Locus	References
22	<i>Calidris ptilocnemis</i>	CytB	42
23	<i>Campylorhynchus brunneicapillus</i>	ND2	43
24	<i>Campylorhynchus rufinucha</i>	ND2	44
25	<i>Cantorchilus nigricapillus</i>	ATP8-ATP6	45
26	<i>Capito wallacei</i>	CytB	46
27	<i>Cardellina pusilla</i>	CytB	47
28	<i>Cardellina rubra</i>	ND2	48
	<i>Cardellina versicolor</i>		
29	<i>Cardinalis cardinalis</i>	ND2	49
30	<i>Catharus fuscater</i>	ND2	28
31	<i>Catharus occidentalis</i>	ND2	50
32	<i>Ceratopipra chloromeros</i>	ND2	50
	<i>Ceratopipra mentalis</i>		
	<i>Ceratopipra erythrocephala</i>		
	<i>Ceratopipra rubrocapilla</i>		
33	<i>Certhia americana</i>	ND2	51
34	<i>Chamaea fasciata</i>	CytB	52
35	<i>Charadrius montanus</i>	CR	53, 54
36	<i>Charadrius nivosus</i>	CR	54
37	<i>Chlorophanes spiza</i>	CytB	37
38	<i>Chlorospingus flavopectus</i>	ATP8-ATP6	55, 56, 57
	<i>Chlorospingus semifuscus</i>		
	<i>Chlorospingus inornatus</i>		
	<i>Chlorospingus tacarcunae</i>		
39	<i>Chrysomus icterocephalus</i>	ND2	58
40	<i>Cinclodes fuscus</i>	ND3	59, 60
	<i>Cinclodes olrogi</i>		
	<i>Cinclodes oustaleti</i>		
	<i>Cinclodes comechingonus</i>		
	<i>Cinclodes antarcticus</i>		
	<i>Cinclodes albidiventris</i>		
41	<i>Colonia colonus</i>	CytB	37
42	<i>Corvus corax</i>	CytB	61
	<i>Corvus cryptoleucus</i>		
43	<i>Cranioleuca antisiensis</i>	ND2	50
	<i>Cranioleuca baroni</i>		
44	<i>Cyanerpes caeruleus</i>	CytB	37

Species	AOS Species	Locus	References
45	<i>Cyanocitta stelleri</i>	ND2	50
46	<i>Cyanocompsa cyanoides</i>	CytB	62
47	<i>Cyanolyca viridicyanus</i>	ND2	28
	<i>Cyanolyca turcosa</i>		
	<i>Cyanolyca armillata</i>		
48	<i>Cyclarhis gujanensis</i>	ND2	50, 63
	<i>Cyclarhis nigristrostris</i>		
49	<i>Cymbilaimus lineatus</i>	CytB	37
50	<i>Dendragapus fuliginosus</i>	CR	64
	<i>Dendragapus obscurus</i>		
51	<i>Dendrocincla fuliginosa</i>	CytB	37
	<i>Dendrocincla anabatina</i>		
52	<i>Dendrocolaptes platyrostris</i>	CytB	65
53	<i>Diglossa caerulescens</i>	ND2	28
54	<i>Diglossa cyanea</i>	ND2	28
55	<i>Drymophila caudata</i>	ND2	28, 66
	<i>Drymophila klagesi</i>		
	<i>Drymophila hellmayri</i>		
	<i>Drymophila striaticeps</i>		
56	<i>Drymophila devillei</i>	ND2	67
57	<i>Dubusia taeniata</i>	ND2	28
58	<i>Empidonax difficilis</i>	ND2	50
	<i>Empidonax occidentalis</i>		
59	<i>Empidonax flavescens</i>	ND2	50
60	<i>Empidonax traillii</i>	CytB	68
61	<i>Forpus coelestis</i>	ND2-CytB	69
	<i>Forpus conspicillatus</i>		
	<i>Forpus xanthops</i>		
	<i>Forpus passerinus</i>		
	<i>Forpus xanthopterygius</i>		
62	<i>Geothlypis tolmiei</i>	ND2	50
63	<i>Geothlypis trichas</i>	ND2	50
	<i>Geothlypis beldingi</i>		
	<i>Geothlypis nelsoni</i>		
	<i>Geothlypis flavovelata</i>		
64	<i>Glyphorhynchus spirurus</i>	CytB	37
65	<i>Habia fuscicauda</i>	ND2	50
66	<i>Habia rubica</i>	ND2	50

Species	AOS Species	Locus	References
67	<i>Hellmayrea gularis</i>	ND2	28
68	<i>Henicorhina leucoptera</i>	ATP8-ATP6	50
69	<i>Henicorhina leucosticta</i>	CytB	37
70	<i>Hirundo rustica</i>	ND2	70
71	<i>Hylophilus ochraceiceps</i>	ND2	63
72	<i>Hylophylax naevioides</i>	ND2	71
	<i>Hylophylax naevius</i>		
73	<i>Hypocnemis cantator</i>	ND2	67, 72, 73
	<i>Hypocnemis flavescens</i>		
	<i>Hypocnemis peruviana</i>		
	<i>Hypocnemis subflava</i>		
	<i>Hypocnemis ochrogyna</i>		
	<i>Hypocnemis striata</i>		
	<i>Hypocnemis rondoni</i>		
74	<i>Icterus galbula</i>	CytB	74
	<i>Icterus abeillei</i>		
75	<i>Icterus pustulatus</i>	CytB	75
76	<i>Lampornis amethystinus</i>	CR	76
77	<i>Lepidocolaptes affinis</i>	ND2	77
78	<i>Lepidocolaptes lacrymiger</i>	ND2	28
79	<i>Lepidothrix coronata</i>	CytB	37
80	<i>Margarornis squamiger</i>	ND2	28
81	<i>Mecocerculus leucophrys</i>	ND2	28
82	<i>Melanerpes formicivorus</i>	CytB	78
83	<i>Melozone fusca</i>	CR	35
84	<i>Microbates cinereiventris</i>	ND2	50, 63, 73
	<i>Microbates collaris</i>		
85	<i>Microcerculus marginatus</i>	CytB	37
86	<i>Mionectes oleagineus</i>	ND2	79
	<i>Mionectes rufiventris</i>		
	<i>Mionectes macconnelli</i>		
87	<i>Mionectes striaticollis</i>	ND2	28
88	<i>Momotus mexicanus</i>	ND2	80
89	<i>Myadestes occidentalis</i>	ND2	39
90	<i>Myioborus miniatus</i>	ND2	50, 81, 82
91	<i>Myiothlypis coronata</i>	ND2	28

Species	AOS Species	Locus	References
92	<i>Myiothlypis fulvicauda</i>	ATP8-ATP7	83
	<i>Myiothlypis rivularis</i>		
93	<i>Myiothlypis leucoblephara</i>	CytB	84
94	<i>Myiothlypis luteoviridis</i>	ND2	28
95	<i>Myrmeciza exsul</i>	ND2	85
96	<i>Myrmeciza hemimelaena</i>	CytB	86
97	<i>Myrmeciza loricata</i>	ND2	87
	<i>Myrmeciza squamosa</i>		
98	<i>Myrmotherula axillaris</i>	CytB	37
99	<i>Myrmotherula schisticolor</i>	ND2	28
100	<i>Nucifraga columbiana</i>	ND2	88
101	<i>Ochthoeca cinnamomeiventris</i>	ND2	28
102	<i>Passerculus sandwichensis</i>	ND2	89
103	<i>Passerina ciris</i>	ND2	90
104	<i>Passerina leclancherii</i>	ND2	80
105	<i>Perisoreus canadensis</i>	ND2	91
106	<i>Petrochelidon fulva</i>	CytB	92
107	<i>Phaethornis guy</i>	ND2	28
108	<i>Pheucticus melanocephalus</i>	ND2	93
109	<i>Phrygilus fruticeti</i>	COI	94
110	<i>Piaya cayana</i>	CytB	37
111	<i>Picoides pubescens</i>	CR-ATP8-ATP6	95
112	<i>Picoides villosus</i>	ND2	96
113	<i>Pinicola enucleator</i>	ND2	97
114	<i>Pipilo erythrophthalmus</i>	ND2	50
	<i>Pipilo maculatus</i>		
115	<i>Pipreola riefferii</i>	ND2	28
	<i>Pipreola intermedia</i>		
116	<i>Piranga flava</i>	ND2	50
117	<i>Piranga ludoviciana</i>	CytB	50
118	<i>Poecile atricapillus</i>	ND6	98
119	<i>Poecile gambeli</i>	ND2	99

Species	AOS Species	Locus	References
120	<i>Polioptila albiloris</i>	ND2	50, 63, 100
	<i>Polioptila nigriceps</i>		
	<i>Polioptila melanura</i>		
	<i>Polioptila californica</i>		
	<i>Polioptila plumbea</i>		
	<i>Polioptila caerulea</i>		
	<i>Polioptila dumicola</i>		
	<i>Polioptila lactea</i>		
121	<i>Premnoplex tatei</i>	ND2	101
	<i>Premnoplex brunnescens</i>		
122	<i>Psaltriparus minimus</i>	ND2	50
123	<i>Pyriglena leucoptera</i>	ND2	102
	<i>Pyriglena atra</i>		
124	<i>Pyrrhomyias cinnamomeus</i>	ND2	28
125	<i>Querula purpurata</i>	CytB	37
126	<i>Quiscalus mexicanus</i>	ND2	103
	<i>Quiscalus major</i>		
127	<i>Rallus longirostris</i>	ND2	104
	<i>Rallus elegans</i>		
128	<i>Ramphocaenus melanurus</i>	ND2	50, 63
129	<i>Regulus calendula</i>	ATP8-ATP6	50
130	<i>Regulus satrapa</i>	ATP8-ATP6	50
131	<i>Saltator coerulescens</i>	ND2	105
	<i>Saltator similis</i>		
	<i>Saltator striatipectus</i>		
132	<i>Saltator grossus</i>	ND2	105
	<i>Saltator cinctus</i>		
	<i>Saltator aurantirostris</i>		
133	<i>Saltator maximus</i>	ND2	105
134	<i>Schiffornis turdina</i>	CytB	37
135	<i>Schiffornis virescens</i>	CR	106
136	<i>Sclerurus mexicanus</i>	CytB	37
	<i>Sclerurus ruficularis</i>		
137	<i>Sclerurus scansor</i>	ND2	107
138	<i>Selasphorus platycercus</i>	CR	108
139	<i>Setophaga coronata</i>	ATP8-ATP6	50
140	<i>Setophaga dominica</i>	CR	109

Species	AOS Species	Locus	References
141	<i>Setophaga graciae</i>	ND2	50
142	<i>Setophaga petechia</i>	CR	110
143	<i>Setophaga ruticilla</i>	CR	111
144	<i>Setophaga striata</i>	CR	112
145	<i>Sialia mexicana</i>	ATP8-ATP6	50
	<i>Sialia currucoides</i>		
	<i>Sialia sialis</i>		
146	<i>Sitta carolinensis</i>	ND2	113
147	<i>Spizella passerina</i>	CR	114
148	<i>Strix occidentalis</i>	CR	115
149	<i>Strix varia</i>	CR	115
150	<i>Sturnella magna</i>	ND2	116
	<i>Sturnella neglecta</i>		
151	<i>Synallaxis azarae</i>	ND2	28
	<i>Synallaxis courseni</i>		
152	<i>Tachycineta bicolor</i>	ND2	117
153	<i>Tangara cyanicollis</i>	CytB	37
154	<i>Tangara gyrola</i>	CytB	37
155	<i>Tangara vassorii</i>	ND2	28
156	<i>Tersina viridis</i>	CytB	37
157	<i>Tityra semifasciata</i>	CytB	37
158	<i>Toxostoma curvirostre</i>	ND2	118
159	<i>Toxostoma redivivum</i>	CytB	119
160	<i>Troglodytes aedon</i>	ND2	50
161	<i>Troglodytes hiemalis</i>	ND2	120
	<i>Troglodytes pacificus</i>		
162	<i>Trogon rufus</i>	CytB	37
163	<i>Vireo atricapilla</i>	ND2	121
164	<i>Vireo gilvus</i>	ND2	50
165	<i>Vireo huttoni</i>	ND2	50
166	<i>Vireo solitarius</i>	ND2	50
	<i>Vireo plumbeous</i>		
	<i>Vireo cassinii</i>		
167	<i>Xenopipo atronitens</i>	ND2	122
168	<i>Xenops minutus</i>	CytB	37
169	<i>Xiphorhynchus elegans</i>	CytB	123
	<i>Xiphorhynchus spixii</i>		
170	<i>Xiphorhynchus fuscus</i>	ND2	124

Species	AOS Species	Locus	References
171	<i>Xiphorhynchus ocellatus</i>	ND2	125
	<i>Xiphorhynchus pardalotus</i>		
172	<i>Xiphorhynchus triangularis</i>	ND2	28
173	<i>Zonotrichia capensis</i>	CR	126

226

227 **SI References**

228

229 1. Reddy S (2014) What's missing from avian global diversification analyses? *Mol. Phylo.*
230 *Evol.* 77:159-165.

231 2. Smith BT, Klicka J (2010) The profound influence of the Late Pliocene Panamanian uplift
232 on the exchange, diversification, and distribution of New World birds. *Ecography* 33:333-
233 342.

234 3. Weir JT, Schluter D (2008) Calibrating the avian molecular clock. *Molecular Ecology*
235 17:2321-2328.

236 4. Ho SYW, et al. (2011) Time-dependent rates of molecular evolution. *Mol. Ecol.* 20:3087-
237 3101.

238 5. Tamura K, Stecher G, Peterson D, Filipinski A, Kumar S (2013) MEGA6: Molecular
239 Evolutionary Genetics Analysis Version 6.0. *Mol. Biol. Evol.* 30:2725-2729.

240 6. Rambaut A, Drummond AJ (2007) Tracer v.1.5. <http://tree.bio.ed.ac.uk/software/tracer>.

241 7. Rambaut A, Drummond A (2008) TreeAnnotator v1.4.8.
242 <http://beast.bio.ed.ac.uk/TreeAnnotator>.

243 8. McKittrick MC, Zink RM (1988) Species concepts in ornithology. *Condor* 90:1-14.

244 9. Gill FB (2014) Species taxonomy of birds: Which null hypothesis? *Auk* 131:150-161.

245 10. Sukumaran J, Knowles LL (2017) Multispecies coalescent delimits structure, not species.
246 *Proc. Nat. Acad. Sci.* 114:1607-1612.

247 11. Orme D, et al. (2013) caper: Comparative analyses of phylogenetics and evolution in R. R
248 package version 0.5.2. <http://CRAN.R-project.org/package=caper>.

249 12. Birdlife International (2014) IUCN Red List for Birds. Downloaded from
250 <http://www.birdlife.org>.

251 13. Sullivan BL, et al. (2009) eBird: A citizen-based bird observation network in the
252 biological sciences. *Biol. Cons.* 142:2282-2292.

253 14. Hijmans RJ, Cameron SE, Parra JL, Jones PG, Jarvis A. (2005) Very high resolution
254 interpolated climate surfaces for global land areas. *Int. J. Climatol.* 25:1965-1978.

255 15. Kipp, FA (1959) Der Handflügel-Index als flugbiologisches Maß. *Vogelwarte* 20:77-86.

256 16. Claramunt S, Derryberry EP, Remsen JV, Brumfield RT (2012) High dispersal ability
257 inhibits speciation in a continental radiation of passerine birds. *Proc. R. Soc. B* 279:1567-
258 1574.

259 17. Dunn PO, Armenta JK, Whittingham LA (2015) Natural and sexual selection act on
260 different axes of variation in avian plumage color. *Sci. Adv.* 1:e1400155.

261 18. Zink RM (2004) The role of subspecies in obscuring avian biological diversity and
262 misleading conservation policy. *Proc. R. Soc. B* 271:561-564.

263 19. Clements JF, et al. (2016) The eBird/Clements checklist of birds of the world v2016.
264 Downloaded from <http://www.birds.cornell.edu/clementschecklist/download/>

- 265 20. Chavez JA, Pollinger JP, Smith TB, LeBuhn G (2007) The role of geography and ecology
266 in shaping the phylogeography of the Speckled Hummingbird (*Adelomyia melanogenys*)
267 in Ecuador. *Mol. Phylo. Evol.* 43:795-807.
- 268 21. Chavez JA, Pollinger JP, Smith TB, LeBuhn G (2007) The role of geography and ecology
269 in shaping the phylogeography of the Speckled Hummingbird (*Adelomyia melanogenys*)
270 in Ecuador. *Mol. Phylo. Evol.* 43:795-807.
- 271 22. Chavez JA, Weir JT, Smith TB (2011) Diversification in *Adelomyia* hummingbirds
272 follows Andean uplift. *Mol. Ecol.* 20: 4564-4576.
- 273 23. Barker FK, Benesh MK, Vandergon AJ, Lanyon SM (2012) Contrasting evolutionary
274 dynamics and information content of the avian mitochondrial control region and ND2
275 gene. *PLoS One* 7:e46403.
- 276 24. Lelevier MJ (2011) Phylogeography of three widespread Neotropical avian taxa: Rufous-
277 tailed Hummingbird, White-breasted Wood-Wren, and Anthracothorax mangos. M.S.
278 Thesis. University of Alaska.
- 279 25. Wenner TJ, Russello MA, Wright TF (2012) Cryptic species in a Neotropical parrot:
280 Genetic variation within the *Amazona farinosa* complex and its conservation implications.
281 *Cons. Genet.* 13:1427-1432.
- 282 26. Eberhard JR, Bermingham E (2004) Phylogeny and biogeography of the *Amazona*
283 *ochrocephala* (Aves: Psittacidae) complex. *Auk* 121:318-332.
- 284 27. Ribas CC, Tavares ES, Yoshihara C, Miyaki CY (2007) Phylogeny and biogeography of
285 Yellow-headed and Blue-fronted parrots (*Amazona ochrocephala* and *Amazona aestiva*)
286 with special reference to the South American taxa. *Ibis* 149:564-574.
- 287 28. Cuervo AM (2013) Evolutionary assembly of the Neotropical montane avifauna. Ph.D.
288 Dissertation. Louisiana State University.
- 289 29. McCracken KG, Johnson WP, Sheldon FH (2001) Molecular population genetics,
290 phylogeography, and conservation biology of the Mottled Duck (*Anas fulvigula*). *Cons.*
291 *Genet.* 2:87-102.
- 292 30. Peters JL, Omland KE (2007) Population structure and mitochondrial polyphyly in North
293 American Gadwalls (*Anas strepera*). *Auk* 124:444-462.
- 294 31. McCormack JE, Heled J, Delaney KS, Peterson AT, Knowles LL (2011) Calibrating
295 divergence times on species trees versus gene trees: Implications for speciation history of
296 *Aphelocoma* jays. *Evolution* 65:184-202.
- 297 32. McCormack JE, Peterson AT, Bonaccorso E, Smith TB (2008) Speciation in the highlands
298 of Mexico: Genetic and phenotypic divergence in the Mexican jay (*Aphelocoma*
299 *ultramarina*). *Mol. Ecol.* 17:2505-2521.
- 300 33. Ribas CC, Miyaki CY (2004) Molecular systematics in *Aratinga* parakeets: Species limits
301 and historical biogeography in the 'solstitialis' group and the systematic position of
302 *Nandayus nenday*. *Mol. Phylo. Evol.* 30:663-675.
- 303 34. Navarro-Sigüenza AG, Peterson AT, Nyari A, García-Deras GM, García-Moreno J (2008)
304 Phylogeography of the *Buarremon* brush-finch complex (Aves, Emberizidae) in
305 Mesoamerica. *Mol. Phylo. Evol.* 47:21-35.
- 306 35. Cadena CD, Cuervo AM (2010) Molecules, ecology, morphology, and songs in concert:
307 how many species is *Arremon torquatus* (Aves: Emberizidae)? *Biol. J. Linn. Soc.* 99:152-
308 176.

- 309 36. Cicero C, Koo MS (2012) The role of niche divergence and phenotypic adaptation in
310 promoting lineage diversification in the Sage Sparrow (*Artemisospiza belli*, Aves:
311 Emberizidae). *Biol. J. Linn. Soc.* 107:332-354.
- 312 37. Smith BT, et al. (2014) The drivers of tropical speciation. *Nature* 515:406-409.
- 313 38. Puebla-Olivares F, et al. (2008) Speciation in the Emerald Toucanet (*Aulacorhynchus*
314 *prasinus*) complex. *Auk* 125:39-50.
- 315 39. Barber BR, Klicka J (2010) Two pulses of diversification across the Isthmus of
316 Tehuantepec in a montane Mexican bird fauna. *Proc. R. Soc. B* 282:2675-2681.
- 317 40. Vilaça ST, Santos FR (2010) Biogeographic history of the species complex *Basileuterus*
318 *culicivorus* (Aves, Parulidae) in the Neotropics. *Mol. Phylo. Evol.* 57:585-597.
- 319 41. Gutiérrez-Pinto N, et al. (2012) Non-monophyly and deep genetic differentiation across
320 low-elevation barriers in a Neotropical montane bird (*Basileuterus tristriatus*; Aves:
321 Parulidae). *Mol. Phylo. Evol.* 64:156-165.
- 322 42. Pruett CL, Winker K (2005) Biological impacts of climatic change on a Beringian
323 endemic: Cryptic refugia in the establishment and differentiation of the Rock Sandpiper
324 (*Calidris ptilocnemis*). *Climatic Change* 68:219-240.
- 325 43. Zink RM, Kessen AE, Line TV, Blackwell-Rago RC (2001) Comparative phylogeography
326 of some aridland bird species. *Condor* 103:1-10.
- 327 44. Vásquez-Miranda H, Navarro-Sigüenza AG, Omland KE (2009) Phylogeography of the
328 Rufous-naped Wren (*Campylorhynchus rufinucha*): Speciation and hybridization in
329 Mesoamerica. *Auk* 126:765-778.
- 330 45. González MA, Eberhard JR, Lovette IJ, Olson SL, Bermingham E (2003) Mitochondrial
331 DNA phylogeography of the Bay Wren (Troglodytidae: *Thryothorus nigricapillus*)
332 complex. *Condor* 105:228-238.
- 333 46. Seeholzer GF, Winger BM, Harvey MG, Weckstein JD (2011) A new species of barbet
334 (Capitonidae: *Capito*) from the Cerros del Sira, Ucayali, Peru. *Auk* 129:551-559.
- 335 47. Kimura M, et al. (2002) Phylogeographical approaches to assessing demographic
336 connectivity between breeding and overwintering regions in a Nearctic-Neotropical
337 warbler (*Wilsonia pusilla*). *Mol. Ecol.* 11:1605-1616.
- 338 48. Barrera-Guzmán AO, Milá B, Sánchez-González LA, Navarro-Sigüenza AG (2012)
339 Speciation in an avian complex endemic to the mountains of Middle America (*Ergaticus*,
340 Aves: Parulidae). *Mol. Phylo. Evol.* 62:907-920.
- 341 49. Smith BT, et al. (2011) The role of historical and contemporary processes on
342 phylogeographic structure and genetic diversity in the Northern Cardinal, *Cardinalis*
343 *cardinalis*. *BMC Evol. Biol.* 11:136.
- 344 50. Smith BT, Seeholzer GF, Harvey MG, Cuervo AM, Brumfield RT (In press) A latitudinal
345 intraspecific diversity gradient in birds. *PLoS Biol.* (doi Pending).
- 346 51. Manthey JD, Klicka J, Spellman GM (2011) Cryptic diversity in a widespread North
347 American songbird: Phylogeography of the Brown Creeper (*Certhia americana*). *Mol.*
348 *Phylo. Evol.* 58:502-512.
- 349 52. Burns KJ, Barhoum DN (2006) Population-level history of the Wrentit (*Chamaea*
350 *fasciata*): Implications for comparative phylogeography in the California Floristic
351 Province. *Mol. Phylo. Evol.* 38:117-129.
- 352 53. Oyler-McCance SJ, St. John J, Knopf FL, Quinn TW (2005) Population genetic analysis
353 of Mountain Plover using mitochondrial DNA sequence data. *Condor* 107:353-362.

- 354 54. Funk WC, Mullins TD, Haig SM (2007) Conservation genetics of Snowy Plovers
355 (*Charadrius alexandrinus*) in the Western Hemisphere: Population genetic structure and
356 delineation of a new subspecies. *Cons. Genet.* 8:1287-1309.
- 357 55. García-Moreno J, Navarro-Sigüenza AG, Peterson AT, Sánchez-González LA (2004)
358 Genetic variation coincides with geographic structure in the Common Bush-Tanager
359 (*Chlorospingus ophthalmicus*) complex from Mexico. *Mol. Phylo. Evol.* 33:186-196.
- 360 56. Weir JT, Bermingham E, Miller MJ, Klicka J, González MA (2008) Phylogeography of a
361 morphologically diverse Neotropical montane species, the Common Bush-Tanager
362 (*Chlorospingus ophthalmicus*). *Mol. Phylo. Evol.* 47:650-664.
- 363 57. Bonaccorso E, Navarro-Sigüenza AG, Sánchez-González LA, Peterson AT, García-
364 Moreno J (2008) Genetic differentiation of the *Chlorospingus ophthalmicus* complex in
365 Mexico and Central America. *J. Avian. Biol.* 39:311-321.
- 366 58. Cadena CD, Gutiérrez-Pinto N, Dávila N, Chesser RT (2011) No population genetic
367 structure in a widespread aquatic songbird from the Neotropics. *Mol. Phylo. Evol.* 58:540-
368 545.
- 369 59. Chesser RT (2004) Systematics, evolution, and biogeography of the South American
370 ovenbird genus *Cinclodes*. *Auk* 121:752-766.
- 371 60. Sanín S, *et al.* (2009) Paraphyly of *Cinclodes fuscus* (Aves: Passeriformes: Furnariidae):
372 Implications for taxonomy and biogeography. *Mol. Phylo. Evol.* 53:547-555.
- 373 61. Omland KE, Tarr CL, Boarman WI, Marzluff JM, Fleischer RC (2000) Cryptic genetic
374 variation and paraphyly in ravens. *Proc. R. Soc. B* 1461:2475-2482.
- 375 62. Bryson RW, *et al.* (2014) Diversification across the New World within the “blue”
376 Cardinalids (Aves: Cardinalidae). *J. Biogeogr.* 41:587-599.
- 377 63. Smith BT, Amei A, Klicka J (2012) Evaluating the role of contracting and expanding
378 rainforest in initiating cycles of speciation across the Isthmus of Panama, *Proc. R. Soc. B*
379 279:3520-3526.
- 380 64. Barrowclough GF, Groth JG, Mertz LA, Gutiérrez RJ (2004) Phylogeographic structure,
381 gene flow, and species status in Blue Grouse (*Dendragapus obscurus*). *Mol. Ecol.* 7:1911-
382 1922.
- 383 65. Cabanne GS, D’Horta FM, Meyer D, Silva J, Miyaki CY (2011) Evolution of
384 *Dendrocolaptes platyrostris* (Aves: Furnariidae) between the South American open
385 vegetation corridor and the Atlantic Forest. *Biol. J. Linn. Soc.* 103:801-820.
- 386 66. Isler ML, Cuervo AM, Bravo GA, Brumfield RT (2012) An integrative approach to
387 species-level systematics reveals the depth of diversification in an Andean Thamnophilid,
388 the Long-tailed Antbird. *Auk* 114:571-583.
- 389 67. Bates JM, Hackett SJ, Goerck JM (1999) High levels of mitochondrial DNA
390 differentiation in two lineages of antbirds (*Drymophila* and *Hypocnemis*). *Auk* 116:1093-
391 1106.
- 392 68. Paxton EH (2000) Molecular genetic structuring and demographic history of the Willow
393 Flycatcher (*Empidonax traillii*). M.S. Thesis. Northern Arizona University.
- 394 69. Smith BT, Ribas CC, Whitney BM, Hernández-Baños BE, Klicka J (2013) Identifying
395 biases at different spatial and temporal scales of diversification: A case study in the
396 Neotropical parrotlet genus *Forpus*. *Mol. Ecol.* 22:483-494.
- 397 70. Dor R, Safran RJ, Sheldon FH, Winkler DW, Lovette IJ (2010) Phylogeny of the genus
398 *Hirundo* and the Barn Swallow subspecies complex. *Mol. Phylo. Evol.* 56:409-418.

- 399 71. Fernandes AM, Wink M, Sardelli CH, Aleixo A (2014) Multiple speciation across the
400 Andes and throughout Amazonia: The case of the Spot-backed Antbird species complex
401 (*Hylophylas naevius/Hylophylax naevioides*). *J. Biogeogr.* 41:1094-1104.
- 402 72. Tobias JA, Bates JM, Hackett SJ, Seddon N (2008) Comment on “The latitudinal gradient
403 in recent speciation and extinction rates of birds and mammals”. *Science* 319:901c.
- 404 73. Naka LN, Bechtoldt CL, Henriques LMP, Brumfield RT (2012) The role of physical
405 barriers in the location of avian suture zones in the Guiana Shield, northern Amazonia.
406 *Am. Nat.* 179:E115-E132.
- 407 74. Kondo B, Baker JM, Omland KE (2004) Recent speciation between the Baltimore Oriole
408 and the Black-backed Oriole. *Condor* 106:674-680.
- 409 75. Cortes-Rodríguez N, Hernández-Baños BE, Navarro-Sigüenza AG, Omland KE (2008)
410 Geographic variation and genetic structure in the Streak-backed Oriole: Low
411 mitochondrial DNA differentiation reveals recent divergence. *Condor* 110:729-739.
- 412 76. Cortes-Rodríguez N, Hernández-Baños BE, Navarro-Sigüenza AG, Peterson AT, García-
413 Moreno J (2008) Phylogeography and population genetics of the Amethyst-throated
414 Hummingbird (*Lampornis amethystinus*). *Mol. Phylo. Evol.* 48:1-11.
- 415 77. Arbeláez-Cortés E, Nyári ÁS, Navarro-Sigüenza AG (2010) The differential effect of
416 lowlands on the phylogeographic pattern of a Mesoamerican montane species
417 (*Lepidocolaptes affinis*, Aves: Furnariidae). *Mol. Phylo. Evol.* 57:658-668.
- 418 78. Honey-Escandón M, Hernández-Baños BE, Navarro-Sigüenza AG, Benítez-Díaz H,
419 Peterson AT (2008) Phylogeographic patterns of differentiation in the Acorn Woodpecker.
420 *Wilson J. Ornith.* 120:478-493.
- 421 79. Miller MJ, *et al.* (2008) Out of Amazonia again and again: Episodic crossing of the Andes
422 promotes diversification in a lowland forest flycatcher. *Proc. R. Soc. B* 275:1133-1142.
- 423 80. Arbeláez-Cortés E, Milá B, Navarro-Sigüenza AG (2014) Multilocus analysis of
424 intraspecific differentiation in three endemic bird species from northern Neotropical dry
425 forest. *Mol. Phylo. Evol.* 70:362-377.
- 426 81. Pérez-Emán JL (2005) Molecular phylogenetics and biogeography of the Neotropical
427 redstarts (*Myioborus*; Aves, Parulinae). *Mol. Phylo. Evol.* 37:511-528.
- 428 82. Pérez-Emán JL, Mumme RL, Jablonski PG (2010) Phylogeography and adaptive plumage
429 evolution in Central American subspecies of the Slate-throated Redstart (*Myioborus*
430 *miniatus*). *Ornith. Monogr.* 1:90-102.
- 431 83. Lovette IJ (2004) Molecular phylogeny and plumage signal evolution in a trans Andean
432 and circum Amazonian avian species complex. *Mol. Phylo. Evol.* 32:512-523.
- 433 84. Batalha-Filho H, Cabanne GS, Miyaki CY (2012) Phylogeography of an Atlantic forest
434 passerine reveals demographic stability through the last glacial maximum. *Mol. Phylo.*
435 *Evol.* 65:892-902.
- 436 85. Miller MJ, Bermingham E, Klicka J, Escalante P, Winker K (2010) Neotropical birds
437 show a humped distribution of within-population genetic diversity along a latitudinal
438 transect. *Ecology Letters* 13:576-586.
- 439 86. Fernandes AM, Wink M, Aleixo A (2012) Phylogeography of the Chestnut-tailed Antbird
440 (*Myrmeciza hemimelaena*) clarifies the role of rivers in Amazonian biogeography. *J.*
441 *Biogeogr.* 39:1524-1535.
- 442 87. Raposo do Amaral F, Albers PK, Edwards SV, Miyaki CY (2013) Multilocus tests of
443 Pleistocene refugia and ancient divergence in a pair of Atlantic Forest antbirds
444 (*Myrmeciza*). *Mol. Ecol.* 22:3996-4013.

- 445 88. Dohms KM, Burg TM (2013) Molecular markers reveal limited population genetic
446 structure in a North American Corvid, Clark's Nutcracker (*Nucifraga columbiana*). *PLoS*
447 *One* 8:e79621.
- 448 89. Zink RM, *et al.* (2005) Mitochondrial DNA variation, species limits, and rapid evolution
449 of plumage coloration and size in the Savannah Sparrow. *Condor* 107:21-28.
- 450 90. Herr CA, Sykes Jr. PW, Klicka J (2011) Phylogeography of a vanishing North American
451 songbird: the Painted Bunting (*Passerina ciris*). *Conserv. Genet.* 12:1395-1410.
- 452 91. van Els P, Cicero C, Klicka J (2012) High latitudes and high genetic diversity:
453 Phylogeography of a widespread boreal bird, the Gray Jay (*Perisoreus canadensis*). *Mol.*
454 *Phylo. Evol.* 63:456-465.
- 455 92. Kirchman JJ, Whittingham LA, Sheldon FH (2000) Relationships among Cave Swallow
456 populations (*Petrochelidon fulva*) determined by comparisons of microsatellite and
457 cytochrome b data. *Mol. Phylo. Evol.* 14:107-121.
- 458 93. van Els P, Spellman GM, Smith BT, Klicka J (2014) Extensive gene flow characterizes
459 the phylogeography of a North American migrant bird: Black-headed Grosbeak
460 (*Pheucticus melanocephalus*). *Mol. Phylo. Evol.* 78:148-159.
- 461 94. Campagna L, *et al.* (2011) A molecular phylogeny of the Sierra-Finches (*Phrygilus*,
462 Passeriformes): Extreme polyphyly in a group of Andean specialists. *Mol. Phylo. Evol.*
463 61:521-533.
- 464 95. Pulgarín-R. PC, Burg TM (2012) Genetic signals of demographic expansion in Downy
465 Woodpecker (*Picoides pubescens*) after the last North American glacial maximum. *PLoS*
466 *One* 7:e40412.
- 467 96. Klicka J, Spellman GM, Winker K, Chua V, Smith BT (2011) A phylogeographic and
468 population genetic analysis of a widespread, sedentary North American bird: The Hairy
469 Woodpecker (*Picoides villosus*). *Auk* 128:346-362.
- 470 97. Drovetski SV, Zink RM, Ericson PGP, Fadeev IV (2010) A multilocus study of Pine
471 Grosbeak phylogeography supports the pattern of greater intercontinental divergence in
472 Holarctic boreal forest birds than in birds inhabiting other high-latitude habitats. *J.*
473 *Biogeogr.* 37:696-706.
- 474 98. Pravosudov VV, *et al.* (2012) Population genetic structure and its implications for
475 adaptive variation in memory and the hippocampus on a continental scale in food-caching
476 Black-capped Chickadees. *Mol. Ecol.* 21:4486-4497.
- 477 99. Spellman GM, Riddle B, Klicka J (2007) Phylogeography of the Mountain Chickadee
478 (*Poecile gambeli*): Diversification, introgression, and expansion in response to Quaternary
479 climate change. *Mol. Ecol.* 16:1055-1068.
- 480 100. Zink R, Groth JG, Vásquez-Miranda H, Barrowclough GF (2013) Phylogeography of the
481 California Gnatcatcher (*Poliophtila californica*) using multilocus DNA sequences and
482 ecological niche modeling: Implications for conservation. *Auk* 130:449-458.
- 483 101. Valderrama E, Pérez-Emán JL, Brumfield RT, Cuervo AM, Cadena CD (2014) The
484 influence of the complex topography and dynamic history of the montane Neotropics on
485 the evolutionary differentiation of a cloud forest bird (*Premnoplex brunnescens*,
486 Furnariidae). *J. Biogeogr.* 41:1533-1546.
- 487 102. Maldonado-Coelho M, Blake JG, Silveira LF, Batalha-Filho H, Ricklefs RE (2013)
488 Rivers, refuges, and population divergence of fire-eye antbirds (*Pyriglena*) in the Amazon
489 Basin. *J. Evol. Biol.* 26:1090-1107.

- 490 103. DaCosta JM, Wehtje W, Klicka J (2008) Historic genetic structuring and paraphyly within
491 the Great-tailed Grackle. *Condor* 110:170-177.
- 492 104. Maley JM, Brumfield RT (2013) Mitochondrial and next-generation sequence data used to
493 infer phylogenetic relationships and species limits in the Clapper/King rail complex.
494 *Condor* 115:316-329.
- 495 105. Chaves JA, Hidalgo JR, Klicka J (2013) Biogeography and evolutionary history of the
496 Neotropical genus *Saltator* (Aves: Thraupini). *J. Biogeogr.* 40:2180-2190.
- 497 106. Cabanne GS, Sari EHR, Meyer D, Santos FR, Miyaki CY (2013) Matrilineal evidence for
498 demographic range expansion, low diversity, and lack of phylogeographic structure in the
499 Atlantic forest endemic Greenish Schiffornis *Schiffornis virescens* (Aves: Tityridae). *J.*
500 *Ornith.* 154:371-384.
- 501 107. d’Horta FM, Cuervo AM, Ribas CC, Brumfield RT, Miyaki CY (2013) Phylogeny and
502 comparative phylogeography of *Sclerurus* (Aves: Furnariidae) reveal constant and cryptic
503 diversification in an old radiation of rain forest understory specialists. *J. Biogeogr.* 40:37-
504 49.
- 505 108. Malpica A, Ornelas JF (2014) Postglacial northward expansion and genetic differentiation
506 between migratory and sedentary populations of the Broad-tailed Hummingbird
507 (*Selasphorus platycercus*). *Mol. Ecol.* 23:435-452.
- 508 109. McKay BD (2009) Evolutionary history suggests rapid differentiation in the Yellow-
509 throated Warbler (*Dendroica dominica*). *J. Avian Biol.* 40:181-190.
- 510 110. Milot EH, Gibbs HL, Hobson KA (2000) Phylogeography and genetic structure of
511 northern populations of the Yellow Warbler (*Dendroica petechia*). *Mol. Ecol.* 9:667-681.
- 512 111. Colbeck GJ, Gibbs HL, Marra PP, Hobson KA, Webster MS (2008) Phylogeography of a
513 widespread North American migratory songbird (*Setophaga ruticilla*). *J. Hered.* 99:453-
514 463.
- 515 112. Ralston J, Kirchman JJ (2012) Continent-scale genetic structure in a boreal forest migrant,
516 the Blackpoll Warbler (*Setophaga striata*). *Auk* 129:467-478.
- 517 113. Spellman GM, Klicka J (2007) Phylogeography of the White-breasted Nuthatch (*Sitta*
518 *carolinensis*): Diversification in North American pine and oak woodlands. *Mol. Ecol.*
519 16:1729-1740.
- 520 114. Milá B, Smith TB, Wayne RK (2006) Postglacial population expansion drives the
521 evolution of long-distance migration in a songbird. *Evolution* 60:2403-2409.
- 522 115. Barrowclough GF, Groth JG, Odom KJ, Lai JE (2011) Phylogeography of Spotted Owl
523 (*Strix occidentalis*): Species limits, multiple refugia, and range expansion. *Auk* 28:696-
524 706.
- 525 116. Barker FK, Vandergon AJ, Lanyon SM (2008) Assessment of species limits among
526 yellow-breasted meadowlarks (*Sturnella* spp.) using mitochondrial and sex-linked
527 markers. *Auk* 4:869-879.
- 528 117. Stenzler LM, *et al.* (2009) Subtle edge-of-range genetic structuring in transcontinentally
529 distributed North American Tree Swallows. *Condor* 111:470-478.
- 530 118. Rojas-Soto OR, Espinosa de los Monteros A, Zink RM (2007) Phylogeography and
531 patterns of differentiation in the Curve-billed Thrasher. *Condor* 109:456-463.
- 532 119. Sgariglia EA, Burns KJ (2003) Phylogeography of the California Thrasher (*Toxostoma*
533 *redivivum*) based on nested-clade analysis of mitochondrial-DNA variation. *Auk* 120:346-
534 361.

- 535 120. Drovetski SV, *et al.* (2004) Complex biogeographic history of a Holarctic passerine. *Proc.*
536 *R. Soc. B* 271:545-551.
- 537 121. Zink RM, Jones AW, Farquhar CC, Westberg MC, Gonzalez Rojas JI (2010) Comparison
538 of molecular markers in the endangered Black-capped Vireo (*Vireo atricapilla*) and their
539 interpretation in conservation. *Auk* 127:797-806.
- 540 122. Capurucho JMG, *et al.* (2013) Combining phylogeography and landscape genetics of
541 *Xenopipo atronitens* (Aves: Pipridae), a white sand campina specialist, to understand
542 Pleistocene landscape evolution in Amazonia. *Biol. J. Linn. Soc.* 110:60-76.
- 543 123. Aleixo A (2004) Historical diversification of a terra-firme forest bird superspecies: A
544 phylogeographic perspective on the role of different hypotheses of Amazonian
545 diversification. *Evolution* 58:1303-1317.
- 546 124. Cabanne GS, Santos FR, Miyaki CY (2007) Phylogeography of *Xiphorhynchus fuscus*
547 (Passeriformes, Dendrocolaptidae): Vicariance and recent demographic expansion in
548 southern Atlantic forest. *Biol. J. Linn. Soc.* 91:73-84.
- 549 125. Sousa-Neves T, Aleixo A, Sequeira F (2013) Cryptic patterns of diversification of a
550 widespread Amazonian woodcreeper species complex (Aves: Dendrocolaptidae) inferred
551 from multilocus phylogenetic analysis: Implications for historical biogeography and
552 taxonomy. *Mol. Phylo. Evol.* 68:410-424.
- 553 126. Loughheed SC, *et al.* (2013) Continental phylogeography of an ecologically and
554 morphologically diverse Neotropical songbird, *Zonotrichia capensis*. *BMC Evol. Biol.*
555 13:58.