

Is speciation driven by species diversity? *Nature* 438, doi:10.1038/nature04308 (2005).

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Unfortunately, the Brief Communications Arising Section of *Nature* does not allow publishing online appendices, and the material presented in this document was judged to be too extensive to be published as part of our comment. In addition, this section of the journal does not include an acknowledgements section with each paper. All this had the unfortunate consequence that the sources of the molecular data we presented could not be cited, and the contributions of multiple individuals could not be recognized. Thus, here we provide details on the sources of data and some explanations regarding the methods we employed.

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Methods. We assembled data on species richness and endemism of resident land birds for 18 West Indian islands (Antigua and Barbuda were considered as a single island as they were connected to each other in the past) based on ref. 1 and we obtained data on island area, maximum elevation, and distance to nearest island from ref. 2. We arcsin-transformed the proportion of endemic species and log-transformed all other variables prior to conducting a forward multiple regression with endemism as response variable and species richness, maximum elevation, and distance to nearest island as predictor variables. Island area was strongly correlated with species richness, so we excluded it from the analysis as Emerson and Kolm³ did in one of their analyses. To illustrate the relationship of species richness and endemism with population persistence times, we collated data on mitochondrial genetic differentiation for 113 populations of 60 bird species occurring on six islands with varying numbers of species and degrees of endemism based on our published and unpublished work and several other sources (see Table 1 below). Most of the sequence data are for the ATPase 6 and 8 genes, but for some species we included data from other genes (CO I, ND2, and cytochrome *b*). Although nucleotide substitution rates across genes vary somewhat, these are minor on the scale of our analysis and thus do not influence the general pattern we document. For each island population for which sequence data were available we calculated the Tamura-Nei distance to the node uniting it with its closest relative, which could be a conspecific population for non-endemic species or a sister species/clade for endemic species. We tested the null hypothesis that there are no differences in the median age of populations (as indexed by genetic distance) among islands using a Kruskal-Wallis test. We used the same statistic on each island individually to test the null hypothesis that the ages of endemic and non-endemic populations are drawn from the same distribution of ages.

Our estimates of the ages of island populations make assumptions that may not be met in all cases, leading to some “noise” in the data. In particular, extinction of island populations could conceal recent nodes in a species phylogeny and lead to overestimated age. However, because the probability of extinction of an island population increases with time, this effect would merely distort the estimated age scale rather than change the relative estimated ages of island populations. Large and diverse islands will continue to exhibit an older age structure of bird populations. In addition, because older populations are more likely to be extinct, nodes that are lost are, on

average, deep rather than shallow, thus reducing this source of bias. Also, as indicated in our Figure 1, a higher proportion of each island's avifauna (and of the endemics) was included in the analyses for islands with reduced diversity and endemism; having already sampled all or nearly all of the endemics for the small and medium-sized islands, adding genetic data for more of the endemics from the larger islands would only exacerbate the already striking differences in mean age of populations. Although the idea of estimating the ages of lineages on the basis of the age of the most recent common ancestor of clades within islands is appealing for cases in which within-island radiations are prominent, this was not possible for Lesser Antillean birds, a system in which within-island speciation occurs only very rarely.

Table 1. Mitochondrial DNA Tamura-Nei genetic distances from island bird populations to the node uniting them with their closest conspecific population or sister taxon. Species are ordered alphabetically; nomenclature follows ref. 1, with modifications according to supplements to the classification of the American Ornithologists' Union. Endemic species are indicated with an asterisk.

Species	Antigua & Barbuda	Monsterrat	Dominica	St. Lucia	Jamaica	Hispaniola	Gene	Ref.
<i>Amazona agilis</i> *					0.0278*		CO I	4
<i>Amazona arausiaca</i> *			0.0118*				CO I	4
<i>Amazona collaria</i> *					0.0125*		CO I	4
<i>Amazona imperialis</i> *			0.0312*				CO I	4
<i>Amazona ventralis</i> *						0.006*	CO I	4
<i>Amazona versicolor</i> *				0.0118*			CO I	4
<i>Chlorostilbon swainsonii</i> *						0.034	ATPase	5
<i>Cichlherminia lherminieri</i>		0	0.032				ATPase	5
<i>Cinclocerthia ruficauda</i>		0	0.003	0.018			ATPase	5
<i>Coereba flaveola</i>	0	0	0	0	0.006	0.006	ATPase	5, 6
<i>Columbina passerina</i>	0	0	0	0	0	0	ATPase	5
<i>Contopus hispaniolensis</i> *						0.019*	ATPase	5
<i>Contopus oberi</i> *				0.019*			ATPase	5
<i>Contopus palidus</i> *					0.061*		ATPase	5
<i>Cyanophaea bicolor</i>			0.01				ATPase	5
<i>Dendroica delicata</i> *				0.013*			ATPase	5
<i>Dendroica petechia</i>	0	0	0	0	0.005		ATPase	5
<i>Dendroica pharetra</i> *					0.044*		ATPase	5
<i>Dendroica plumbea</i>			0.002				ATPase	5
<i>Dendroica subita</i> *	0.018*						ATPase	5
<i>Dulus dominicus</i> *						0.077*	cyt <i>b</i>	7
<i>Elaenia fallax</i>					0.026	0.0335	ATPase	5
<i>Elaenia martinica</i>	0						ATPase	5
<i>Eulampis holosericeus</i>	0	0	0				ATPase	5
<i>Eulampis jugularis</i>		0	0	0			ATPase	5
<i>Euneornis campestris</i> *					0.047*		cyt <i>b</i>	8
<i>Geotrygon montana</i>			0	0			ATPase	5
<i>Hyetornis ruficularis</i> *						0.013*	ND2	9
<i>Icterus laudabilis</i> *				0.044*			ATPase	5
<i>Icterus oberi</i> *		0.04*					ATPase	5
<i>Loxigilla violacea</i>					0.033	0.007	ATPase	5
<i>Loxipasser anoxanthus</i> *					0.069*		ATPase	5
<i>Margarops fuscatus</i>	0	0	0				ATPase	5
<i>Margarops fuscus</i>			0	0.003			ATPase	5
<i>Melanospiza richardsoni</i> *				0.044*			ATPase	5
<i>Mimus gilvus</i>			0	0			ATPase	5
<i>Myadestes genibarbis</i>			0.004	0.001	0.019	0.005	ATPase	5
<i>Myiarchus barbirostris</i> *					0.0133*		ATPase	10
<i>Myiarchus oberi</i>	0		0	0			ATPase	5
<i>Myiarchus stolidus</i>					0	0	ATPase	5
<i>Myiarchus validus</i> *					0.0357*		ATPase	10
<i>Nesopsar nigerrimus</i> *					0.0375*		cyt <i>b</i>	11
<i>Orthorhyncus cristatus</i>	0	0	0	0			ATPase	5
<i>Priotelus roseigaster</i> *						0.097*	ND2	12
<i>Quiscalus lugubris</i>		0	0	0			ATPase	5
<i>Saltator albicollis</i>			0.002	0			ATPase	5
<i>Saurothera longirostris</i> *						0.010*	ND2	9

Species	Antigua &						Gene	Ref.
	Barbuda	Monsterrat	Dominica	St. Lucia	Jamaica	Hispaniola		
<i>Saurothera vetula</i> *					0.024*		ND2	9
<i>Tiaris bicolor</i>	0	0	0	0	0	0	ATPase	5
<i>Tiaris olivacea</i>						0.002	ATPase	5
<i>Todus angustirostris</i> *						0.041*	ATPase	13
<i>Todus subulatus</i> *						0.043*	ATPase	13
<i>Todus todus</i> *					0.056*		ATPase	13
<i>Troglodytes aedon</i>			0.032				ATPase	5
<i>Turdus jamaicensis</i> *					0.042*		ATPase	5
<i>Turdus nudigenis</i>				0			ATPase	5
<i>Turdus plumbeus</i>			0			0.003	ATPase	5
<i>Tyrannus dominicensis</i>	0	0	0	0		0	ATPase	5
<i>Tyrannus caudifasciatus</i>					0		ATPase	5
<i>Vireo altiloquus</i>	0	0	0	0			ATPase	5

Abbreviations: CO I = cytochrome oxidase subunit I, ATPase = ATP-synthase 6 and ATP-synthase 8, cyt *b* = cytochrome *b*, ND2 = NADH dehydrogenase subunit 2.

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