

Supporting Text

Taxon Sampling.—We sampled exemplars of every passerine family recognized by Sibley and Monroe (1), save one, the monotypic oscine passerine family Hypocoliidae (Table 3), whose single species (*Hypocolius ampelinus*) is distributed through Iraq and Iran. We also have not sampled the enigmatic New World genus *Sapayoa*, whose true relationships appear to lie the Old World suboscine radiation (2). We included samples from all subfamilies and all but one tribe (the Mohouini) of Sibley and Monroe's family Corvidae, which encompasses many traditionally-recognized families (3), has previously been shown to be paraphyletic (4), and harbors taxa of unexpectedly ancient derivation (5). We also included a number of enigmatic taxa the placement of which has been controversial: *Arcanator* and *Modulatrix* (6), *Chaetops* and *Picathartes* (family Picathartidae; 7), *Culicicapa* and *Elminia* (8), *Erpornis* [*Yuhina*] *zantholeuca* (9), and *Promerops* (7). In many cases we have included multiple congeneric samples in order to provide control for sample identification errors and/or errors in sequence contig formation. A total of 144 passerine samples was included in this study. Rooting of the passerine tree was accomplished with two outgroups, *Gallus gallus* and *Coracias caudata* (see below).

Collection of Sequence Data.—We amplified and sequenced a large portion of the single exons of the nuclear genes RAG-1 (GenBank LocusLink ID #5896; 10), using primers previously described (4, 11), and RAG-2 (GenBank LocusLink ID #5897; 10), using primers listed in Table 6. The former gene has been used to recover deep-level relationships within birds, and shows little evidence of substitutional saturation, even at the deepest levels of comparison (11). The two RAG genes are closely physically linked in *Homo* and in *Gallus* (separated by ~10 kilobases in the latter; 12), share similar compositional and evolutionary properties, and thus should provide

congruent phylogenetic information. However, recombination rates and thus the degree of genetic linkage in this region are poorly known in *Gallus*, and completely unknown in passerines. This study focuses on sampling a single gene region thoroughly, in order to obtain a robust and fully-resolved estimate of relationships for passerines: addition of substantial data sets gathered from other regions of the genome will provide robust tests of the hypotheses adduced here. Methods of genomic DNA extraction, enzymatic amplification, and sequencing were as previously described (4). RAG-1 sequences for taxa previously sequenced (4) were obtained from GenBank (see Table 3 for accession numbers). The RAG-2 sequences of *Gallus* and *Coracias* were provided by Drs. George Barrowclough and Jeff Groth (American Museum of Natural History).

Phylogenetic Inference.—New sequences obtained from all taxa have been deposited in GenBank (see Table 3). Sequences of each gene varied in length among taxa (RAG-1: 2854-2932 bases; RAG-2: 1143-1152 bases), and alignment of sequences was performed manually, guided by inferred amino acid translations. The final alignment of RAG-1 yielded 2974 positions, and that of RAG-2 1152 positions, for a total of 4126: these alignments have been submitted to the EMBL database (Accessions ALIGN_000669 for RAG-1 and ALIGN_000671 for RAG-2). Prior to phylogenetic analysis, the data were evaluated for apparent stationarity of base composition. The only taxon showing significant deviations from stationarity was *Sitta carolinensis*, at both RAG-1 and RAG-2 (χ^2 goodness-of-fit = 41.4, $p < 0.01$ with correction for multiple comparisons). In a previous study (4), sequences of RAG-1 from *Sitta pygmaea* were shown to be GC-rich at degenerate sites, and this is true of the congener *S. carolinensis* included in this study. The observation that the closely-linked RAG-2 gene is also GC-rich adds support

to the hypothesis that this gene region has shifted its position relative to local spatial structuring of genomic base composition (isochores *sensu lato*; 4, 13). Consequently, the phylogenetic position of *Sitta* must be interpreted with caution, and sequences of the genus were excluded from molecular clock analyses (see below).

These alignments were analyzed using parsimony, maximum likelihood (ML) and Bayesian methods, as implemented in PAUP* v4.0b10 (14), PHYML (15) and MrBayes v3.0 (16, 17). Trees were rooted at *Gallus*, using both *Gallus* and *Coracias* as outgroups. The sister group to passerines is not known with any confidence (e.g., 18, 19), though a recent study of ordinal relationships using the seventh intron of the α -fibrinogen gene (FGB-I7) suggested that the Piciformes is a good candidate (20). Unfortunately, complete RAG-1 and RAG-2 sequences from Piciformes are not currently available. However, we note that rooting of our ingroup sample with all available near-full-length RAG-1 sequences (from 10 avian orders and two crocodylians, as well as eutherian and metatherian mammals) yielded the same ingroup topology as that obtained using *Gallus* and *Coracias* alone (not shown). Combined phylogenetic analysis of the data was preceded by a test of congruence between the two genes (the incongruence length difference test; 21). The large taxon sample necessitated an abbreviated form of this test (100 replicates, taxa added stepwise to the closest branch, nearest-neighbor interchange [NNI] branch-swapping), which was non-significant ($p = 0.81$). Known problems with this test (22-24) yield excessive Type I error: failure to reject the null should be conservative with regard to the hypothesis of shared history (e.g., 25). Separate analyses of the two data sets yielded largely congruent estimates of phylogeny (not shown), as might be expected for physically linked loci. However, we note that our much smaller RAG-2 data set resolves some relationships that remain

equivocal with RAG-1 alone (e.g., monophyly of *Irena* + *Chloropsis*, separate trees not shown), suggesting that the phylogenetic signal of the two genes is not redundant.

Parsimony analysis of the combined data set was accomplished using the “parsimony ratchet” (26), as implemented in PAUPRat (27). The ratchet search was run for 200 iterations using the default settings, yielding 90 minimum-length trees (length = 9431 steps, ensemble consistency index (CI) = 0.36, ensemble retention index (RI) = 0.56). These trees were submitted to tree-bisection and reconnection (TBR) branch-swapping, which yielded 342 additional trees of the same length. The strict consensus of these trees was well resolved, retaining 131 of 143 possible nodes. Nodal robustness under the parsimony criterion was evaluated using the non-parametric bootstrap (28), by analyzing 100 replicates generated using the SeqBoot program of PHYLIP (29), with the same parsimony ratchet procedures as used for the original data set, modified by the use of NNI branch-swapping after identification of candidate shortest trees by the ratchet (NNI and TBR branch-swapping had similar efficiencies in recovering the set of shortest trees for several replicates examined). Tree weights for bootstrap replicates recovering multiple equally-parsimonious trees were added after these analyses, and used in calculation of the nodal bootstrap values as in the normal PAUP* implementation (Figure 3).

ML and Bayesian analyses of the data were performed using the general time-reversible model of sequence evolution (30), including a proportion of invariant sites and allowing rates at variable sites to follow a discrete approximation to the Γ distribution (GTR+I+ Γ ; 31), as used previously (4). ML analysis was performed by initial tree estimation with PHYML (15), followed by NNI branch swapping with PAUP*, under the best fit model estimated on the initial tree obtained from PHYML. Robustness of nodal support under ML was estimated by non-parametric bootstrapping, with 100 pseudoreplicates analyzed using PHYML. In Bayesian

analyses, prior distributions for all parameters were set to uniform intervals, except for base composition, which was assigned a Dirichlet prior, and branch lengths, which were assigned exponential priors (16). The probability density of the posterior was estimated by Metropolis-coupled Markov chain Monte Carlo (MC³), using either three or four incrementally-heated chains, taking advantage of the parallel implementation of MrBayes v3.0 β 3 (17; compiled on a 16 processor Sun Fire™ 6800, with 64-bit, 900 MHz UltraSparc III architecture, Sun Microsystems, Santa Clara, CA). In total, six independent runs of 10⁶ generations (sampling every 100) were performed, two each with three and four heated chains. For this large sample problem, the burn-in time was considerable, with chains not reaching apparent stationarity until 3·10⁵ generations, leaving 7·10⁵ generations per run. Since all chains converged on the same log-likelihood and parameter values, the results were combined, yielding 7000·6 = 42,000 sampled generations for estimation of the posterior density (Figure 3).

Most conflicts among the optimal trees and Bayesian posterior consensus involved relationships among the New World suboscines and the Corvoidea, but few of the conflicts were well supported. The ML and Bayesian analyses favored a pectinate relationship of the Furnariidae (*Campylorhamphus* and *Furnarius*) with *Formicarius*, *Scytalopus*, *Conopophaga*, and *Thamnophilus* as successively more divergent relatives (recovered in 61, 95, 79, and 100% of bootstrap replicates for each, estimated Bayesian posteriors of 0.89, 1.00, 0.56, 1.00), whereas parsimony placed *Thamnophilus* as sister to *Conopophaga* in the shortest trees and 67% of bootstrap replicates, and *Scytalopus* as sister to *Formicarius* in 65%. Additionally, the Bayesian consensus conflicted with both the parsimony and likelihood analyses in the arrangement of *Monarcha* and *Grallina* in a clade sister to *Melampitta* ($p = 0.97$, parsimony and ML placed these genera as sister to a clade containing *Corvus*, *Cyanocitta*, *Lanius*, and *Corvinella* in their optimal

trees and 69% and 56% of bootstrap replicates, respectively). All other conflicts had estimated posterior values < 0.95 or bootstrap values $< 50\%$.

Hypothesis Testing.—The goodness-of-fit of the molecular data to the phylogenetic hypotheses implied by Sibley and Ahlquist's DNA-DNA hybridization phenogram (the Tapestry; 7) was evaluated under the maximum likelihood criterion, using the test of Shimodaira and Hasegawa (SH test; 32). Taxon sampling of the current study and that of Sibley and Ahlquist (7) was made equivalent by pruning of genera not held in common between the two. This procedure left a total of 112 shared genera (Table 3), for which a tree matching Sibley and Ahlquist's phenogram was constructed by hand in MacClade v4.0 (33). Search constraints corresponding to the nodes in this tree (a total of 105 resolved nodes) were generated using TreeRot v2c (34). For all nodes which conflicted with our optimal maximum likelihood estimate, we performed a heuristic maximum likelihood search enforcing the corresponding constraint. Due to the large number of searches performed, and the computational burden imposed by the large size of the data set, we used a search strategy of initial tree formation using neighbor-joining with maximum likelihood distances (using parameter estimates from our initial ML searches, see above), followed by NNI branch swapping. After these constraint trees were found, they were compiled into a set along with our maximum likelihood estimate (with unshared taxa pruned). The deviation of constraint trees from the maximum likelihood estimate was evaluated by the SH test, as implemented in PAUP* (14), using 10,000 reestimated log-likelihood (RELL) bootstrap replicates (Table 4).

Biogeographic Analysis.—All species of passerines were assigned to higher taxa as defined by our preferred hypothesis of relationships (the ML tree), and by the taxonomy of Sibley and

Monroe (1). Species were coded to the lowest taxonomic level possible, given the current density of taxon sampling, which varied from tribal to subfamilial to familial. Monophyly of higher taxa was assumed where we had no data suggesting otherwise; where our hypothesis conflicted with Sibley and Monroe, conflicting taxa were either reassigned to a higher group or coded separately in the analysis. The distribution of each species was coded as Australasian, Old World outside of Australasia, and New World. The boundary between Australasia and the remainder of the Old World was defined according to Wallace's line (35), and distributional data were taken from sources previously cited (4). Table 7 gives the higher taxa and distributional data used in this analysis. A complete list of all passerine species, including distributional data and higher taxon assignments, is available from the authors. Because of incomplete taxon sampling and non-monophyly of the tribes Falcunculini and Pachycephalini, we were unable to code unambiguously the oscine genera *Rhagologus*, *Eulacestoma*, and *Turnagra*. All three genera are monotypic, the former two genera endemic to New Guinea, and the latter to New Zealand. Given this distribution, their placement at any point in the oscine phylogeny cannot substantially alter the overall conclusions drawn here. Also, we could not include the monotypic family Hypocoliidae (see above), which is supposed to be Passeridan (possibly related to the silky flycatchers Bombycillidae; (7): placement of this taxon among basal oscine lineages where it would affect our inferred biogeographic history is unlikely. The number of species in coded higher taxa distributed in the three recognized areas was tallied, and taxa coded as present or absent in each area. The ancestral area for all groups defined by interior nodes of particular trees analyzed was inferred from these distributional data, using dispersal-vicariance analysis (36, 37), without constraints on the number of areas allowed for ancestral state reconstructions. As resolution at the base of the "core Corvoidea" was particularly poor, ancestral state reconstruction for this

group was repeated for the set of unique trees (3611) from one of the six Bayesian runs performed (see above), and the results of these analyses weighted by their estimated posterior probabilities.

Molecular Clock Analyses.—Sequences of *Sitta carolinensis* (see above) and *Gallus* (due to large divergence levels) were excluded from the clock analysis, and branch lengths optimized on the ML tree estimate using the GTR+I+ Γ model with *Coracias* as an outgroup. A likelihood ratio test (38) rejects the molecular clock for the pruned data set ($-2 \ln \lambda = 492$, $df=142$, $p<0.001$), necessitating application of rate-smoothing procedures. Relative nodal ages were established both by non-parametric rate smoothing (39) and penalized likelihood (40). Rate smoothing of the optimized tree was performed with r8s (41). The optimal smoothing parameter for the penalized likelihood analysis was empirically determined to be 60 via cross-validation (40). Bootstrap estimates of the standard error (42) of the relative divergences were derived from by rate smoothing 100 pseudoreplicate data sets. Initial analyses using parametric methods (43) yielded highly congruent temporal scaling (not shown). The relative timescale derived from non-parametric analysis was calibrated using the divergence of *Acanthisitta* versus other passerines, assuming it was coincident with rifting of New Zealand from Antarctica (44). This calibration yields a divergence date for oscines and suboscines (77 Ma, Table 2) nearly contemporaneous with an independently-derived date (77.1 ± 11.6 Ma; 45). However, given the controversial nature of this timescale (e.g., 46), we sought additional corroboration by applying a gene-specific clock (47) to divergences at the mitochondrial locus cytochrome *b*, among closely-related species sampled in our tree (mostly congeners, including comparisons with $p < 0.16$, at the limit of resolution for this gene), and projecting back to the basal divergence of *Acanthisitta*. The taxa

used in this comparison are noted in Table 3 by inclusion of a cytochrome *b* accession. A GTR+I+ Γ model of sequence evolution was estimated by ML for these taxa on a pruned version of the ML tree, and divergences for each pair estimated using these parameters. These ML distances were converted to estimated divergence dates using a passerine-specific cytochrome *b* calibration based on divergences among dated volcanic islands ($t_{\text{divergence}} = d_{\text{ML}}/0.016$; 47), and calibrated against rate-smoothed nuclear divergences (d_{NPRS}) for the same pairs using Model II regression. The best-fit regression line ($\text{age} = 1.817 [\text{s.e.} = 1.334] + 559.35 [\text{s.e.} = 41.80] \cdot d_{\text{NPRS}}$; $r^2 = 0.88$; Figure 4) predicts a divergence date of 87.5 Ma for *Acanthisitta*, a value only 5.5 Myr greater than the assumed New Zealand vicariance calibration, and very close to the credible range of timing for that event (Table 5).

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Table 3. Taxon sampling, specimen information, and GenBank accession numbers for sequences

Sibley and Monroe (1) taxonomy				GenBank accession nos.						
Suborder	Parvorder	Superfamily	Family	Representative taxa ^a	Specimen data ^a	RAG-1	RAG-2	Cytochrome b ^b		
Tyranni			Acanthisittidae	<i>Acanthisitta chloris</i>	Unvouchered (RIF002), <i>vide</i> A.J. Baker, ROM	AY056975				
				<i>Acanthisitta chloris</i>	Unvouchered (RIF001), <i>vide</i> A.J. Baker, ROM		AY443102			
			Pittidae	<i>Pitta sordida</i>	AMNH (PRS712)	AY443319	AY443206			
			Eurylaimidae	<i>Smithornis rufolateralis</i>	AMNH 827484 (CGS5226)	AY057031	AY443228			
				<i>Psarisomus dalhousiae</i>	AMNH 22993 (PRS629)	AY057025	AY443214			
			Philepittidae	<i>Philepitta castanea</i>	FMNH 345690	AY057018	AY443201			
				<i>Neodrepanis coruscans</i>	FMNH 393232	AY443306	AY443181			
			Tyrannidae	<i>Mionectes [Pipromorpha] macconnelli</i>	AMNH (GFB2886)	AY443302	AY443174			
				<i>Tyrannus tyrannus</i>	AMNH 24560 (PRS1298)	AF143739	AY443243			
				<i>Schiffornis turdinus</i>	AMNH (GFB2223)	AY443330	AY443225			
				<i>Tityra semifasciata</i>	AMNH (GFB1035)	AY443337	AY443237			
				<i>Rupicola rupicola</i>	AMNH 22747 (PRS802)	AY057029	AY443224			
				<i>Pipra coronata</i>	AMNH 9360 (SC804)	AY057020	AY443204			
			Thamnophilidae	<i>Thamnophilus nigrocinereus</i>	AMNH 18074 (GFB2200), Deaccessioned	AY057034	AY443235			
			Furnariidae	<i>Furnarius rufus</i>	AMNH NA (PRS1836)	AY056995	AY443149			
				<i>Campylorhamphus trochilirostris</i>	AMNH (ALP145)	AY443264	AY443112			
				<i>Formicarius colma</i>	AMNH 9343 (SC721)	AY056993	AY443147			
			Formicariidae	<i>Conopophaga ardesiaca</i>	AMNH (MV25)	AY443271	AY443125			
			Conopophagidae	<i>Scytalopus magellanicus</i>	AMNH (RTC449)	AY443331	AY443226			
			Rhinocryptidae	<i>Cormobates leucophaea</i>	ANWC 49979	AY443274	AY443130	AY064278 [placens]		
			Climacteridae	<i>Climacteris erythropus</i>	UWBM 57635	AY443268	AY443121	U58501 [rufus]		
				<i>Climacteris picumna</i>	UWBM 57695 (SVE1092)	AY056987	AY443122			
			Menuridae	<i>Menura novaehollandiae</i>	ANWC 43660	AY057004	AY443171			
			Ptilonorhynchidae	<i>Aluroedus melanotis</i>	BPBM 110138	AY443260	AY443105	X74257		
				<i>Ptilonorhynchus violaceus</i>	Unvouchered (QM, Lab 3119)	AY057026	AY443216	X74256		
			Meliphagoidea	Maluridae	<i>Malurus melanocephalus</i>	Unvouchered (AM, Lab 1109), <i>in litt.</i> W. Boles	AY057001	AY443162		
				Meliphagidae	<i>Meliphaga analoga</i>	KUMNH 5171 (AM983), unvouchered <i>vide</i> A. Mack	AY057003	AY443170		
					<i>Ephthianura tricolor</i>	UWBM 57574	AY443285	AY443144		
				Pardalotidae	<i>Pardalotus punctatus</i>	AM [Lab 1141]	AY443313	AY443193		
					<i>Pardalotus striatus</i>	AM [Lab 1062]	AY057015	AY443194		
			Corvoidea	Petroicidae	<i>Microeca papuana</i>	KUMNH 5225 (AM1089)	AY443301	AY443172		
					<i>Eugerygone rubra</i>	KUMNH 5246 (AM1114)	AY443286	AY443145		
					<i>Melanodryas [Petroica] cucullata</i>	UWBM 60860	AY443300	AY443169		
					<i>Tregellasia leucops</i>	KUMNH 4701 (AM819), voucher BPBM	AY057037	AY443239	AY443259	
					<i>Peneothello bimaculatus</i>	KUMNH 5151 (AM962)	AY443315	AY443199	AY443256	
					<i>Pachycephalopsis poliosoma</i>	KUMNH 4691 (AM803)	AY443311	AY443190		
			Irenidae	<i>Irena cyanogaster</i>	FMNH 350955	AY056999	AY443158			
				<i>Chloropsis cochinchinensis</i>	AMNH 22997 DA-Singapore (PRS717)	AY056984	AY443118			
			Orthonychidae	<i>Orthonyx teminkii</i>	ANWC 46865	AY443309	AY443187			
				<i>Orthonyx spaldingii</i>	ANWC 34489	AY057012	AY443186			
			Pomatostomidae	<i>Pomatostomus isidorei</i>	KUMNH 5099 (AM890), voucher BPBM	AY057023	AY443210			
				<i>Pomatostomus halli</i>	UWBM 57737	AY443321	AY443209			
			Laniidae	<i>Lanius excubitor</i>	AMNH (LMC95-23)	AY443293	AY443160			
				<i>Corvinella corvina</i>	LSUMNS B39326	AY443275	AY443131			
			Vireonidae	<i>Vireo philadelphia</i>	AMNH 24546 (PRS1035)	AY057041	AY443245			
				<i>Hylophilus poicilotis</i>	FMNH 395482	AY443291	AY443156			
			Corvoidea	<i>Ptiliorhoa caerulescens</i>	KUMNH 5107 (AM899)	AY443326	AY443218			
	<i>Corcorax melanorhamphos</i>	AM [Lab 1146]	AY443273	AY443129	AY064274					
	<i>Struthidea cinerea</i>	AM [FB 40, SVE071]	AY443335	AY443231	AY064277					
	<i>Daphoenositta chrysoptera</i>	ANWC 43773	AY443281	AY443138						
	<i>Falcunculus frontatus</i>	AM [Lab 1150]	AY443287	AY443146						
	<i>Oreoica gutturalis</i>	ANWC 46761	AY443307	AY443183	AY443255					
	<i>Pachycephala hyperthra</i>	KUMNH 5123 (AM921)	AY443310	AY443188						
	<i>Pachycephala soror</i>	KUMNH 4692 (AM804), voucher BPBM	AY057013	AY443189						
	<i>Colluricincla harmonica</i>	UWBM 57495	AY443270	AY443124						
	<i>Pitohui cristatus</i>	KUMNH 4697 (AM812)	AY443318	AY443205	AY443257					
	<i>Cyanocitta cristata</i>	Unvouchered (AMNH, JLC)	AY443280	AY443137						
	<i>Corvus corone</i>	AMNH 24068 (PRS1288)	AY056989	AY443132	AF094613					
	<i>Corvus orru</i>	AM [Lab 1163]	AY443277	AY443134						
	<i>Corvus coronoides</i>	AMNH (PRS2285)	AY443276	AY443133	AF197837					
	<i>Melampitta lugubris</i>	KUMNH 5257 (AM1126)	AY443298	AY443166	AY443253					
	<i>Melampitta gigantea</i>	SNZP, <i>vide</i> R. Fleischer	AY443297	AY443165	AY443252					
	<i>Loboparadisea sericea</i>	KUMNH 4720 (AM843)	AY443294	AY443161	AF197843					
	<i>Cnemophilus loriae</i>	KUMNH 5220 (AM1083)	AY443269	AY443123	AF197841 [macgregorii]					
	<i>Manucodia atra</i>	KUMNH 5108 (AM900)	AY443295	AY443163	AY443250					
	<i>Manucodia chalybata</i>	KUMNH 5157 (AM968)	AY443296	AY443164	AY443251					
	<i>Ptiloris magnificus</i>	KUMNH 5212 (AM1031)	AY443325	AY443217	X74254					
	<i>Paradisaea raggiana</i>	ZSSD AO48924 (27731)	AY057014	AY443191	U25738, U15204					
	<i>Cracticus quoyi</i>	KUMNH 5084 (AM873)	AY443278	AY443135	AY443248					
	<i>Gymnorhina tibicen</i>	Unvouchered (AMNH, JLC)	AY443289	AY443153	AF197867					
	<i>Strepera graculina</i>	UQ, <i>vide</i> L. Joseph	AY443334	AY443230						
	<i>Artamus leucorhynchus</i>	FMNH 345096	AY056980	AY443109						
	<i>Artamus cyanopterus</i>	MV 00133	AY443262	AY443108						
	<i>Oriolus xanthonotus</i>	ANSP 1176	AY443308	AY443185						
	<i>Oriolus larvatus</i>	AMNH 25750 (JGG1280)	AY057011	AY443184						
	<i>Sphecotheres viridis</i>	AM [Lab 1189]	AY443333	AY443229						
	<i>Coracina novaehollandiae</i>	AM [Lab 1142]	AY443272	AY443128						
	<i>Coracina lineata</i>	AMNH 23412 (MKL64)	AY056988	AY443127						
	<i>Lalage leucomela</i>	UWBM 57518	AY443292	AY443159						
	<i>Pericrocotus ethologus</i>	FMNH 347842	AY443316	AY443200						
	<i>Rhipidura hyperthra</i>	KUMNH 5169 (AM981)	AY443329	AY443223						
	<i>Chaetorhynchus papuensis</i>	KUMNH 4690 (AM802)	AY443267	AY443117						
	<i>Dicrurus adsimilis</i>	AMNH 25749 (JGG1301)	AY056991	AY443140						
	<i>Dicrurus hottentottus</i>	KUMNH 5098 (AM889)	AY443283	AY443141						
	<i>Elminia [Trochocercus] nigromitratus</i>	AMNH (PRS2106)	AY443338	AY443240	AF096474					
	<i>Monarcha axillaris</i>	KUMNH 4716 (AM838), voucher BPBM	AY057006	AY443176						
	<i>Monarcha chrysomela</i>	KUMNH 5202 (AM1021)	AY443304	AY443177	AY443254					
	<i>Grallina cyanoleuca</i>	AM [Lab 1144]	AY443288	AY443152						
	<i>Grallina cyanoleuca</i>	AM [FB 1509 #15]			AY443249					
	<i>Aegithina tiphia</i>	AMNH 22963 (PRS691)	AY056977	AY443104						
	<i>Dryoscopus cubla</i>	DM (D-9)	AY443284	AY443142						
	<i>Telophorus dohertyi</i>	FMNH 358004	AY443336	AY443234						
	<i>Prionops plumatus</i>	ZMUC (LPZ-089, tube 102)	AY443322	AY443211						
	<i>Batis mixta</i>	ZMUC (SMG-4619, tube 465)	AY443263	AY443110						
	<i>Vanga curvirostris</i>	FMNH 352878	AY057040	AY443244						
Callaeatidae	<i>Philesturnus [Creaedion] carunculatus</i>	SNZP (1695), <i>vide</i> J. Dumbacher	AY443317	AY443202						
Picathartidae	<i>Chaetops frenatus</i>	PFI (PFI18421)	AY443266	AY443116						

incertae sedis
Table 3, continued.

Sibley and Monroe (1) taxonomy				GenBank accession nos.					
Suborder	Parvorder	Superfamily	Family	Representative taxa ¹	Specimen data ¹	RAG-1	RAG-2	Cytochrome b ²	
Passeri	<i>incertae sedis</i>	Passerida	Picathartidae	<i>Picathartes gymnocephalus</i>	AMNH 827716 (AC350)	AY057019	AY443203		
			Bombycillidae	<i>Bombycilla garrulus</i>	Unvouchered (AMNH, PRS1417)	AY056981	AY443111	AF285796	
				Muscicapoidea	<i>Ptilogonys cinereus</i>	FMNH (ATP6132)	AY443324	AY443215	AY443258
				Cinclidae	<i>Cinclus cinclus</i>	AMNH NA (PRS2328)	AY056985	AY443119	
				Muscicapidae	<i>Catharus ustulatus</i>	Unvouchered (AMNH, JLC)	AY443265	AY443114	AY049507
					<i>Turdus falcklandii</i>	AMNH NA (PRS1825)	AY057039	AY443242	AF197835 [migratorius]
					<i>Muscicapa ferruginea</i>	AMNH (PRS2233)	AY443305	AY443179	
					<i>Culicicapa ceylonensis</i>	AMNH (JGG1172)	AY443279	AY443136	AF096453
					<i>Sturnus vulgaris</i>	FMNH 389606 (MCP96-437)	AY057032	AY443232	
					<i>Mimus patagonicus</i>	AMNH NA (PRS1711)	AY057005	AY443173	
			Sylvioidea	Sittidae	<i>Sitta carolinensis</i>	AMNH (MGL253)	AY443332	AY443227	
				Certhiidae	<i>Certhia familiaris</i>	FMNH 351158 (S87-0026)	AY056983	AY443115	
					<i>Troglodytes aedon</i>	FMNH 343273 (MEX331)	AY057038	AY443241	AY352547
					<i>Poliophtila caerulea</i>	FMNH 343322 (MEX167)	AY443320	AY443208	AY352535
				Paridae	<i>Remiz pendulinus</i>	ZMUC 117640 (O1851)	AY443328	AY443222	
					<i>Parus major</i>	AMNH (PRS2335)	AY443314	AY443197	AF347962
					<i>Parus inornatus</i>	AMNH 23656 (PRS1015)	AY057017	AY443196	X60944
				Aegithalidae	<i>Aegithalos iouschensis</i>	AMNH 831357 (JGG1052)	AY056976	AY443103	
				Hirundinidae	<i>Hirundo rustica</i>	Unvouchered (AMNH, JLC)	AY443290	AY443155	AF074577
					<i>Hirundo pyrrhonota</i>	AMNH 23653 (PRS1013)	AY056997	AY443154	AF074591
				Regulidae	<i>Regulus calendula</i>	AMNH 24545 (PRS1080)	AY057028	AY443220	AJ004327
					<i>Regulus satrapa</i>	AMNH (GFB3235)	AY443327	AY443221	AJ004329
				Pycnonotidae	<i>Pycnonotus barbatus</i>	AMNH 24822 (PRS2125)	AY057027	AY443219	
				Cisticolidae	<i>Cisticola anonymus</i>	AMNH 832156 (PB159)	AY056986	AY443120	
				Zosteropidae	<i>Zosterops senegalensis</i>	FMNH 346671 (JCK0607)	AY057042	AY443247	AY352549
				Sylviidae	<i>Garrulax milleti</i>	AMNH 833160 (PRS2191)	AY056996	AY443151	
					<i>Modulatrix stictigula</i>	ZMUC 118730 (O2941)	AY443303	AY443175	
					<i>Arcanator orostruthus</i>	ZMUC 118184 (OZ395)	AY443261	AY443107	
					<i>Erpornis [Yuhina] zantholeuca</i>	AMNH (PRS2248)	AY443339	AY443246	
					<i>Sylvia nana</i>	AMNH 23211 (LMC95-22)	AY057033	AY443233	Z73494 [atricapilla]
			Passeroidea	Alaudidae	<i>Alauda arvensis</i>	AMNH NA (PRS2316)	AY056978	AY443106	
				Nectariniidae	<i>Promerops cafer</i>	PFI, <i>vide</i> T. Crowe	AY443323	AY443212	
					<i>Dicaeum aeneum</i>	AMNH (MKL115)	AY443282	AY443139	
					<i>Nectarinia olivacea</i>	AMNH 831874 (RWD23779)	AY057008	AY443180	
				Melanocharitidae	<i>Melanocharis nigra</i>	KUMNH 5153 (AM964), voucher BPBM	AY057002	AY443167	
					<i>Melanocharis versteri</i>	KUMNH 4708 (AM830)	AY443299	AY443168	
					<i>Toxorhamphus novaeguineae</i>	KUMNH 5102 (AM894), voucher BPBM	AY057036	AY443238	
					<i>Oedistoma iliophorum</i>	KUMNH 5145 (AM956), voucher BPBM	AY057010	AY443182	
				Paromythidae	<i>Paromythia montium</i>	MV (FB15)	AY443312	AY443192	
				Passeridae	<i>Passer montanus</i>	AMNH 22967 (PRS697)	AF143738	AY443198	
					<i>Motacilla cinerea</i>	UWBM 46534 (GAV158)	AY057007	AY443178	
					<i>Prunella collaris</i>	AMNH 831301 (JGG1154)	AY057024	AY443213	
					<i>Ploceus cucullatus</i>	AMNH 831877 (RWD23772)	AY057022	AY443207	
				Fringillidae	<i>Fringilla montifringilla</i>	ROM (MKP1553)	AY056994	AY443148	
					<i>Emberiza schoeniclus</i>	MVZUC O480	AY056992	AY443143	
					<i>Parula americana</i>	Unvouchered (AMNH, PRS152)	AY057016	AY443195	AF256503
					<i>Thraupis cyanocephala</i>	AMNH 24097 (GFB3133)	AY057035	AY443236	AF489898 [bonariensis]
				<i>Cardinalis cardinalis</i>	AMNH 23188 (PRS930)	AY056982	AY443113	AF447363	
				<i>Icterus parisorum</i>	AMNH 832513 (JGG1243)	AY056998	AY443157	AF089035	
Outgroups			Coraciidae	<i>Coracias caudata</i>	AMNH 22703 (PRS756)	AF143737	AY443126		
			Phasianidae	<i>Gallus gallus</i>	Unvouchered, <i>vide</i> M. Zuk, U. C. Riverside	AF143730	AY443150		

¹Passerine genera unsampled by Sibley and Ahlquist (2) are highlighted in bold.

²AM, Australian Museum, Sydney; AMNH, American Museum of Natural History, New York; BPBM, Bernice Parks Bishop Museum, Hawaii; ANWC, Australian National Wildlife Collection, Commonwealth Scientific and Industrial Research Organization; DM, Durban Museum; FMNH, Field Museum of Natural History, Chicago; KUMNH, University of Kansas, Museum of Natural History; MV, Museum Victoria, Melbourne; PFI, Percy Fitzpatrick Institute of Ornithology, University of Cape Town; SNZP, Smithsonian National Zoological Park; UQ, University of Queensland; QM, Queensland Museum, Brisbane; UWBM, Burke Museum, University of Washington, Seattle; ZMUC, Zoological Museum, University of Copenhagen; ZSSD, Zoological Society of San Diego; DA, deaccessioned; NA, not accessioned. Numbers in parentheses are collector's numbers. All KUMNH specimen numbers are tissue numbers. Australian Museum specimens with "Lab" or "FB" numbers in many cases lack vouchers (W. Boles, personal communication).

³In some cases, cytochrome b sequences from a different species within a genus were used in the mtDNA calibration analysis, and these are indicated in brackets.

1. Sibley, C.G. & Monroe, B.L., Jr. (1990) *Distribution and Taxonomy of the Birds of the World* (Yale Univ. Press, New Haven, CT)
2. Sibley, C.G. & Ahlquist, J.E. (1990) *Phylogeny and Classification of Birds: A Study in Molecular Evolution* (Yale Univ. Press, New Haven, CT).

Table 4. Monophyly of and significance of paraphyly of groups present in Sibley and Ahlquist's (1) hypothesis of passerine relationships, including only genera sampled in common with the current study

Node	Description	Taxon	Rank	Monophyletic	Likelihood	Difference	P
1	Garrulax, Sylvia	Sylviidae	Family	No	53898.79	18.53	0.88
2	1, Zosterops			Yes			
3	2, Cisticola			Yes			
4	3, Pycnonotus			Yes			
5	4, Regulus			No	53971.97	91.70	0.04
6	5, Hirundo			No	53974.74	94.48	0.04
7	6, Aegithalos			No	53935.08	54.82	0.26
8	Parus, Remiz	Paridae	Family	Yes			
9	7, 8			No	53940.80	60.53	0.20
10	Poipitia, Troglodytes			Yes			
11	10, Certhia	Certhiidae	Family	No	53897.10	16.84	0.91
12	11, Sitta			Yes			
13	9, 12	Sylviodea	Superfamily	No	53942.98	62.72	0.19
14	Ploceus, Prunella			No	53901.96	21.70	0.83
15	14, Motacilla			No	53909.57	23.31	0.67
16	15, Passer	Passeridae	Family	No	53906.93	26.66	0.73
17	Cardinalis, Icterus			No	53956.03	75.77	0.10
18	17, Thrupis			No	53931.97	51.70	0.31
19	18, Parula			No	53902.36	22.09	0.80
20	19, Emberiza	Emberizinae	Subfamily	Yes			
21	20, Fringilla	Fringillidae	Family	Yes			
22	Dicaeum, Nectarinia	Nectariniinae	Subfamily	Yes			
23	22, Promerops	Nectariniidae	Family	No	53903.40	23.13	0.80
24	Oedistoma, Toxorhamphus	Toxorhamphini	Tribe	Yes			
25	24, Melanocharis	Melanocharitidae	Family	Yes			
26	25, Paramythia			No	53926.75	46.48	0.38
27	23, 26			No	54050.19	169.92	<0.01
28	21, 27			No	54185.99	305.73	<0.01
29	16, 28			No	54070.52	190.25	<0.01
30	29, Alauda	Passeroidea	Superfamily	No	54122.87	242.60	<0.01
31	13, 30			No	54074.18	193.92	<0.01
32	Bombycilla, Ptilogonyx	Bombycillidae	Family	Yes			
33	Catharus, Turdus	Turdinae	Subfamily	Yes			
34	33, Muscipapa	Muscicapidae	Family	Yes			
35	Mimus, Sturnus	Sturnidae	Family	Yes			
36	34, 35			No	53899.15	18.88	0.86
37	36, Cinclus			Yes			
38	32, 37	Muscicapodea	Superfamily	Yes			
39	31, 38	Passerida	Parvorder	Yes	54046.29	166.02	<0.01
40	Chaetops, Picathartes	Picathartidae	Family	No			
41	Alluroedus, Ptilonorhynchus	Ptilonorhynchidae	Family	Yes			
42	41, Menua			No	53936.31	56.05	0.26
43	Climacteris, Cormobates	Climacteridae	Family	Yes			
44	42, 43	Menuroidea	Superfamily	No	53910.74	30.48	0.65
45	Ephthianura, Meliphaga	Meliphagidae	Family	Yes			
46	45, Pardalotus			Yes			
47	46, Malurus	Meliphagoidea	Superfamily	Yes			
48	Microeca, Tregellasia	Petroicidae	Family	Yes			
49	Chloropsis, Irena	Irenidae	Family	Yes			
50	Lanius, Corvinella	Laniidae	Family	Yes			
51	Hylophilus, Vireo	Vireonidae	Family	Yes			
52	Corcorax, Struthidea	Corcoracinae	Subfamily	Yes			
53	Colluricincla, Pachycephala, Pitohui	Pachycephalini	Tribe	No	54009.62	129.35	0.01
54	53, Oreocia, Falco			No	53888.09	7.83	0.97
55	54, Daphoenositta	Pachycephalinae	Subfamily	No	53898.23	17.96	0.84
56	Dryoscopus, Telophorus	Malaconotini	Tribe	Yes			
57	Batis, Prionops	Vangini	Tribe	No	53880.26	5.86	0.98
58	56, 57	Malaconotinae	Subfamily	No	53882.14	1.88	0.98
59	58, Aegithina			Yes			
60	Grallina, Monarcha	Monarchini	Tribe	Yes			
61	60, Chaetorhynchus, Dicrurus			No	53925.55	45.29	0.40
62	61, Rhipidura	Dicrurinae	Subfamily	No	53908.79	28.52	0.69
63	59, 62			No	54014.84	134.58	0.01
64	Corvus, Cyanocitta	Corvini	Tribe	Yes			
65	Paradisaea, Ptilons			Yes			
66	65, Manucodia			Yes			
67	66, Melampitta	Paradisaeini	Tribe	No	53893.77	13.50	0.95
68	Coracina, Lalage			Yes			
69	68, Pericrocotus			Yes			
70	Oniulus, Sphecotheres			Yes			
71	69, 70	Oriolini	Tribe	No	53889.26	8.99	0.93
72	Cracticus, Gymnorhina			Yes			
73	72, Strepera			Yes			
74	73, Artamus	Artamini	Tribe	Yes			
75	71, 74			No	53953.17	72.91	0.13
76	67, 75			No	54044.63	164.37	<0.01
77	64, 76	Corvinae	Subfamily	No	54075.58	195.31	<0.01
78	63, 77			No	53995.93	115.66	0.01
79	78, Pachycephalinae			No	54013.71	133.45	<0.01
80	79, Corcoracinae			No	53964.92	84.66	0.06
81	80, Ptilorhoa (Cinclosomatinae)	Corvidae	Family	No	53972.14	91.88	0.03
82	81, Vireonidae			No	53968.31	88.05	0.05
83	82, Laniidae			No	53996.47	16.21	0.88
84	83, Pomatosotomidae			No	53959.92	79.65	0.06
85	84, Orthonychidae			No	53952.53	72.27	0.12
86	85, Irenidae			No	54067.42	187.15	<0.01
87	86, Petroicidae	Corvoidea	Superfamily	No	54066.54	186.28	<0.01
88	47, 87			No	54100.17	219.91	<0.01
89	44, 88	Corvida	Parvorder	No	54179.99	299.73	<0.01
90	Corvida, Passerida	Passeri	Suborder	Yes			
91	Campylorhamphus, Furnarius	Furnariidae/Furnarioidea	Family/Parvorder	Yes			
92	Conopophaga, Scytalopus			No	53912.61	32.34	0.61
93	92, Formicarius	Formicarioidea	Superfamily	No	53917.36	37.10	0.52
94	91, 93	Furnariida	Parvorder	Yes			
95	94, Thamnophilus			Yes			
96	Pipra, Rupicola			No	53903.93	23.66	0.76
97	Schiffornis, Tityra	Tityrinae	Subfamily	Yes			
98	97, Tyrannus			No	53902.13	21.87	0.80
99	96, 98			No	53904.67	24.41	0.76
100	99, Mionectes	Tyrannidae/Tyrannida	Family/Parvorder	Yes			
101	93, 100	Tyrannides	Infraorder	Yes			
102	Psarisomus, Smithornis	Eurylaimidae	Family	Yes			
103	102, Pitta	Eurylaimides	Infraorder	Yes			
104	101, 103			Yes			
105	104, Acanthisitta	Tyranni	Suborder	No	53908.38	28.12	0.70

The columns *Node* and *Description* can be used to reconstruct Sibley and Ahlquist's (1) tree for the genera shared with the current study. Groups which represent named higher taxa (1, 2) are indicated, as is their status on our preferred hypothesis of relationships (Figs. 1 and 3). For groups appearing paraphyletic in our analyses, the negative log-likelihood of the best tree consistent with the group, its difference from the best fit, and the significance of the difference (as indicated by the test of Shimodaira and Hasegawa, see *Methods* and ref. 3) are given.

1. Sibley, C.G. & Ahlquist, J.E. (1990) *Phylogeny and Classification of Birds: A Study in Molecular Evolution* (Yale Univ. Press, New Haven, CT).
2. Sibley, C.G. & Monroe, B.L., Jr. (1990) *Distribution and Taxonomy of the Birds of the World* (Yale Univ. Press, New Haven, CT)
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Table 5. An approximate timescale for important Late Cretaceous and Cenozoic geophysical and climatic events

Event	Date	Reference
New Zealand/West Antarctica separation	85-82 Ma	10
Australia/East Antarctica separation	65-64 Ma	9
End of North Atlantic connection between North America and Europe	55-53 Ma	7
Collision of India with Eurasia	60-49 Ma	2
End of terrestrial connections between South America and Antarctica	40-30 Ma	1
Major uplift of the Andes (southern)	15 Ma	8
Major uplift of the Andes (northern, central)	10-0 Ma	4, 6
Initiation of Miocene climatic deterioration	13-12 Ma	11
Opening of Panamanian isthmus	3.5-3.1 Ma	3

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Table 6. Location and sequence of RAG-2 specific primers used

Direction	Name	Sequence	Position
Forward	R2F4	GGTTCTTCCCTGCTGAATTTTGATGG	77
Forward	R2-1	TCTTTTTTGGGCAGAAGGGATG	107
Forward	R2F1	CAGAAGGGATGGCCGAAGAGATCCTG	122
Forward	R2-27	AGAGGCAATGCAGAGTCTGA	260
Forward	R2-11	GATGTCCCTGAAGCTAGATA	413
Forward	R2K1	GCTCAAGATGGACTTTCTTTCCA	620
Forward	R2F2	CAGGATGGACTTTCCTTCCATGT	623
Forward	R2-31	GGGATATCTGTGTCAAGTGCT	783
Reverse	R2-8	TCATTGTTAGGKGTTCCTCCAC	284
Reverse	R2-22	ACGCTCATGCTTTTTCCC	286
Reverse	R2-10	CTGGCAACTGAAACATGGA	617
Reverse	R2R2	CGACACAGATATTCCTCCTGGCAA	754
Reverse	R2R4	CTGGTAGCCCCCAACAAGGACAA	812
Reverse	R2K4	TGAGTGGTAGCCACCRACAA	818
Reverse	R2-6	TTTCTGGTTGTCAGACTGGTAG	828
Reverse	R2-14	CAGTAGCCCGTTTCTGATTCATCTTCTTCATCATCTT	1214
Reverse	R2-16	GACCCAGGTGTTAATGTC	1279
Reverse	R2R1	CTGTTGAATAGAAAGGCACCCAGGT	1288
Reverse	R2R5	GATCCATGCACTGTGCATGAACCCA	1360

Locations of 3' primer nucleotides are given relative to GenBank Accession #M58531 (1). The names of primers used most extensively are highlighted in bold.

1. Carlson, L.M., Oettinger, M.A., Schatz, D.G., Masteller, E.L., Hurley, E.A., McCormack, W.T., Baltimore, D., & Thompson, C.B. (1991) *Cell* **64**, 201-208.

Table 7. Taxonomy and distribution of passerines

Suborder	Infraorder	Parvorder	Coded Group	Australasia, New Zealand, South Pacific Islands	Eurasia and Africa	New World
Tyranni	Acanthisittides		Acanthisittidae	1	0	0
Tyranni	Eurylaimides	Pittoidea	Pittidae	1	1	0
Tyranni	Eurylaimides	Eurylaimoidea	<i>Smithornis</i>	0	1	0
Tyranni	Eurylaimides	Eurylaimoidea	Other Eurylaimidae	0	1	0
Tyranni	Eurylaimides	Eurylaimoidea	Philepittidae	0	1	0
Tyranni	<i>incertae sedis</i>		<i>Sapayoa</i>	0	0	1
Tyranni	Tyrannides		Tyrannides	0	0	1
Passeri		Corvida	Climacteridae	1	0	0
Passeri		Corvida	Menuridae	1	0	0
Passeri		Corvida	Ptilonorhynchidae	1	0	0
Passeri		Corvida	Maluridae	1	0	0
Passeri		Corvida	Meliphagidae	1	1	0
Passeri		Corvida	Pardalotidae	1	1	0
Passeri		Corvida	Petroicidae	1	0	0
Passeri		Corvida	Irenidae	0	1	0
Passeri		Corvida	Orthonychidae	1	0	0
Passeri		Corvida	Pomatostomidae	1	0	0
Passeri		Corvida	Laniidae	1	1	1
Passeri		Corvida	Vireonidae and <i>Yuhina zantholeuca</i>	0	1	1
Passeri		Corvida	Cinclosomatinae	1	1	0
Passeri		Corvida	Corcoracinae	1	0	0
Passeri		Corvida	Neosittini	1	0	0
Passeri		Corvida	Mohouini	1	0	0
Passeri		Corvida	<i>Falcunculus</i>	1	0	0
Passeri		Corvida	<i>Rhagologus</i>	1	0	0
Passeri		Corvida	Pachycephalini (part)	1	1	0
Passeri		Corvida	<i>Pitohui</i> and <i>Oreoica</i>	1	0	0
Passeri		Corvida	<i>Eulacestoma</i>	1	0	0
Passeri		Corvida	<i>Turnagra</i>	1	0	0
Passeri		Corvida	Corvini	1	1	1
Passeri		Corvida	<i>Melampitta</i>	1	0	0
Passeri		Corvida	<i>Cnemophilus</i> and <i>Loboparadisea</i>	1	0	0
Passeri		Corvida	Paradisaeini (part)	1	0	0
Passeri		Corvida	Artamini	1	1	0
Passeri		Corvida	<i>Oriolus</i>	1	1	0
Passeri		Corvida	<i>Sphecotheres</i>	1	0	0
Passeri		Corvida	Campephagidae	1	1	0
Passeri		Corvida	Rhipidurini	1	1	0
Passeri		Corvida	<i>Chaetorhynchus</i>	1	0	0
Passeri		Corvida	<i>Dicrurus</i>	1	1	0
Passeri		Corvida	Monarchini (part)	1	1	0
Passeri		Corvida	Aegithininae and Malaconotinae	0	1	0
Passeri		Corvida	Callaeatidae	1	0	0
Passeri		<i>incertae sedis</i>	Picathartidae	0	1	0
Passeri		Passerida	Bombycillidae	0	1	1
Passeri		Passerida	Cinclidae	0	1	1
Passeri		Passerida	Turdinae	1	1	1
Passeri		Passerida	Muscicapinae (part)	1	1	1
Passeri		Passerida	Sturnini	1	1	0
Passeri		Passerida	Mimini	0	0	1
Passeri		Passerida	Sittidae+Certhiidae	0	1	1
Passeri		Passerida	Paridae	1	1	1
Passeri		Passerida	<i>Culicicapa</i> and <i>Elminia</i>	1	1	0
Passeri		Passerida	Aegithalidae	0	1	1
Passeri		Passerida	Hirundinidae	1	1	1
Passeri		Passerida	Regulidae	0	1	1
Passeri		Passerida	Pycnonotidae	1	1	0
Passeri		Passerida	<i>Hypocoliidae</i>	0	1	0
Passeri		Passerida	Cisticolidae	1	1	0
Passeri		Passerida	Zosteropidae and Sylviidae (part)	1	1	1
Passeri		Passerida	<i>Arcanator</i> and <i>Modulatrix</i>	0	1	0
Passeri		Passerida	Alaudidae	1	1	1
Passeri		Passerida	Promeropinae	0	1	0
Passeri		Passerida	Nectariniinae	1	1	0
Passeri		Passerida	Melanocharitidae	1	0	0
Passeri		Passerida	Paramythiidae	1	0	0
Passeri		Passerida	Passerinae	0	1	0
Passeri		Passerida	Motacillinae	1	1	1
Passeri		Passerida	Prunellinae	0	1	0
Passeri		Passerida	Ploceinae+Estrildinae	1	1	0
Passeri		Passerida	Fringillidae	1	1	1

Taxonomy follows Sibley and Monroe (1). Distributions are drawn from Sibley and Monroe (1) and a variety of regional sources. Entries under "Coded Group" indicate higher taxa, which were coded for biogeographic analysis (see *Methods*). Highlighted taxa are unsampled taxa with uncertain relationships (in most cases due to non-monophyly of other sampled members of the same group). These taxa have been excluded from analysis (see *Methods*).

1. Sibley, C.G. & Monroe, B.L., Jr. (1990) *Distribution and Taxonomy of the Birds of the World* (Yale Univ. Press, New Haven, CT)

Figure 3. Maximum likelihood estimate of passerine relationships based on combined RAG-1 and RAG-2 sequences. Integers above each node represent the percentage of likelihood (top) and parsimony (bottom) bootstrap replicates (n=100) in which that node appeared, and decimal values below each node indicate its estimated posterior probability in Bayesian analysis of the data (n=42,000 sampled generations; see Materials and Methods).

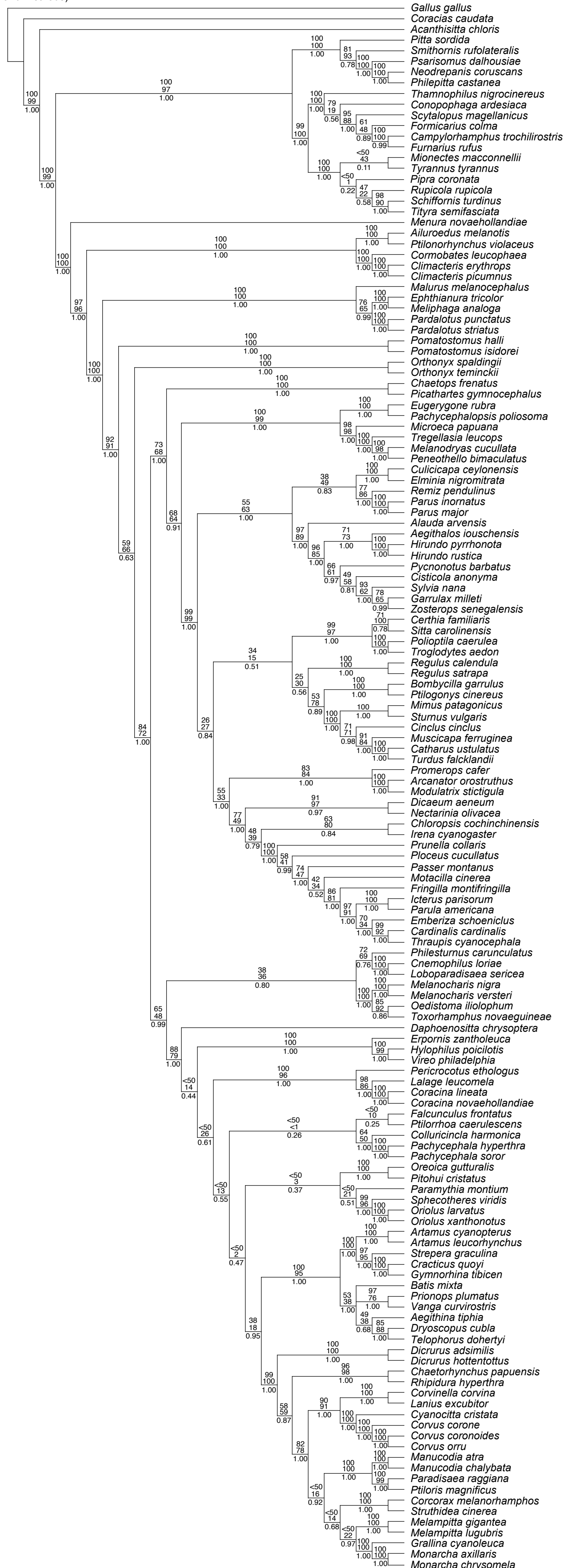


Figure 4. Secondary calibration of the basal passerine divergence, using a mitochondrial clock (Fleischer et al. 1998). The abscissa is the non-parametrically rate-smoothed nuclear sequence divergence for 22 independent sister-taxon comparisons, and the ordinate is the estimated divergence times of those sister taxa based on cytochrome *b* distances and a gene-specific evolutionary rate (see Materials and Methods). The solid line is the best-fit Model II regression, and the dashed lines depict the 95% CI of the regression slope. The solid circular point in the upper right quadrant is the 82 Ma calibration assumed by Ericson et al. (2002), plotted at our corrected nuclear divergence for *Acanthisitta*. The solid diamond is the 77.1 Ma figure estimated by van Tuinen and Hedges (2001) for the "suboscine"/oscine divergence (i.e., excluding *Acanthisitta*), plotted at our corrected nuclear divergence for that split.

