

Supporting Information

Jönsson et al. 10.1073/pnas.1018956108

SI Methods

Dating Analyses. We used the relaxed Bayesian molecular clock implemented in Multidivtime to estimate divergence dates (1, 2). The best fitting parameters for each gene were estimated in PAML (3) using the F84 model of nucleotide substitution and five discrete categories. These parameters were then entered into the program Estbranches to calculate the branch lengths of the rooted maximum likelihood (ML) tree from the analysis of the partitioned data set, and their variance-covariance matrix under each of the corresponding partitions. Second, a priori knowledge was incorporated as gamma distributions: (i) the root age, (ii) the substitution rate at the root, and (iii) the degree of autocorrelation among the substitution rates along the branches. These priors were specified as means and SDs of the three distributions according to the Multidivtime guidelines. The posterior distributions of node times were approximated through four independent Markov Chain Monte Carlo (MCMC) runs of 50 million generations and the “burn-in” was set at one million generations. Finally, convergence diagnostics were checked graphically.

To calibrate the tree to estimate absolute dates, we used a combination of geological calibration points (4) and secondary calibration points (5). We used (i) the age of Acanthisittidae versus other passerines at 76 ± 8 My SD (age within 95% confidence intervals = 62.8–89.2 My), (ii) the age of Old World versus New World suboscines at 70 ± 2 My SD (confidence intervals = 66.7–73.3 My), (iii) the split between *Menura noveahollandiae* and the rest of the oscines 63 ± 2 My SD (confidence intervals = 59.7–66.3 My), and (iv) the split between *Coracina typica* from Mauritius and *Coracina newtoni* from Reunion at 1.5 million y (My) \pm 0.25 SD (age within 95% confidence intervals = 1.09–1.91 My).

To further corroborate the absolute date estimates, we assessed the molecular rate of evolution for ND2 for nodes younger than 12 My. It has been shown that, for cytochrome *b*, the rate of evolution of ca. 2.1% per My is maintained over a 12-My interval for birds (6). The corresponding rate for ND2 has been demonstrated to be somewhat higher at approximately 2.8% per million years (7).

Biogeographic Analyses. Bayes-diva. We used Bayes-DIVA to elucidate ancestral patterns (8), with particular emphasis on the nodes around the core Corvoidea. In a standard dispersal-vicariance analysis (9), as implemented in the software DIVA (10), ancestral areas are optimized onto internal nodes of a phylogeny by minimizing the number of dispersal and extinction events required to explain the terminal distributions (11). We sampled 20,000 trees (by thinning the chain; i.e., sampling every n^{th} generation) from the MCMC output and ran DIVA on all of them. The frequency of ancestral areas for clades was then recorded and plotted as marginal distributions on the majority-rule consensus tree derived from the MCMC. The major advantage of the Bayes-DIVA method is that the marginal distributions for the alternative ancestral areas at each node in the tree are the product of the phylogenetic uncertainty in the rest of the tree and the uncertainty in the biogeographic reconstruction of the node of interest.

We assigned 10 geographic areas for the Bayes-DIVA analysis (Fig. 1), considering evidence of historical relationships of geological plates and terranes in the Indo-Pacific (12–14) but otherwise sticking to major continental areas. The analysis was carried setting maxareas = 2 but we also explored the importance of changing the maxareas (setting maxareas = 3, 4, and 5). **BayesTraits.** We used BayesTraits ver. 1.0 (15) to test the validity of New Guinea as the area of origin of the core Corvoidea.

BayesTraits estimates the instantaneous forward and backward rates among all specified states (in this case areas of origin) to compute probabilities of a state change in a given branch (16). To contrast the New Guinean origin hypothesis for the core Corvoidea clade, we used a local approach (17) and compared state reconstructions at this specific node (Node 2: core Corvoidea). Thus, we constrained the Most Recent Common Ancestor for the core Corvoidea node at one of the ten potential states (areas of origin). MCMC was used to explore the samples and the space of rate parameter values of 20,000 trees generated in the combined MrBayes analysis. Because we have no information concerning the rates, priors on uniform distributions were set between 0 and 100. BayesTraits computes the likelihood and a rate for any new combination in a tree. Using Metropolis-Hastings evaluation, this new state of the chain will be either accepted or rejected. The ratedev parameters (rate of parameter changes) were set at the start of each run. Accordingly, the acceptance rate of the proposed transition range between ranges between 20 and 40%. The MCMC chain was run for 10,000,000 generations and rate parameters were sampled every 10,000 generations. Two chains were run independently to sample rate parameters and to derive overall likelihoods of the reconstructions when the node of interest was constrained at its alternative state. Bayes factors were then calculated to determine the support for New Guinea compared with the nine remaining alternative biogeographic states.

Lineage diversity. To generate a visual overview of the distributions of the various clades of oscine passerine birds, we generated lineage diversity maps at the time when the proto-Papuan archipelago emerged in the Oligocene. Lineage diversity maps (Fig. 2) were generated from a global dataset of bird distributions (presence-absence data in a grid of $1 \times 1^\circ$) (17) by combining the distributions of all species representing a lineage. We assumed that the current distribution of the representatives of a lineage represents the combined historical distribution of that lineage, and for visual presentation we overlaid the distributions of all lineages that had diverged at 25 Mya. For the core Corvoidea, we generated lineage diversity maps for three time frames (35, 30, or 25 Mya) to accommodate the uncertainty associated with any date estimate. We chose these points in time for two reasons: (i) they mark the transition between initial (deeper) branching of the core Corvoidea and several strong secondary radiations in some subgroups outside Australo-Papua; (ii) they mark the transition between the existence of isolated Papuan islands and continuous land connections with Australia (12, 13) (see maps in Fig. 1). Our assumption is that lineage endemism and the peak of lineage diversity reflects the center of radiation in the Late Eocene/Oligocene.

Morphological measurements. One of us (R.E.R.) measured two to four individuals of 158 species distributed among all lineages of contemporary species represented in the phylogenetic reconstruction at an age of 25 Mya. These individuals included 84 species from the 34 lineages of core Corvoidea, 36 species from the 12 transitional lineages, and 38 species from the 11 lineages of basal oscines (for details on number of lineages, see Tables S2 and S3). Measurements were made in several collections, including the Field Museum of Natural History in Chicago, the American Museum of Natural History in New York, the United States National Museum in Washington, D.C., and the Zoologisches Staatssammlung in Munich, Germany. Traits were the \log_{10} -transformed lengths of the wing, tail, tarsus, and middle toe, and the length, width, and depth of the culmen measured at the base (see ref. 19).

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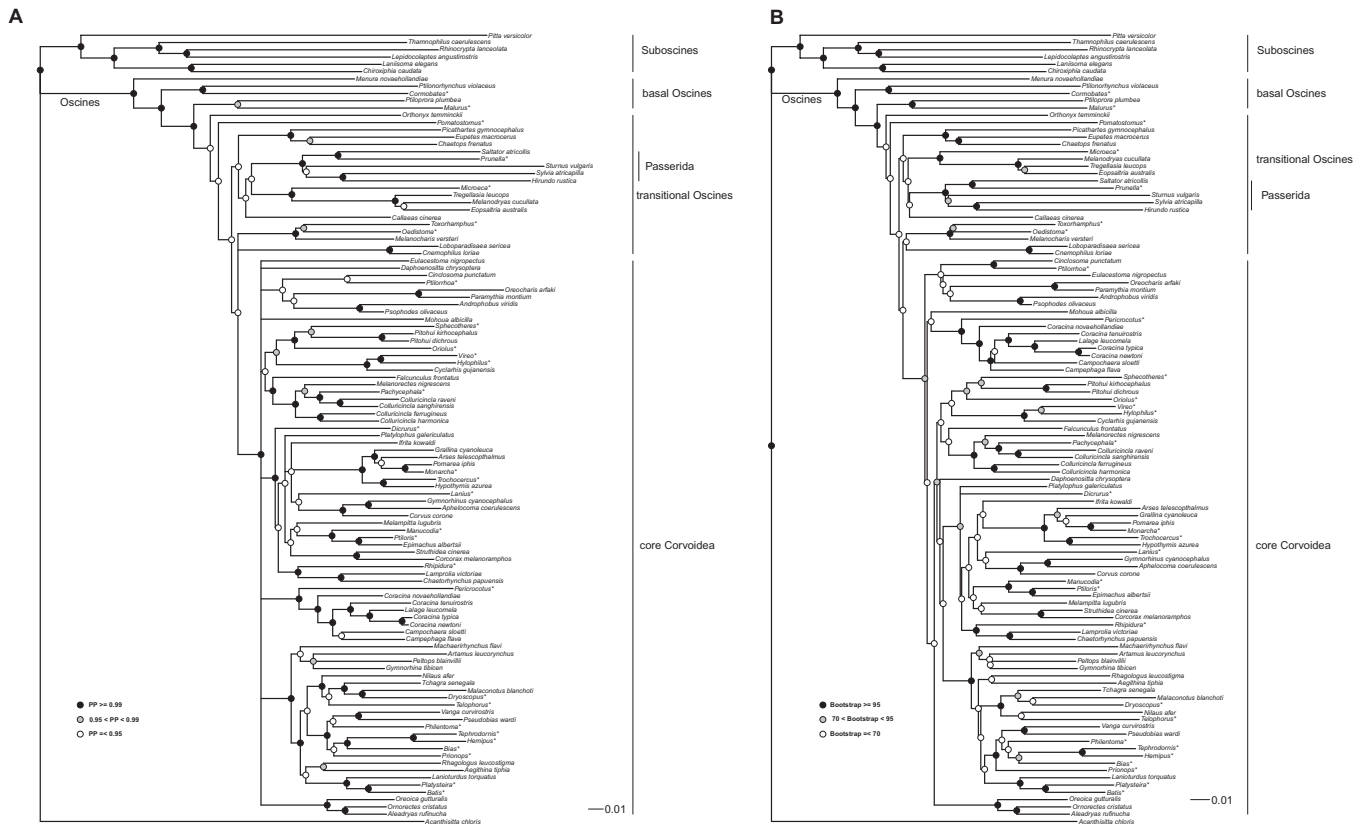


Fig. S1. (A) The 50% majority rule consensus tree obtained from the Bayesian analysis of 6,676 bp of the combined dataset (ODC, Myo2, ND2, RAG-1, and RAG-2). BI harmonic mean: $-\ln 86881.07$. The substitution model GTR+I+ Γ was determined with MrModeltest (1), using the Akaike Information Criterion (2, 3). In the Bayesian analyses (4, 5) the Markov Chain Monte Carlo (MCMC) was run using Metropolis-coupling, with one cold and three heated chains, for 60 million iterations with trees sampled every 500 iterations. The number of iterations discarded before the posterior probabilities were calculated (i.e., the length of the “burn-in” period) was graphically estimated using AWTY (6, 7) by monitoring the change in cumulative split frequencies. Two independent runs initiated from random starting trees were performed, and the log-likelihood values and posterior probabilities for splits and model parameters were checked to ascertain that the chains had reached apparent stationarity. Circles at nodes represent posterior probabilities (PP) (circles: black ≤ 0.99 , gray $0.99 \leq PP \leq 0.95$, white $0.95 \leq PP \leq 0$). (B) The Maximum Likelihood tree obtained from the RaXML analysis of 6676 bp of the combined dataset (ODC, Myo2, ND2, RAG-1 and RAG-2). Likelihood value $-\ln 80480.84$. The substitution model GTR+I+ Γ was determined with MrModeltest (1), using the Akaike Information Criterion (2, 3). Circles at nodes represent ML bootstrap support (circles: black 100–95%, gray 95–70%, white 70–0%). The 50% majority rule consensus trees obtained from the Bayesian analysis of the full data for each of these markers is available from K.A.J.

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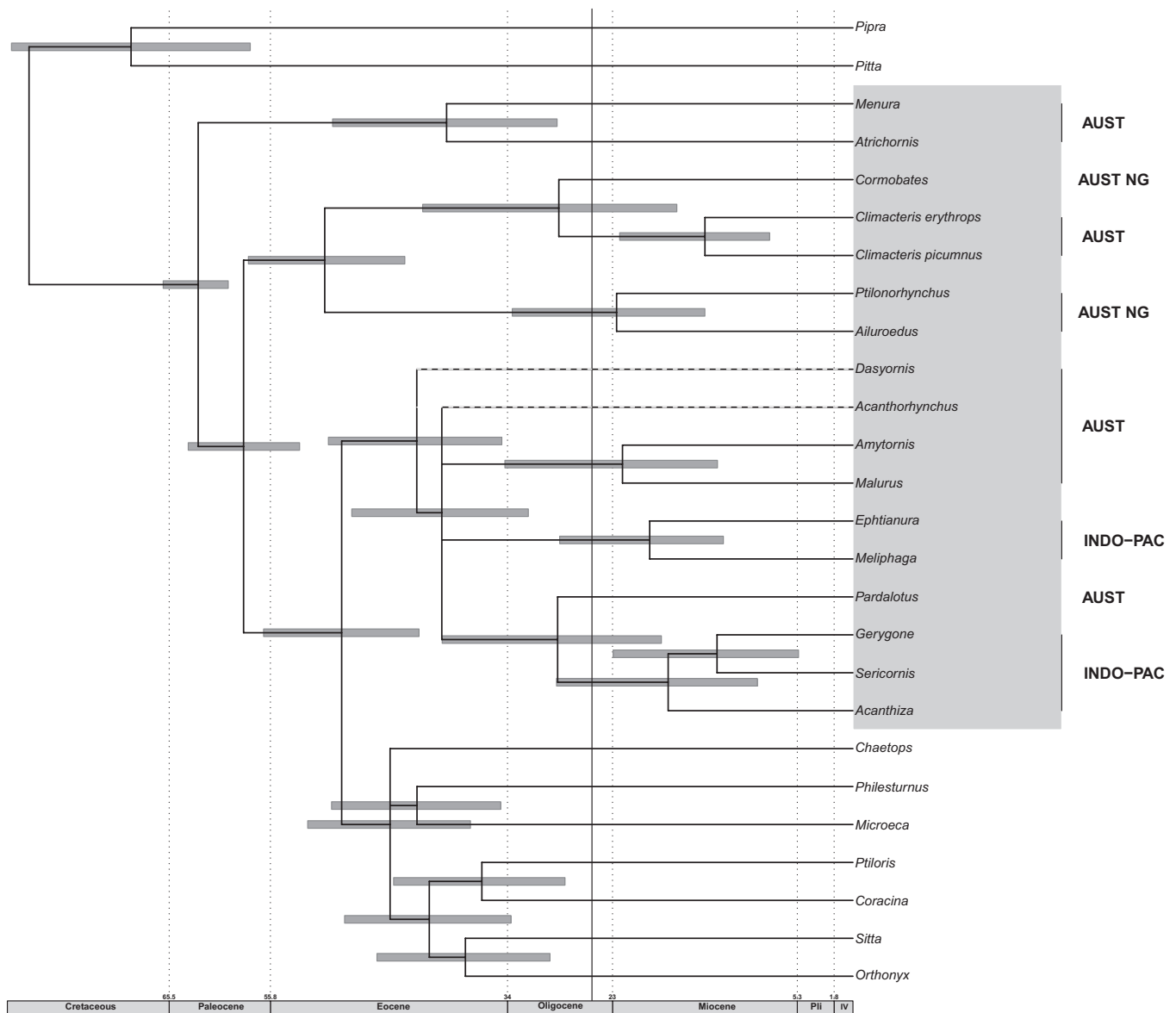


Fig. S2. Chronogram for the basal oscine lineages. Basal oscine lineages are shaded gray. Bayesian analysis was performed on 2,872 bp of the Recombination Activating Gene 1 (RAG-1). BI harmonic mean $-\ln 11500.49$. The substitution model GTR+I+ Γ was determined with MrMODELTEST (1), using the Akaike Information Criterion (2, 3). In the Bayesian analyses (4, 5) the MCMC was run using Metropolis-coupling, with one cold and three heated chains, for 20 million iterations with trees sampled every 500 iterations. The number of iterations discarded before the posterior probabilities were calculated (i.e., the length of the “burn-in” period) was graphically estimated using AWTY (6, 7) by monitoring the change in cumulative split frequencies. Two independent runs initiated from random starting trees were performed, and the log-likelihood values and posterior probabilities for splits and model parameters were checked to ascertain that the chains had reached apparent stationarity. Divergence times were estimated from the RAG1 dataset with a Bayesian relaxed molecular clock method (8, 9). Two genera for which we did not have RAG-1 available were added to the basal oscine chronogram (with dashed lines) because other studies have demonstrated that they represent deep branches in the tree.

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Table S1. Results of the BayesTraits analysis

Hypothesis	Likelihood value	Harmonic mean	Bayes factor against Hypothesis 3
1: New Zealand	-164.18	-172.17	6.48**
2: Australia	-162.23	-170.29	2.73*
3: New Guinea	-155.88	-168.93	0
4: Philippines	-160.11	-172.57	7.29**
5: Wallacea	-170.12	-174.25	10.65***
6: Eurasia	-160.65	-170.3	2.76*
7: Africa	-164.76	-170.76	3.66*
8: America	-159.28	-171.91	5.96**
9: Pacific islands	-159.71	-173.05	8.25**
10: Indian ocean islands	-161.08	-170.43	3.01*

Ancestral area state reconstructions at the most recent common ancestor of the core Corvoidea clade. Bayes Factors (BF) measure twice the difference between the harmonic mean (HM) returned by the model when the Most Recent Common Ancestor is successively set at its 10 possible biogeographic states (New Guinea, New Zealand, Australia, Philippines, Wallacea, Asia, Africa, America, Pacific Ocean islands, and Indian Ocean islands), with a difference of 2 to 5 considered as positive evidence (*), 5 to 10 considered strong evidence (**), and >10 very strong evidence (***) (1). The harmonic mean (-168.9) of the constrained ancestral biogeographic state reconstruction was significantly higher for the New Guinea hypothesis than for the other nine biogeographic states. Furthermore, the state returning the highest marginal likelihood value is New Guinea (155.88).

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Table S2. Specimen data: core Corvoidea and transitional oscine lineages at 25 Mya

Lineages	Species	Myo	ODC	ND2	RAG1	RAG2	References
core Corvoidea							
1	<i>Aleadryas rufinucha</i>	EU273395	EU273355	EF592289	FJ821040	/	1, 2
	<i>Oreoica gutturalis</i>	FJ821094	/	EF592284	AY443307	AY443183	1, 3, 4
	<i>Ornorectes cristatus</i>	EU273411	EU273370	GQ494087	AY443318	AY443205	2, 3, 5
2	<i>Batis poensis/mixta*</i>	AY529907	EU272120	AY529941	AY443263*	AY443110*	3, 6
	<i>Laniorturdus torquatus</i>	AY529924	/	AY529959	AY799819	AY799838	6, 7
	<i>Platysteira chalybeal/castanea*</i>	AY529919	/	AY529954	DQ376531*	DQ376521*	6, 8
3	<i>Bias flammulatus/musicus*</i>	AY529927	/	AY529962	DQ376529*	DQ376519*	6, 8
	<i>Hemipus picatus/hirundinaceus*</i>	DQ406637	/	DQ411309	DQ376527*	DQ376517*	8, 9
	<i>Prionops retzii/plumatus*</i>	AY529931	EU380457	AY529966	AY443322*	AY443211*	3, 6, 10
	<i>Tephrodornis pondicerianus/gularis*</i>	EF052762	/	EF052689	DQ376526*	DQ376516*	8, 11
4	<i>Philentoma velatal/pyrhopterum*</i>	AY816221	/	AY816228	DQ376525*	DQ376515	8, 9
	<i>Pseudobias wardi</i>	AY529933	/	AY529968	DQ376530	DQ376520	6, 8
	<i>Vanga curvirostris</i>	AY701505	/	AY701508	AY057040	AY443244	3, 12, 13
5	<i>Dryoscopus gambensis/cubla*</i>	AY529918	/	AY529953	AY443284*	AY443142*	3, 6
	<i>Malaconotus blanchoti</i>	AY529926	/	AY529961	/	/	6
	<i>Tchagra senegalus</i>	AY529937	/	AY529972	DQ376528	DQ376518	6, 8
	<i>Telophorus sulfureopectus/dohertyi*</i>	AY529912	EU380413	AY529947	AY443336*	AY443234*	3, 6, 10
6	<i>Nilaus afer</i>	AY529928	/	AY529963	/	/	6
7	<i>Aegithina tiphia</i>	AY816225	/	AY816232	AY056977	AY443104	3, 9, 12
	<i>Rhagologus leucostigma</i>	EU273416	/	EF592323	FJ821071	/	1, 2
8	<i>Artamus leucorynchus</i>	FJ821079	/	DQ096729	AY056980	AY443109	14
	<i>Gymnorhina tibicen</i>	AY064741	EU272119	AY064756	FJ358100	AY443153	3, 15, 16
	<i>Peltops blainvillii</i>	FJ821099	/	/	FJ821065	/	4
9	<i>Machaerirhynchus flaviventer</i>	FJ821090	/	DQ084072	FJ821057	/	1, 4
10	<i>Campephaga flava</i>	EF052822	EU380410	AY529944	AF295184	/	11, 17
	<i>Campochaera sloetii</i>	EU380489	EU380412	HM002951	/	/	2, 18
	<i>Coracina newtoni</i>	HM002941	HM003014	HM002973	/	/	18
	<i>Coracina novaehollandiae</i>	EF052834	EU380425	EF052779	AY443272	AY443128	3, 10, 11
	<i>Coracina tenuirostris</i>	HM002945	HM003019	HM002987	/	/	18
	<i>Coracina typica</i>	HM002946	HM003020	HM002988	/	/	18
	<i>Lalage leucomela</i>	EF052840	EU380438	EF052785	AY443292	AY443159	3, 10, 11
11	<i>Pericrocotus divaricatus/lethologus*</i>	EU380514	EU380449	GQ255857	AY443316*	AY443200*	2, 3, 19
12	<i>Chaetorhynchus papuensis</i>	EU726214	EU726224	/	AY443267	AY443117	3, 20
	<i>Lamprolia victoriae</i>	EU726215	EU726225	/	/	/	20
13	<i>Rhipidura rufifrons/hyperthra*</i>	DQ084100	EU272115	DQ084073	AY443329*	AY443223*	3, 14, 21
14	<i>Corcorax melanoramphos</i>	AY064737	EF441236	AY064747	AY443273	AY443129	15, 16
	<i>Struthidea cinerea</i>	AY064738	/	AY064757	AY443335	AY443231	3, 15
15	<i>Epimachus albertisi</i>	AY064735	EU380436	AY064745	AY037850	/	10, 15
	<i>Manucodia ater</i>	EU726218	EU726228	/	AY443295	AY443163	20
	<i>Ptiloris magnificus</i>	EU726219	EU726229	AY064761	AY443325	AY443217	3, 15, 20
16	<i>Melampitta lugubris</i>	EU726213	EU726221	EF592281	AY443298	AY443166	1, 3, 20
17	<i>Aphelocoma coerulescens</i>	AY395580	/	DQ912601	/	/	22, 23
	<i>Corvus corone</i>	AY529914	EU272116	AY529949	AY056989	AY443132	3, 6, 21
	<i>Gymnorhinus cyanocephalus</i>	AY395589	/	DQ912615	/	/	22, 23
18	<i>Lanius collurio/excubitor*</i>	EF635052	EF637073	EU166959	AY228042	AY443160*	3, 24, 25
19	<i>Arses telescopthalmus</i>	DQ084104	/	DQ084077	/	/	14
	<i>Grallina cyanoleuca</i>	DQ084101	/	DQ084074	AY443288	AY443152	3, 14
	<i>Hypothymis azurea</i>	EF052768	EU726223	EF052695	/	/	11, 20
	<i>Monarcha melanopsis/laxillaris*</i>	DQ084110	EU272114	DQ084083	FJ821059	AY443176*	3, 4, 14, 21
	<i>Pomarea iphis</i>	DQ084119	/	DQ084097	/	/	14
	<i>Trochocercus nitens</i>	/	/	EU652702	/	/	26
20	<i>Ifrita kowaldi</i>	EU273402	/	EF592280	FJ821054	/	1, 2
21	<i>Platylophus galericulatus</i>	EU380517	EU380456	/	/	/	10
22	<i>Dicrurus bracteatus/ladsmilis*</i>	EF052839	EU272113	EF052784	FJ821049	AY443140*	3, 4, 11, 21
23	<i>Eulacestoma nigropectus</i>	EU273400	/	EF592278	FJ821051	/	1, 2, 4
24	<i>Colluricincla ferrugineus</i>	EU273413	EU273372	GQ494089	/	/	2, 5
	<i>Colluricincla harmonica</i>	EU273396	EU273356	GQ494091	AY443270	AY443124	2, 5
	<i>Coracornis raveni</i>	EU380503	EU380434	GQ494106	/	/	5, 10
	<i>Coracornis sanghirensis</i>	EF441256	EF441235	GQ494110	/	/	5, 10
	<i>Melanorectes nigrescens</i>	EU273415	EU273373	GQ494090	/	/	2
	<i>Pachycephala pectoralis/hyperthra*</i>	EU273407	EU273366	EU600813	AY443310*	AY443188*	2, 3, 27
25	<i>Falcunculus frontatus</i>	FJ821086	/	EF592279	AY443287	AY443146	1, 3, 4

Table S2. Cont.

Lineages	Species	Myo	ODC	ND2	RAG1	RAG2	References
26	<i>Cyclarhis gujanensis</i>	EU380504	EU380435	AY030129	/	/	10, 28
	<i>Hylophilus ochraceiceps/poicilotis*</i>	EU272100	EU272109	AY030133	AY443291*	AY443156*	3, 10, 28
	<i>Vireo olivaceus/philadelphia*</i>	EU272101	EU272110	AY136614	AY057041*	AY443245*	12, 21, 29
27	<i>Oriolus flavocinctus/xanthonotus*</i>	EF441258	EF441243	GQ901758	AY443308*	AY443185*	3, 16, 30
28	<i>Pitohui dichrous</i>	EU273412	EU273371	GQ494088	/	/	2, 5
	<i>Pitohui kirhocephalus</i>	EU273414	/	EF592318	/	/	1, 2
29	<i>Sphecotheres vieillotii/iridis*</i>	FJ821107	GQ901707	GQ901761	AY443333*	AY443229*	3, 4, 30
30	<i>Mohoua albicilla</i>	FJ821091	/	/	FJ821058	/	4
31	<i>Androphobus viridis</i>	/	HQ456529	/	/	/	Present study
	<i>Psophodes olivaceus</i>	FJ821102	/	EF592322	FJ821069	/	1, 4
32	<i>Oreocharis arfaki</i>	HQ456526	HQ456530	/	/	/	Present study
	<i>Paramythia montium</i>	HQ456527	HQ456531	/	AY443312	AY443192	3, present study
33	<i>Cinclosoma punctatum</i>	FJ821080	/	/	FJ821043	/	4
	<i>Ptilorrhoa leucosticta/caerulescens*</i>	EF441261	EF441255	/	AY443326*	AY443218*	3, 16
34	<i>Daphoenositta chrysoptera</i>	EU380505	/	/	AY443281	AY443138	3, 10
Transitional oscines							
1	<i>Cnemophilus lorae</i>	EU272107	EU272126	/	AY443269	/	3, 21
	<i>Loboparadisaea sericea</i>	EU272106	EU272125	/	AY443294	AY443161	3, 21
2	<i>Melanocharis versteri</i>	EU272103	EU272121	/	AY443299	AY443168	3, 21
3	<i>Oedistoma pygmaeum/liliolophum*</i>	EU272104	EU272122	/	AY057010*	AY443182*	3, 12, 21
4	<i>Toxorhamphus poliopterus/novaeguineae*</i>	EU272105	EU272123	/	AY057036*	AY443238*	3, 12, 21
5	<i>Callaesa cinerea</i>	EU272108	EU272124	/	DQ469294	/	21, 31, 32
6	<i>Eopsaltria australis</i>	AY064732	EF441238	AY064749	AY064262	/	15, 16
	<i>Melanodryas cucullata</i>	HQ612121	HQ612165	EF592282	AY443300	AY443169	1, 3, present study
	<i>Tregellasia leucops</i>	HQ612130	HQ612174	HQ456528	AY057037	AY443239	3, 12, present study
7	<i>Microeca fascians/papuana*</i>	HQ612122	HQ612166	EF592283	AY443301*	AY443172*	1, 3, present study
8	<i>Chaetops frenatus</i>	AY228289	EF441234	/	AY443266	AY443116	3, 33
9	<i>Eupetes macrocerus</i>	EF441257	EF441239	/	/	/	16
10	<i>Picathartes gymnocephalus</i>	AY228314	EF441247	DQ125989	AY057019	AY443203	3, 16, 33, 34
11	<i>Orthonyx temminckii</i>	AY064728	EF441244	AY064755	AY443309	AY443187	3, 15, 16
12	<i>Pomatostomus temporalis/halli*</i>	AY064730	EF441248	AY064758	AY443321*	AY443209*	3, 15, 16
Passerida							
	<i>Hirundo rustica</i>	AY064258	EF441240	DQ176584	AY443290	AY443155	3, 15, 16, 35
	<i>Prunella modularis/collaris*</i>	AY228318	EF441249	AF407038	AY057024*	AY443213*	3, 16, 33, 36
	<i>Saltator atricollis</i>	AY228320	EF441252	EF529914	AY228036	/	16, 33, 37
	<i>Sturnus vulgaris</i>	AY228322	EF441253	FJ177342	AY057032	AY443232	3, 12, 16, 33, 38
	<i>Sylvia atricapilla</i>	AY228323	EF441254	DQ125994	EF568261	EF568285	16, 33, 34, 39
Basal oscines							
Family: Climacteridae							
	<i>Cormobates placens/leucophaeus*</i>	AY064731	EF441237	AY064748	AY064260	AY443130*	3, 15, 16
Family: Maluridae							
	<i>Malurus amabilis/melanocephalus*</i>	AY064729	EF441241	AY064752	AY037847	AY443162*	3, 15, 16
Family: Menuridae							
	<i>Menura novaehollandiae</i>	AY064744	EF441242	NC_007883	AY057004	AY443171	3, 12, 15, 16, 40
Family: Ptilonorhynchidae							
	<i>Ptilonorhynchus violaceus</i>	AY064742	EF441250	AY064759	AY057026	AY443216	3, 12, 15, 16
Family: Meliphagidae							
	<i>Ptiloprora plumbea</i>	AY064736	EF441251	AY064760	AY037848	/	15, 16
Suboscines							
	<i>Chiroxiphia caudata</i>	DQ435516	DQ435477	AY136620	AF453802	FJ501792	41–44
	<i>Laniisoma elegans</i>	EU231747	EU231848	DQ363975	FJ501651	FJ501831	44–46
	<i>Lepidocolaptes angustirostris</i>	AY065767	DQ435486	AY089838	FJ461168	FJ460984	43, 47–49
	<i>Pitta versicolor</i>	DQ786002	DQ785966	EF501927	DQ320617	DQ320581	50–52
	<i>Rhinocrypta lanceolata</i>	AY065775	DQ435499	AY370596	FJ461221	FJ460995	43, 48, 49, 53
	<i>Thamnophilus caerulescens</i>	AY065783	DQ435504	EF030294	FJ461176	FJ461066	43, 48, 49, 54
Acanthisittidae							
	<i>Acanthisitta chloris</i>	EU272612	EU272620	AY325307	AY056975	AY443102	3, 12, 20

List of taxa with GenBank accession numbers that were used for the main analyses in the present study. References are given to the studies for which the sequences were originally generated.

*Taxa for which two species from the same genus were used in the analyses.

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Table S3. Specimen data: Basal oscine lineages at 25 Mya

Lineages	Species	RAG-1	References
Basal oscines			
1	<i>Menura novaehollandiae</i>	AF295191	1
2	<i>Atrichornis clamosus</i>	EF463008	2
3	<i>Cormobates placens</i>	AY064260	3
4	<i>Climacteris erythroptera</i>	AY443268	3
	<i>Climacteris picumnus</i>	AY056987	3
5	<i>Ailuroedus melanotis</i>	AY443260	3
	<i>Ptilonorhynchus violasceus</i>	AY057026	3
6	<i>Dasyornis</i>	No data	4
7	<i>Acanthorhynchus</i>	No data	4
8	<i>Amytornis striatus</i>	FJ821041	5
	<i>Malurus melanocephalus</i>	AY057001	3
9	<i>Ephthianura tricolor</i>	AY443285	3
	<i>Meliphaga analoga</i>	AY057003	3
10	<i>Pardalotus punctatus</i>	AY443313	3
11	<i>Acanthiza chrysorrhoa</i>	FJ821039	5
	<i>Gerygone fusca</i>	FJ821053	5
	<i>Sericornis frontalis</i>	FJ821074	5
Transitional oscines			
	<i>Orthonyx temminckii</i>	AY443309	3
	<i>Microeca papuana</i>	AY443301	3
	<i>Chaetops frenatus</i>	AY443266	3
	<i>Philesturnus carunculatus</i>	AY443317	3
Passerida			
	<i>Sitta carolinensis</i>	AY443332	3
core Corvoidea			
	<i>Ptiloris magnificus</i>	AY443325	3
	<i>Coracina lineata</i>	AY056988	3
Suboscines			
	<i>Pipra coronata</i>	AY057020	3
	<i>Pitta sordida</i>	AY443319	3
Acanthisittidae			
	<i>Acanthisitta chloris</i>	AY056975	3

List of taxa with GenBank accession numbers that were used for the analyses of basal oscine lineages. References are given to the studies for which the sequences were originally generated.

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