

Supporting Information

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SI Text

Section A: Phylogenetic Boundaries of a Monophyletic Tanager (Thraupidae) Radiation.

To define a monophyletic tanager radiation for use in the present study, a Bayesian phylogeny of 136 genera and 200 species of nine-primaried oscines was constructed using cytochrome-b sequence data. The analysis was run in MrBayes 3.0b444 under the GTR-gamma model of sequence evolution for 30 million generations, sampled every 400 generations, and the first 16 million generations were discarded as the burnin. A consensus phylogeny was constructed from remaining sampled trees (Fig. S1). The analysis was rooted with *Sylvia layardi* (Genbank sequence AJ534528) and in-group sequences were taken from Genbank (AF489878, AF089005, AF089066, AF089006, AF089007, AF089011, AF447362, AY117723, AF089014, AF290162, AF006211, AF310061, AF382994, AF382997, AF489879, AF006212, AY117717, AY117706, AF089017, AF472384, AY117718, AF089018, AF284073, AF006213, AF108802, AF108792, AF108795, AF447363, AF310049, AF383024, AF108805, AF006214, AF006215, AF006217, AF006218, AF006219, AF006220, AF006221, AF006222, AF489881, AF489883, AF383000, AF006223, AF447366, AF006224, AF006224, AF089020, AF006225, AY190167, AF301462, AF301460, AF006226, AF006227, AF006228, AF256504, AF489884, AF382996, AF383002, AF006229, AF089021, AF089022, AF006230, AF284081, AF284080, AF284083, AF284082, AF290157, AY228057, AF383010, AF006231, AF489885, AF089023, AF383009, AF108778, AF383003, AF089025, AF382995, AF301449, AF089026, AY117699, AF089053, AF006233, AF290156, AF383004, AF383019, AF383020, AF006235, AF006236, AF383028, AF099277, AF099278, AF099288, AF099296, AF089033, AF099302, AF099307, AY190169, AF006237, AF290161, AF089037, AF006238, AF006239, AF089038, AF383005, AF489886, AF489888, AF089039, AF310043, AY156182, AY156181, AF383021, AF284079, AF006240, AF383006, AF089041, AF089042, AF089043, AF383031, AF006241, AF006242, AF006243, AF089045, AF489889, AF472382, AF383017, AF383029, AF006244, AF089046, AF310055, AF489890, AF447371, AF284078, AY124544, AF301447, AF489891, AF006245, AF310057, AF310058, AF108790, AF284075, AF290160, AF006246, AF011772, AF011780, AF011781, AF284074, AF310052, AF383030, AF472383, AY117698, AF472368, AF089051, AF006249, AF089054, AF089057, AF089058, AF310048, U15718, AY228082, AF089059, AF383107, AF489892, AF089060, AF006250, AF383007, AF383001, AF383008, AF489893, AF383018, AF006252, AF089061, AF118231, AF255710, AF310054, AF310053, AF489896, AF290149, AF089062, AF089063, AF089064, AF006253, AF489897, AF006254, AF382999, AF006255, AF006256, AF489898, AF290153, AF489899, AF310042, AF489900, AF108807, AF489901, AF489903, AF383016, AF089067, AF006257, AF383022, AF382998, AF284076, AF383023, AY228056, AF255705, AF171659, AF310066, AF290142, AF342883, AF447364, AF342866, AF342869, AF006216, AY228055, AF342871, AF290143, AF383014, AF006232, AF310067, AF447368, L77903, AF342875, AF015760, AF015755, AF015754, AY156385, AF342877, AF015757, AF342879, AF015763, AF015758, AF015761, AF015759, AF342882, AF015762, AF342884, L76265, L76263, AF365877, AF015756, U46769, ACU46776, U46774, ATU46775, U46777, AF526468, AY228045, AF290138, AY228068, AY030117, AY030118,

AY228074, AF290139, AY228061, AF290141, AF255709, AY228080, AJ534526, AF376887, AY124542, AY124540, AJ534528).

Several taxa traditionally considered tanagers grouped with the Cardinalidae, Parulidae (several genera of “tanagers” and warblers formed a monophyletic radiation endemic to the Caribbean that was sister to a clade containing all other members of the Parulidae), Emberizidae, and Fringillidae, while genera traditionally placed in Cardinalidae, Parulidae, and Emberizidae grouped within the tanagers (see Fig. S1 and Table S1). The blackbirds (Icteridae) were the only nine-primaried oscine family whose traditional taxonomic boundaries were supported by the analysis in Fig. S1. While taxonomic revisions in nine-primaried oscines require multigene datasets, the analysis presented here was used to define a monophyletic radiation of tanagers for the specific purpose of investigating the GABI.

Section B: Additional Details of Methods. Categories of crossing events.

The following are four categories of crossing events between North and South America.

Category 1. These crossing events are represented by the same species in both North and South America. Because the land bridge formed relatively recently, and because tropical taxa often require 3 or more million years to be recognized as distinct species (1), the majority of interchange events [woodcreepers, $n = 15$; antbirds, $n = 21$; tanagers, $n = 29$; blackbirds, $n = 12$] are considered to be the same species on either side of the land bridge.

Category 2. These crossing events are represented by a pair of sister species with one species endemic to North America and the other to South America. Six tanager and five blackbird interchange events fall into this category.

Category 3. These crossing events are represented by deeper-level splits in a phylogenetic tree in which a clade of two or more endemic species in one continent is sister to an endemic clade of one or more species in the other. Blackbirds and woodcreepers each have one crossing event that fall within this category. Tanagers have two.

Category 4. These crossing events are represented by dispersal events that are not represented by endemic clades in each continent. This category occurs when an initial crossing event is followed by one or more recent crossing events that are phylogenetically nested within the same clade. Unlike the other categories of crossing events, this category relies on ancestor-state reconstruction in order to determine at which nodes crossing events occurred. Blackbirds and tanagers each have four, antbirds one, and woodcreepers two crossing events that fall within this category.

Dating of crossing events. A crossing event between North and South America occurs when a lineage colonizes from one continent to the other and establishes a breeding population there. Each crossing event that has left descendants to the present (i.e. has not gone extinct) produces a node on a phylogenetic tree, with one of the daughter lineages occurring in North America and the other in South America. We were certain to include these nodes in our phylogenies by obtaining samples from either continent for all four categories of crossing events (except in a few cases where a sample from one continent was not available: see below). The date of this node will, in most cases, closely approximate the date of colonization, provided gene flow between the continents was severed following colonization.

For most land bird species straddling both continents, the land

bridge probably represents a phylogenetic break. Highland areas within the land-bridge region are separated by lowland barriers between the Andes and the Darien highlands and between the Darien highlands and highlands of western Panama and Costa Rica, which limit gene flow between populations of a highland species following a crossing event. Lowland species also appear to have a phylogenetic break between populations on the two continents. For example, a general pattern occurs where closely related sister species (Category 2 crossing events) exhibit a contact zone along the Isthmus of Panama in the region between the Canal Zone and the Darien highlands, with one species occurring to the northwest and the other to the southeast. This common biogeographic pattern is often mirrored within lowland species that straddle the land bridge (lowland Category 1 crossing events). For example, our samples of *Ramphocelus flammigeus icterocephalus* from western Panama south into the Isthmus of Panama are genetically differentiated from those south of the Darien highlands in the Choco region of South America (≈ 1.8 Ma divergence), despite the fact that they constitute the same subspecies. These patterns suggest that upon dispersal across the land bridge, genetic differentiation occurs in either continent because subsequent gene flow is greatly reduced or absent across the narrow isthmus region.

For those species that occur in both continents but do not yet appear to be greatly differentiated in cytochrome *b*, we assume that the lack of genetic differentiation results from the recent expansion across the land bridge (habitat changes associated with Pleistocene climatic cycles may have facilitated dispersal). However, in some cases ongoing gene flow between Central and South American populations within a species may render the genetic estimates of their colonization date to be younger than the true date at which colonization occurred. This is unlikely to be a major problem because colonization prior to land bridge completion would almost certainly have resulted in genetically differentiated lineages in each continent (i.e. because of marine barriers). Of the 61 species of antbirds, woodcreepers, tanagers, and blackbirds that occur in both continents (for which we had samples from each continent) 43 were genetically undifferentiated or exhibited at most low genetic divergence in cytochrome *b* (less than $\approx 2\%$) between Central America and northwest South America. However, 26 of these possess a genetically differentiated sister population (usually in the Amazon or southern Andes) or sister species that dates within the past 4 million years, a pattern suggesting that colonization between continents was indeed post-land bridge (see Fig. S2).

Ancestor-state reconstruction. Because most crossing events between North and South American will naturally give rise to a node in our trees (see above), the most appropriate of the currently available methods for ancestor-state reconstruction is to treat North America and South America as discrete character states. Our methods assume that all lineages (including ancestral lineages) in our phylogenies occur in either one state or the other but not both simultaneously. For species that occur in both geographic regions, this means sampling the local populations in each and treating them as distinct lineages in the analysis.

For analysis of character evolution (in our case biogeographic states), branch lengths should be used only when analyzing character traits that may evolve at any time along a branch. In biogeographic models where the character states represent discrete geographic regions, it may be more appropriate to ignore branch-length information because a character-state transition (dispersal between regions) will create nodes on the tree (2), and we have argued above that this is the most likely case here. Therefore, we constrained branch lengths to be equal in our analysis, which has the effect of associating crossing events with nodes. Forcing branch lengths to be equal effectively gives each node the same probability of representing a crossing event in ancestor-state reconstructions and the one-rate model we

used to analyze character evolution. In the two-rate model, branch lengths are used only to determine whether a node occurs before or after a breakpoint in time. If a node dates before the breakpoint, the branches immediately descending from the node are set to 1; if after the breakpoint, branches descending from a node are set to a parameter f , which is estimated by the model. This effectively gives each node predating the breakpoint the same probability of representing a crossing event, while nodes following the breakpoint are assigned a different probability.

To test the validity of the equal branch-length assumption, we compared support for that model with one that has branch lengths proportional to time. The model transforms branches by raising them to the power K (3). When K is 0, branches are all equal to 1 (the model used here, which ignores branch lengths). When K is 1, branch lengths are equal to their original values in the dated phylogeny. Values of K between 0 and 1 produce branch lengths between the original and constrained values. For each of our four focal families, we estimated the likelihood of a range of K values using our two-rate model and the best supported time of breakpoint (Fig. 1A). In all four families, likelihoods increased as K decreased and a value of 0 received strongest support in each case (Table S2). This result best supports a model in which branch lengths are constrained to be equal. However, we obtained the same qualitative result when we analyzed the data using the original branch lengths: rates were elevated in each family following the best-supported breakpoint, and the increase in rates was strongest in woodcreepers and antbirds. The similarity of these results suggest that our overall findings are robust to assumptions about branch lengths.

Section C: Phylogenetic Trees and Ancestor-State Reconstructions for Woodcreepers, Antbirds, Tanagers, and Blackbirds.

Here we discuss additional details of reconstructions of ancestral geographic range used for antbirds, woodcreepers, tanagers, and blackbirds (see Fig. S2). Maximum-likelihood reconstructions were performed using the best breakpoint, as shown in Fig. 1. Branches descending from nodes postdating the breakpoint were given length f (see above), and those before were set to 1. Reconstructions were performed with either forward and backward rates constrained to be equal (symmetrical model) or allowed to vary (asymmetrical model). The two models reconstructed identical character states at nodes for blackbirds and almost identical states for woodcreepers, antbirds, and tanagers. The only difference in the latter three families was that the asymmetrical model gave stronger support to a South American state for nodes, which in the symmetrical model had approximately equal support for either state. Here we report results for only the simpler symmetrical model, except as noted.

Antbirds, woodcreepers, and tanagers were reconstructed as having a South American and blackbirds a North American origin. Tanagers evolved and radiated in South America following early colonization of a nine-primaried oscine of North American affinity (see Fig. S1) during the Miocene. Very few clades of tanager have colonized the Caribbean, and those that have are mostly associated with finch-billed morphology and are not confined to tropical forest.

For antbirds, both parsimony and a maximum-likelihood reconstruction (one-rate punctuated model with branchlengths set to 1) were ambiguous regarding the reconstruction for *Thamnophilus bridgesi* and *T. atrinucha*. Either an initial colonization event of North America occurred at 5.6 Ma followed by a back-colonization of South America less than 1 Ma, or two separate colonizations of North America occurred, the first at ≈ 3 Ma, the second at earlier than 1 Ma. The asymmetrical model supported the double invasion of North America. The double-invasion reconstruction is consistent with the lack of pre-land bridge colonization events in the rest of the tree and we assume it is correct in our analysis.

For woodcreepers, antbirds, and blackbirds, we sampled all species involved in the interchange. In tanagers we sampled all species involved, with the exception of four crossing events where a South American clade colonized North America, producing an endemic species there (Category 2 or 3 crossing events). In these latter four cases, we sampled the representative species from one side of the land bridge but lacked a sample from the other. We detail these here: (i) *Chrysothlypis salmomi* is missing and was placed as sister to the only other species in its genus, *C. chrysomelas*. (ii) *Tangara cabanisi* is missing and was placed as sister to *T. palmeri*, with whom a sister-species relationship based on plumage and biogeographic considerations has been suggested by Isler and Isler (4). These investigators also state that these two species “are alike in appearance, habitat preference and voice.” Most of the other species groups of *Tangara* defined by Isler and Isler (4) have turned out to represent monophyletic groups in a recent molecular phylogenetic analysis (5). (iii) The South American ancestor of the Central American endemic *Bangsia arcaei* is unsampled. We believe *Bangsia melanochlamys* to be the sister species to *B. arcaei* based on biogeographic considerations (it is the species that is closest to Central America) and plumage similarity, and have added it manually to the tree. However, it is possible that one of the several other Andean species in this genus (or a clade of multiple Andean species) is the sister to *B. arcaei*. In either case, the reconstruction will not be altered (see Fig. S2). (iv) *Oryzoborus nuttingi* is missing. This species was formerly considered conspecific with the South American *O. crassirostris*/*O. maximiliani* complex (6, 7) and is considered to form a superspecies with *O. crassirostris* and *O. maximiliani*. Given these considerations, we place it as sister to our sample of *O. crassirostris*.

For 22 crossing events representing the same species on either side of the land bridge (Category 1 crossing events), we sample the species from one side of the land bridge but lacked a sample from the other side. The missing population was added manually to the tree as sister to the conspecific population that we sampled.

We lacked samples for a number of additional species that were not involved in the interchange and these were ignored in ancestor-state reconstruction (though we do correct for their missing branch length in our analysis in Figs. 1B and 2). We do not expect these missing species to affect our dating or ancestor-state reconstructions for two reasons. First, most missing species come from genera that occur in only South America (e.g., the tanager genera *Conirostrum*, *Poospiza*, and *Hemispingus*, among others) and, thus, we know they were not involved in interchange. Adding them amounts to adding additional South American twigs to our phylogenies in parts of these trees that failed to colonize North America. Second, missing species from genera that did colonize between continents are presumed not to alter our reconstruction because the colonization occurred either within a species (Category 1-type of colonization) or they belong to a different superspecies complex than the ones involved in colonization. If a superspecies boundary is incorrectly defined, then we may have failed to sample the most closely related South America species to the North American one. Such error in dating is conservative with respect to our null hypothesis of an increase in interchange rates.

Section D: Phylogenetic Trees and Ancestor-State Reconstructions for Earliest Dates of Interchange for Families in Table 2. This section includes the parsimony and maximum-likelihood reconstructions

of ancestral geographic range used for the additional families in Table 2 that were not included in the previous section (Fig. S3). For each family, a phylogenetic tree is presented for the family as a whole or for a specific clade within that family. See additional notes on species sampling and ancestor state reconstruction associated with each family in Fig. S3.

Section E: Analysis of Extinction Rates. Our neontological approach uses molecular phylogenetic dating methods to reconstruct the ages of colonization events between North and South America. This approach is unable to reconstruct ages of colonization events that left no descendants at the present. If extinction rates are high, then the dates of crossing events alone cannot determine whether land bridge completion precipitated a wave of interchange. To correct for extinction, we calculated per-lineage rates of interchange. Provided that per-lineage extinction rates are the same for lineages that crossed and lineages that remained behind within the same family, then extinction is factored out by calculating per-lineage rates of interchange between the continents. To test this assumption, we used newly developed methods (8) implemented in Mesquite (9) to estimate extinction rates separately for lineages in each continent. To implement this analysis, we included clock-like branch lengths obtained from our BEAST analysis. We compared a model in which extinction rates were free to vary in colonizing versus noncolonizing lineages with a model in which extinction rates were constrained to be the same in all clades. The models differ by one free parameter and were compared using a likelihood-ratio test as done in Table 1. Because the extinction estimates assume complete species sampling, we present results in Table S3 only for woodcreepers and blackbirds for which we sampled most species. Results for these two families suggest very low extinction rates in both lineages that colonize and those that remain. Estimates of extinction were thousands of times slower than speciation rates (see Table S3). Moreover, the two-rate extinction model did not provide a significantly better fit than the one-rate extinction model. These results fail to reject our assumption that extinction rates are similar in clades that colonize versus those that do not. This analysis has several caveats. First, branch lengths were included in order to estimate speciation and extinction rates. However, a robust model of geographic character change that incorporates branch lengths has not been developed. The simple model used here has the undesirable property of allowing direct transition between continents along branches rather than just at nodes. This is unlikely to be a major issue because our previous analysis suggested inclusion of branch lengths has little effect on estimates of transition rates between continents. Second, crossing events represented by the same species in each continent (Category 1 crossing events) have a representative sample from each continent in the tree and, thus, add a node to the tree that may not represent a true speciation event. To determine whether these additional nodes might alter our estimates of extinction, we compared extinction rates for the entire tree with and without the additional samples within species. We did this using the simplest model, which estimates speciation and extinction rates but ignores character states and is equivalent to the method developed by Nee et al. (10, 11). Excluding multiple samples per species increased extinction rate estimates slightly, but these rates remained very low (woodcreepers: with additional samples extinction = 5.63, without additional samples extinction = 5.11×10^{-6} ; blackbirds: with additional samples extinction = 1.88×10^{-6} , without additional samples extinction = 4.827×10^{-6}).

1. Weir JT, Schluter D (2007). The latitudinal gradient in recent speciation and extinction rates of birds and mammals. *Science* 316:1574–1576.
2. Weir JT (2006). Different timing and patterns of species accumulation in lowland and highland Neotropical birds. *Evolution* 61:842–845.

3. Pagel M (1994). Detecting correlated evolution on phylogenies: A general method for the comparative analysis of discrete characters. *Proc R Soc Lond B* 255:37–45.
4. Isler ML, Isler RI (1999). *The Tanagers: Natural History, Distribution, and Identification*. (Smithsonian Inst Press, Washington, DC).

5. Burns KJ, Naoki K (2004). Molecular phylogenetics and biogeography of neotropical tanagers in the genus *Tangara*. *Mol Phylogenet Evol* 32:838–854.
6. Wetmore A (1970). Description of additional forms of birds from Panama and Colombia. *P Biol Soc Wash* 82:761–776.
7. Stiles FG (1984). The Nicaraguan Seed-Finch (*Oryzoborus nuttingi*) in Costa Rica. *Condor* 86:118–122.
8. Maddison WP, Midford PE, Otto SP (2007). Estimating a binary character's effect on speciation and extinction. *Syst Biol* 56:701–710.
9. Maddison WP, Maddison DR (2006) Mesquite: A modular system for evolutionary analysis, v1.12.
10. Nee S, Holmes EC, May RM, Harvey PH (1994a) Extinction rates can be estimated from molecular phylogenies. *Phil Trans R Soc Lond B* 344:77–82.
11. Nee S, May RM, Harvey PH. (1994b) The reconstructed evolutionary process. *Phil Trans R Soc Lond B* 344:305–311.

Antbird parsimony ancestor state reconstruction

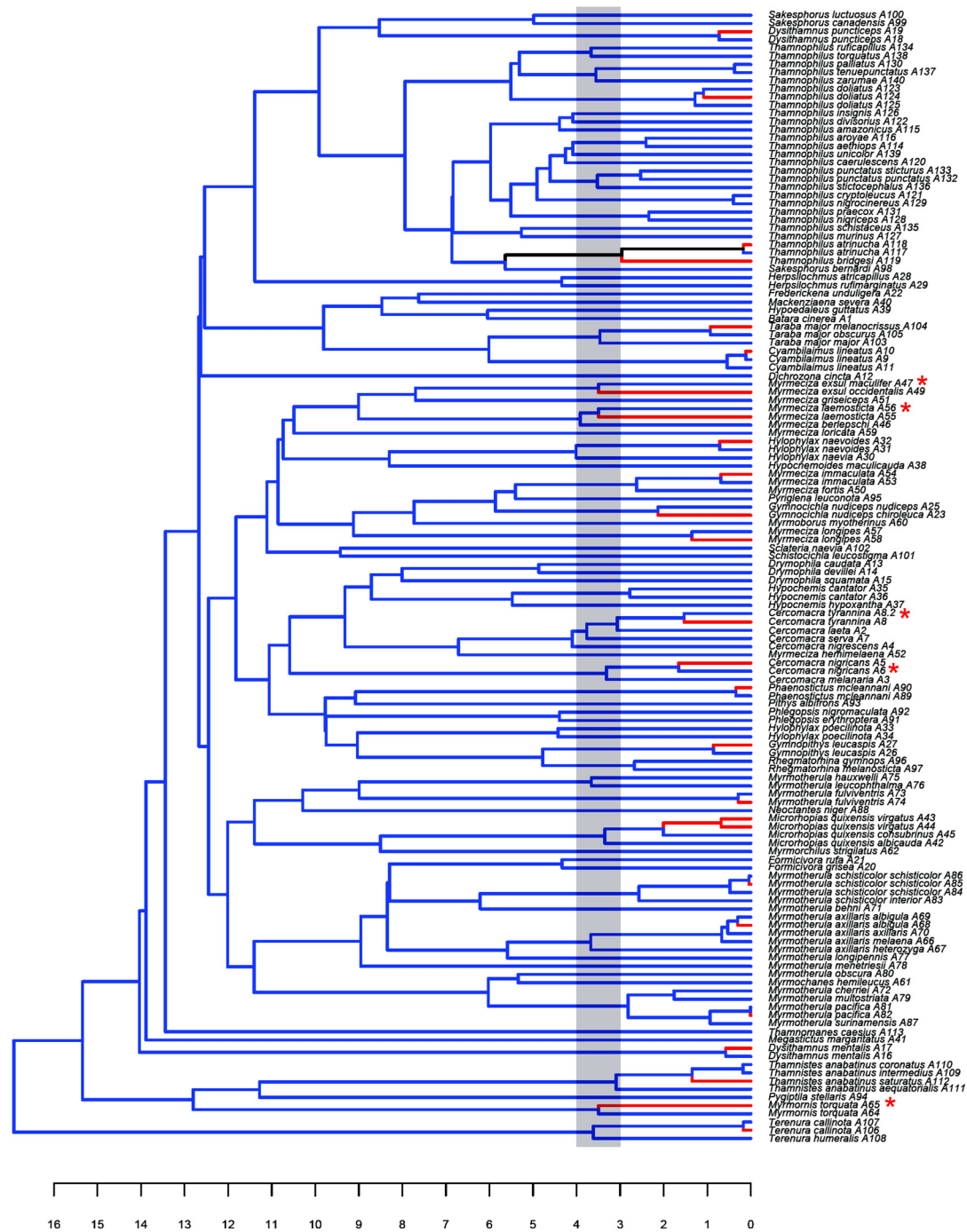


Fig. S2. Continued.

Tanager parsimony ancestor state reconstruction

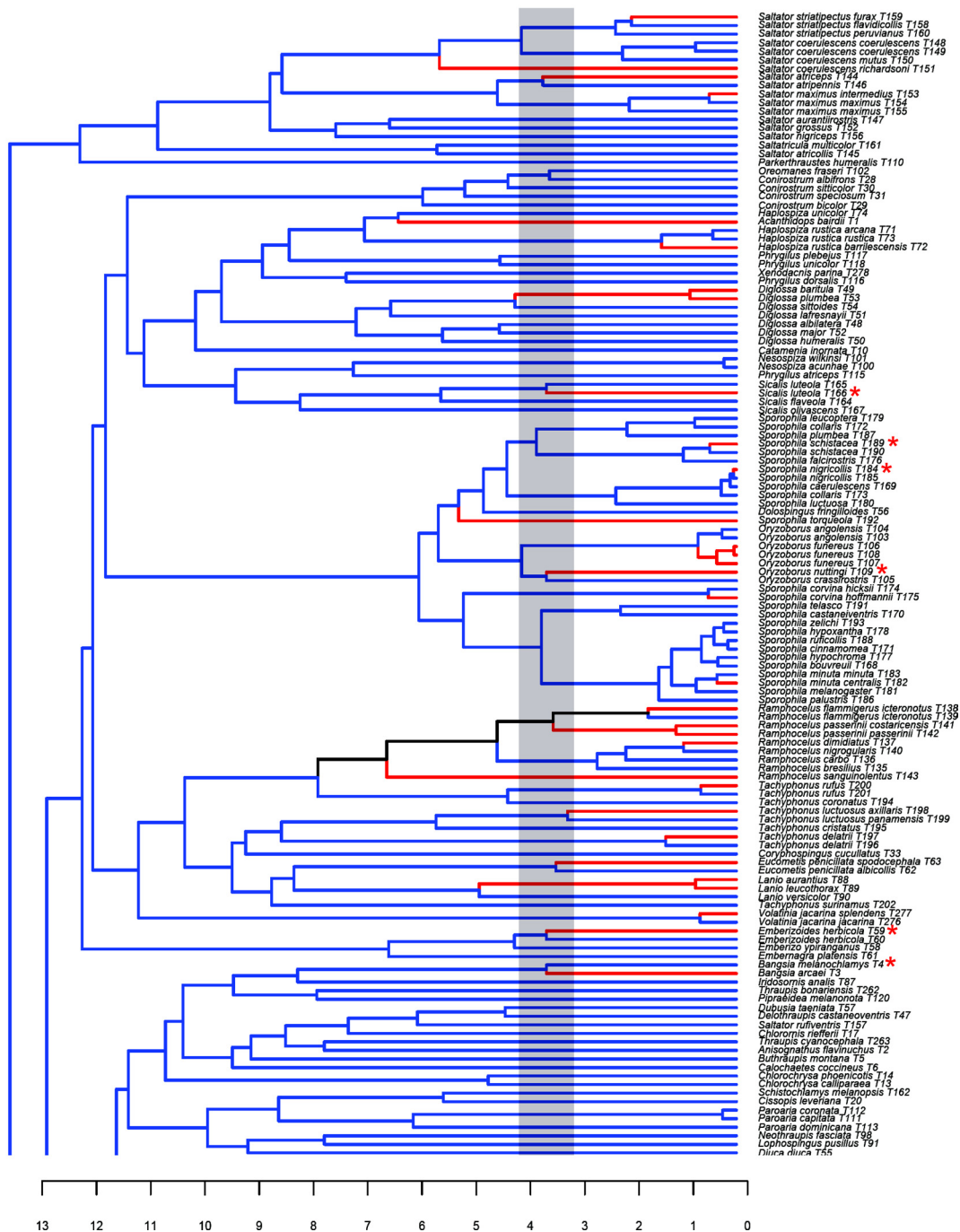


Fig. S2. Continued.

Tanager maximum likelihood ancestor state reconstruction

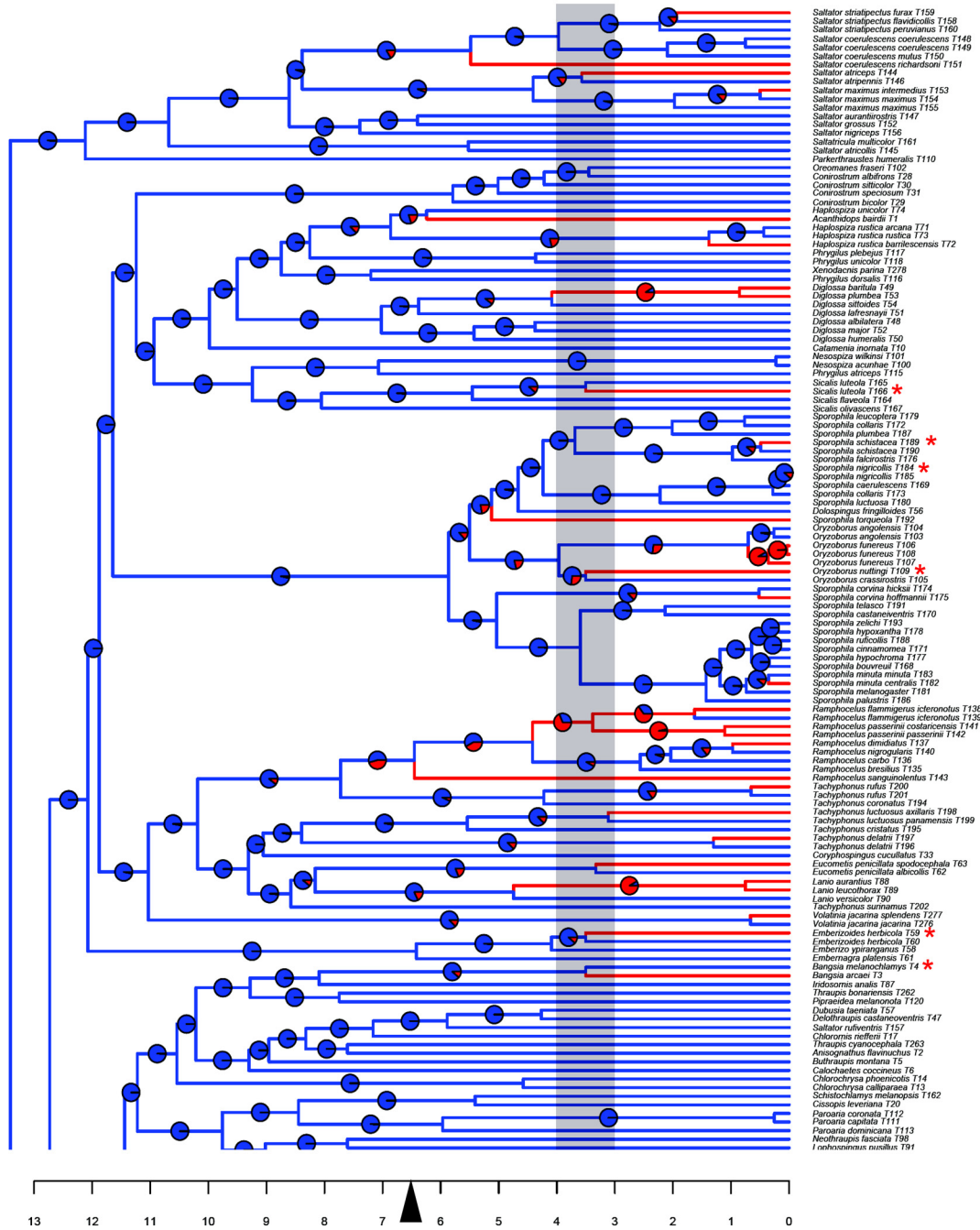


Fig. S2. Continued.

Tanager maximum likelihood ancestor state reconstruction continued

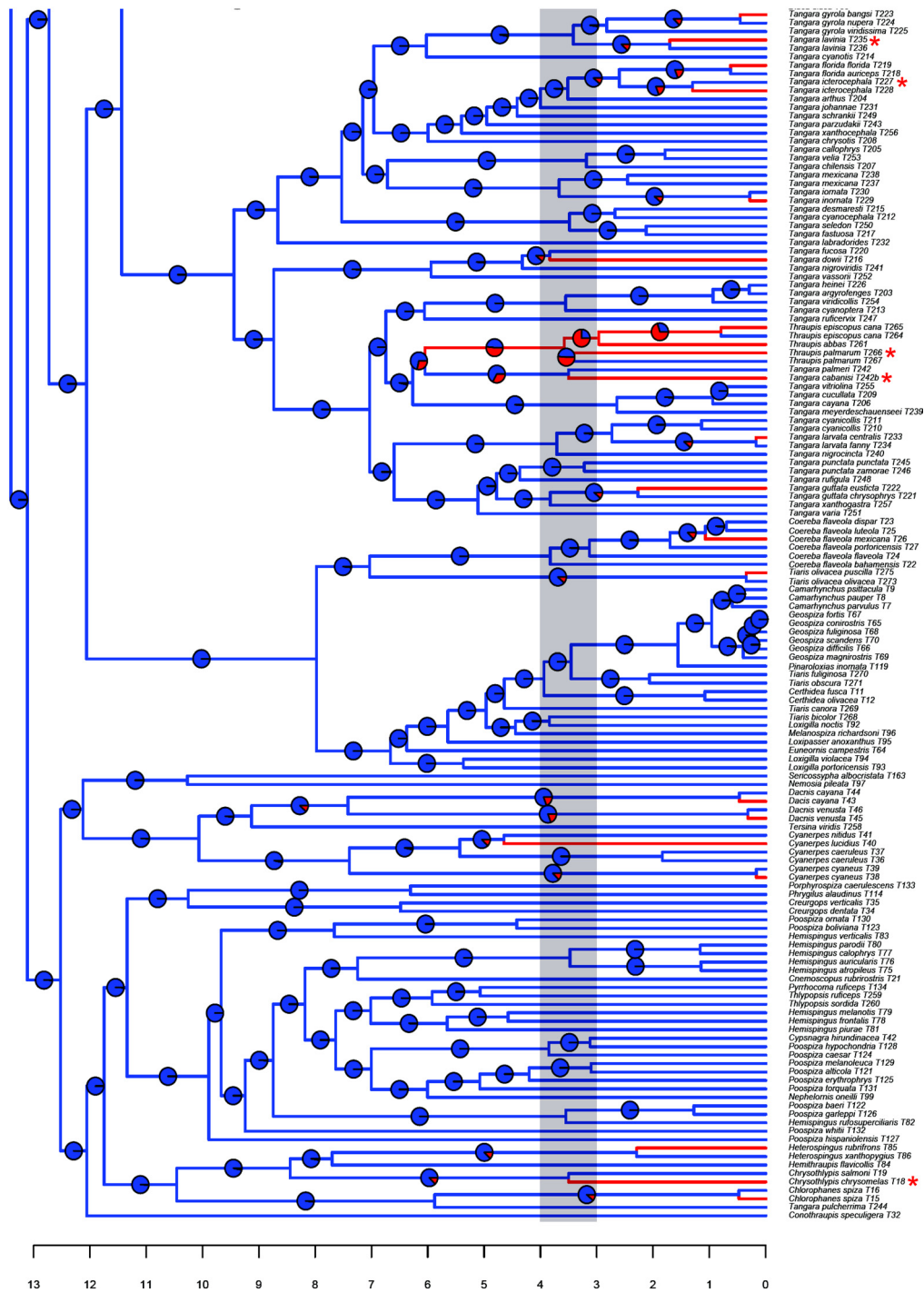


Fig. S2. Continued.

Blackbird parsimony ancestor state reconstruction

NOTE: *Molothrus bonariensis* is a primarily SA species which has invaded NA in historical times. Thus the most parsimonious reconstruction here is incorrect and this branch should be colored blue (SA) ▼

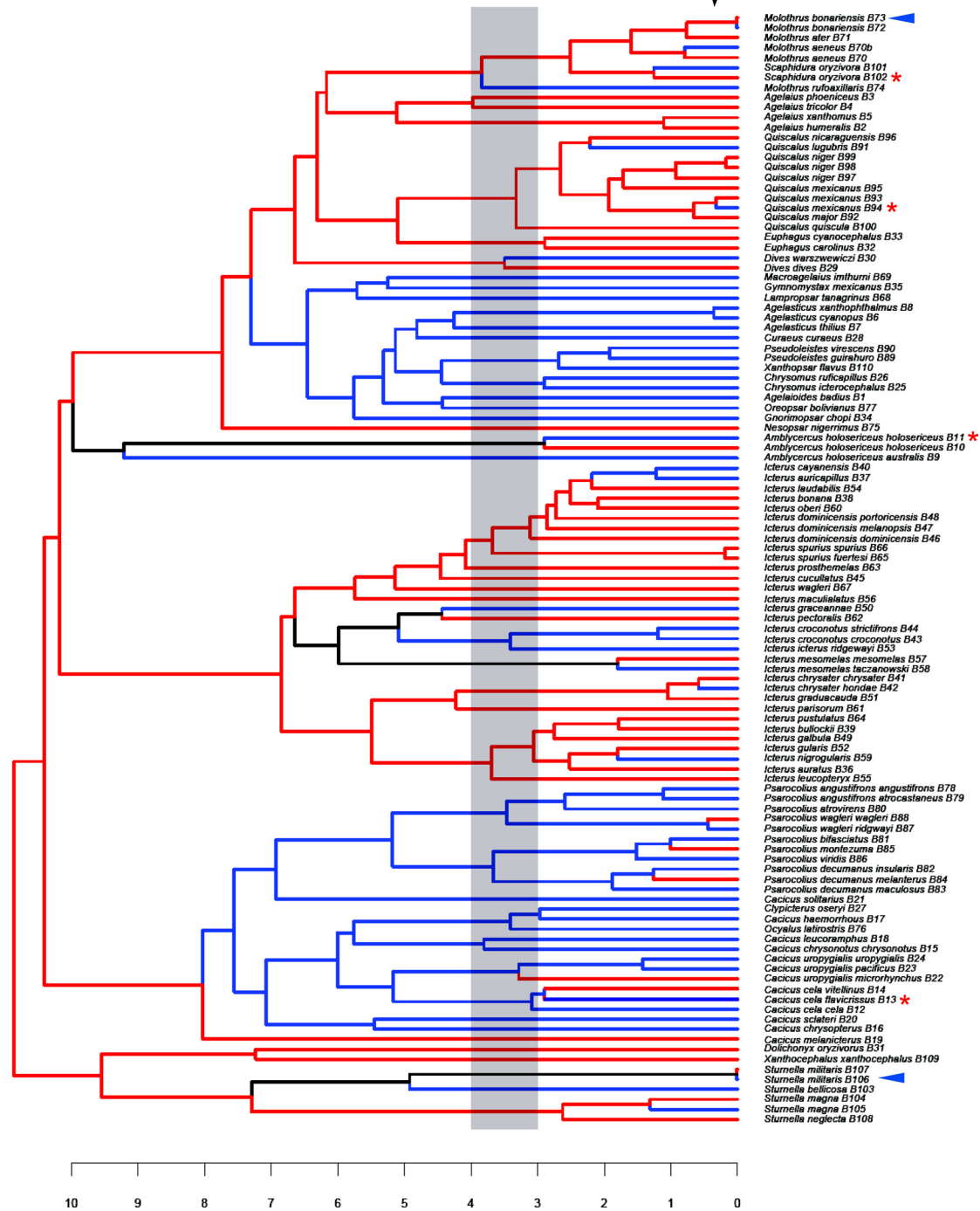


Fig. S2. Continued.

Blackbird maximum likelihood ancestor state reconstruction

NOTE: *Molothrus bonariensis* is a primarily SA species which has invaded NA in historical times. Thus the reconstruction here is incorrect and this branch should be colored blue (SA).

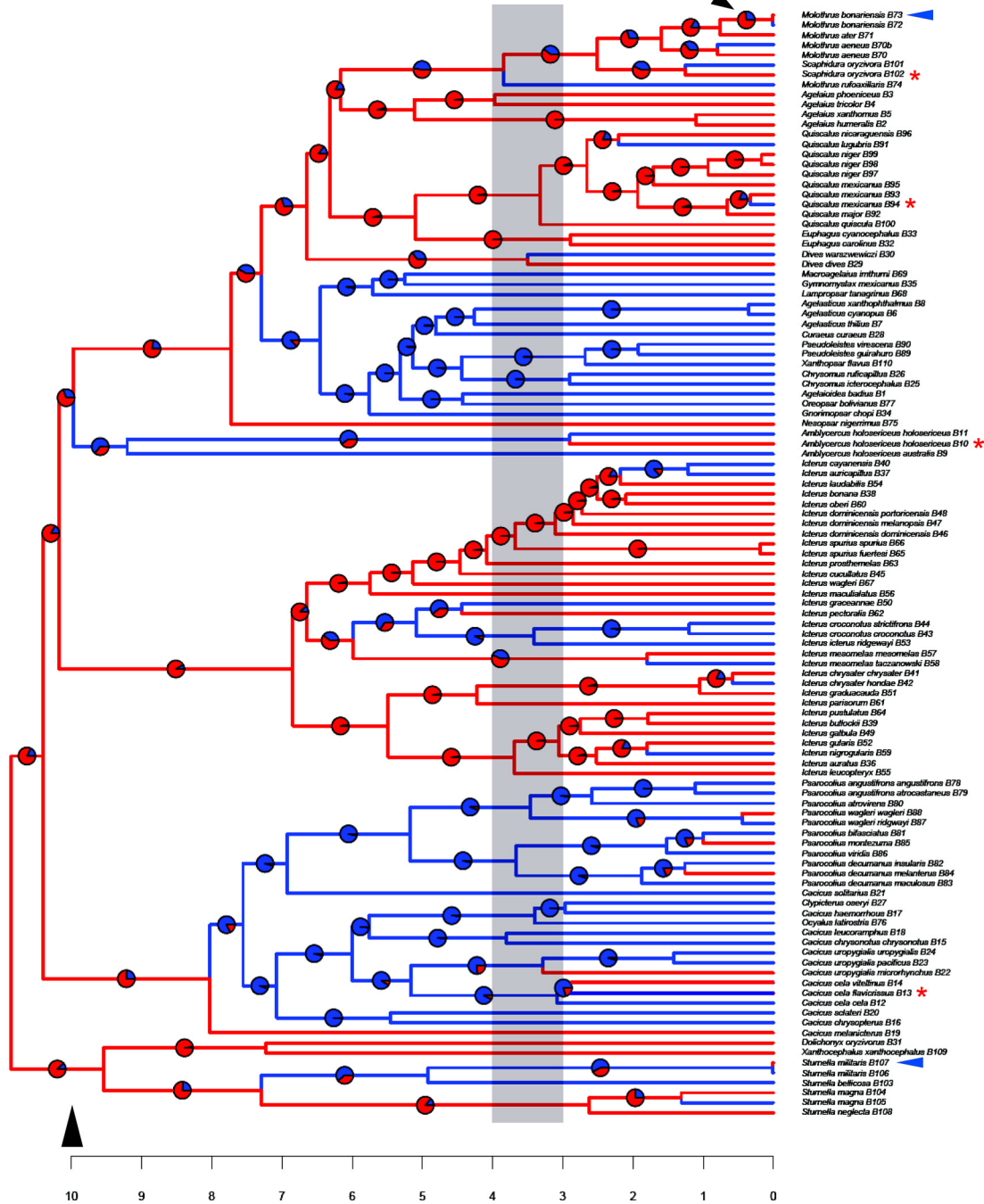
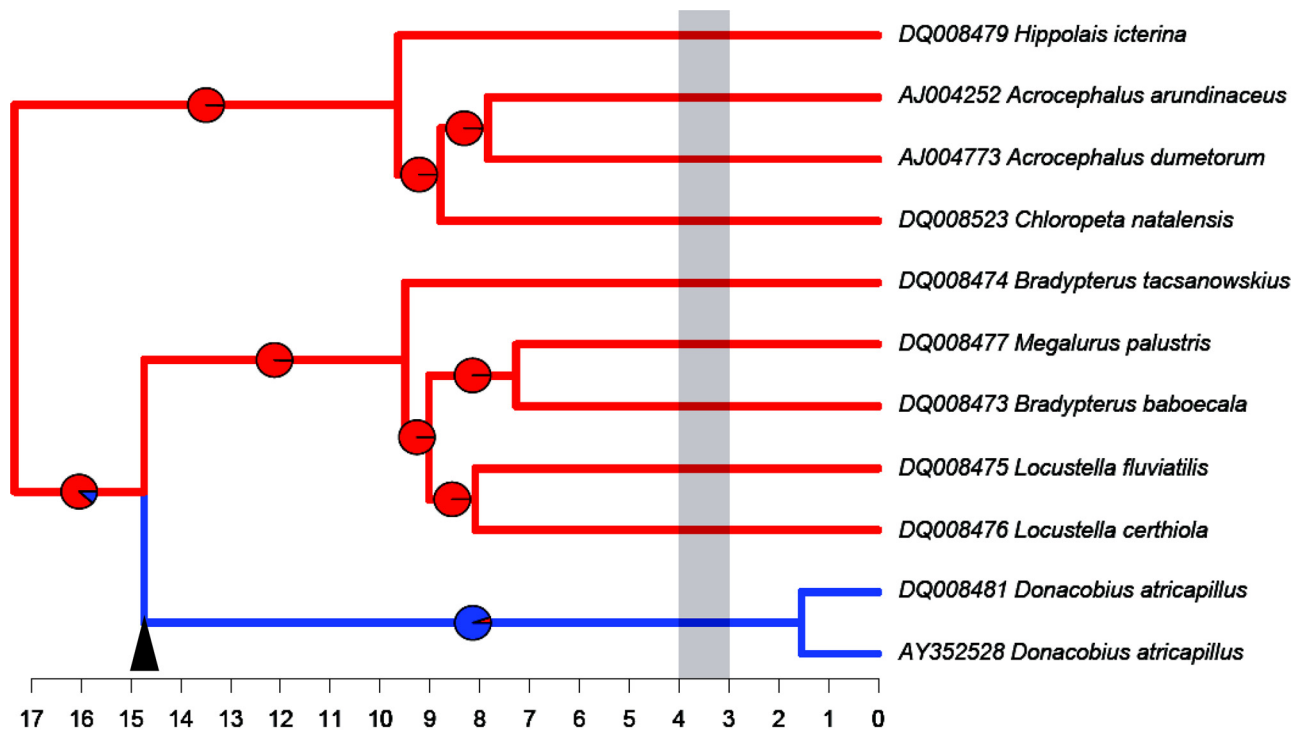


Fig. S2. Continued.

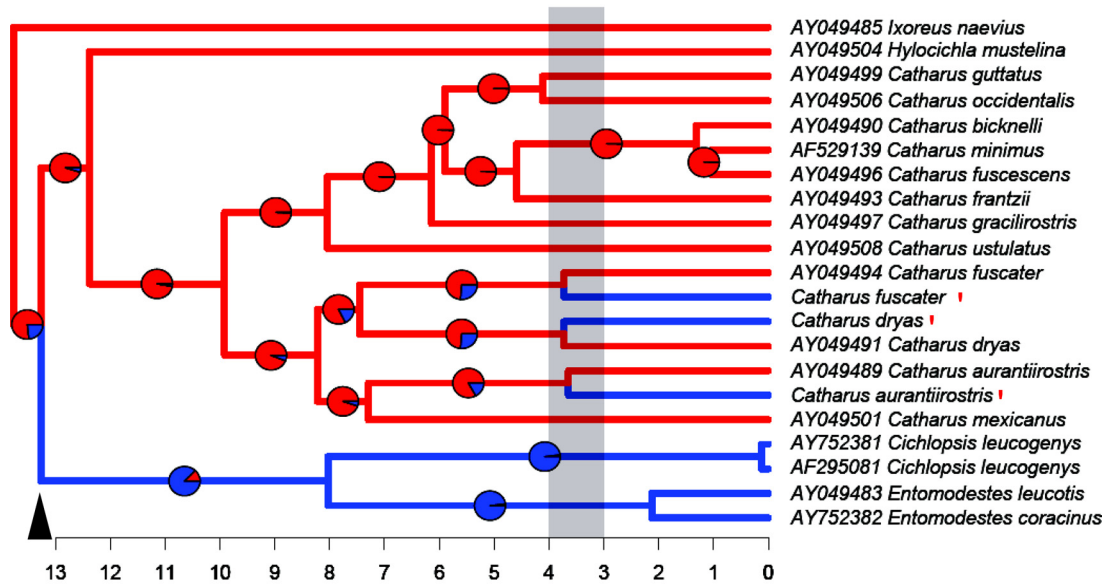
Donacobius parsimony and maximum likelihood reconstruction reconstruction



Comments: *Donacobius* has recently been shown to be sister to the Megaluridae and we include it in that family. Whether it colonized South America via North America is unknown for certain as the family currently is restricted to the Old World and South America. The only New World species is sampled. It is not certain but seems likely that colonization of South America occurred via North America. Red here indicates Old World distribution.

Fig. S3. Bayesian phylogenies and parsimony and maximum-likelihood ancestor-state reconstructions of geographic range (unless otherwise stated, red represents North America, blue represents South America, yellow represents Old World, and black is uncertain) for the additional families listed in Table 2. North American distribution is indicated by black and South American by white. Branches on parsimony reconstructions in gray indicate that either character state is equally parsimonious for that branch. Maximum-likelihood reconstructions are based on a punctuated one-rate model in which all branch lengths were set to a value of one. Scale bars indicate time in millions of years. The time period between 4 and 3 Ma, when the land bridge was completed, is highlighted in gray. Missing lineages added manually to trees are followed by a red asterisk and the date at which they join the tree is arbitrary. Pie diagrams show proportional likelihoods (i.e., they sum to 1). Transition events between continents occur at nodes in these reconstructions and pie diagrams are placed along the lineage leading up to a node to indicate the state of that lineage. The date of first interchange is shown by a black triangle. A second black triangle is shown for some families to illustrate an alternative first date of interchange. GenBank numbers precede species names.

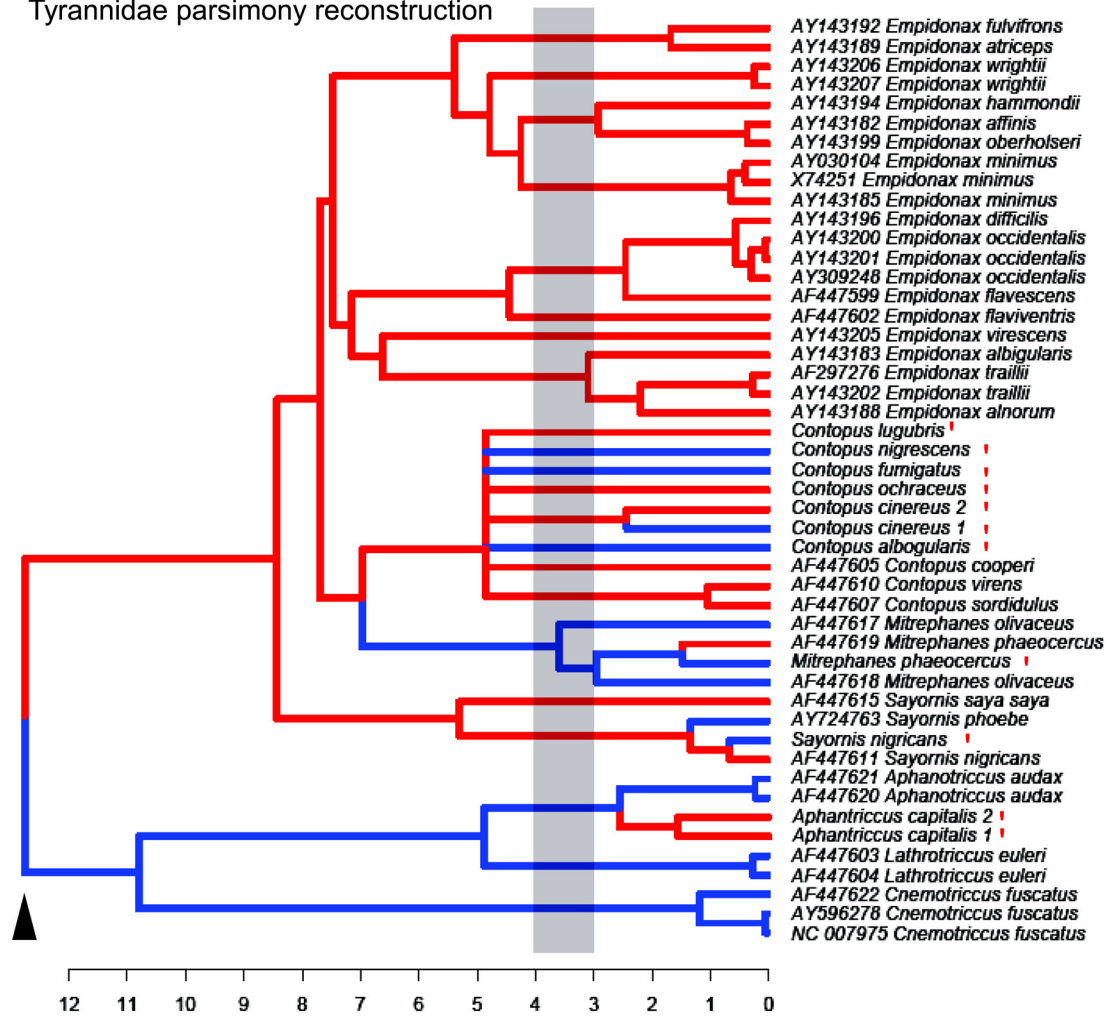
Turdidae parsimony and maximum likelihood reconstruction



Comments: Certain clades of thrushes may have colonized North and South America independently from the Old World. The earliest date of interchange at 13.3 Ma refers to the colonization of South American *Cichlopsis* and *Entomodestes* from a primarily North American clade dominated by *Catharus* and its relatives. Older dates of interchange in other clades within the family are unlikely. This monophyletic clade (see 8) within the Turdidae is almost confined to the New World (*Catharus minimus* also occurs in eastern Siberia). One species is missing: *Ridgwayia pinicola*. The analysis of Klicka et al. (8) suggest *Ridgwayia* is sister to *Hylocichla*. It's inclusion would not alter the reconstruction.

Fig. S3. Continued [(8) Klicka J, Voelker G, Spellman GM (2005) A molecular phylogenetic analysis of the "true thrushes" (Aves: Turdidae). *Mol Phylogenet Evol* 34:486–500].

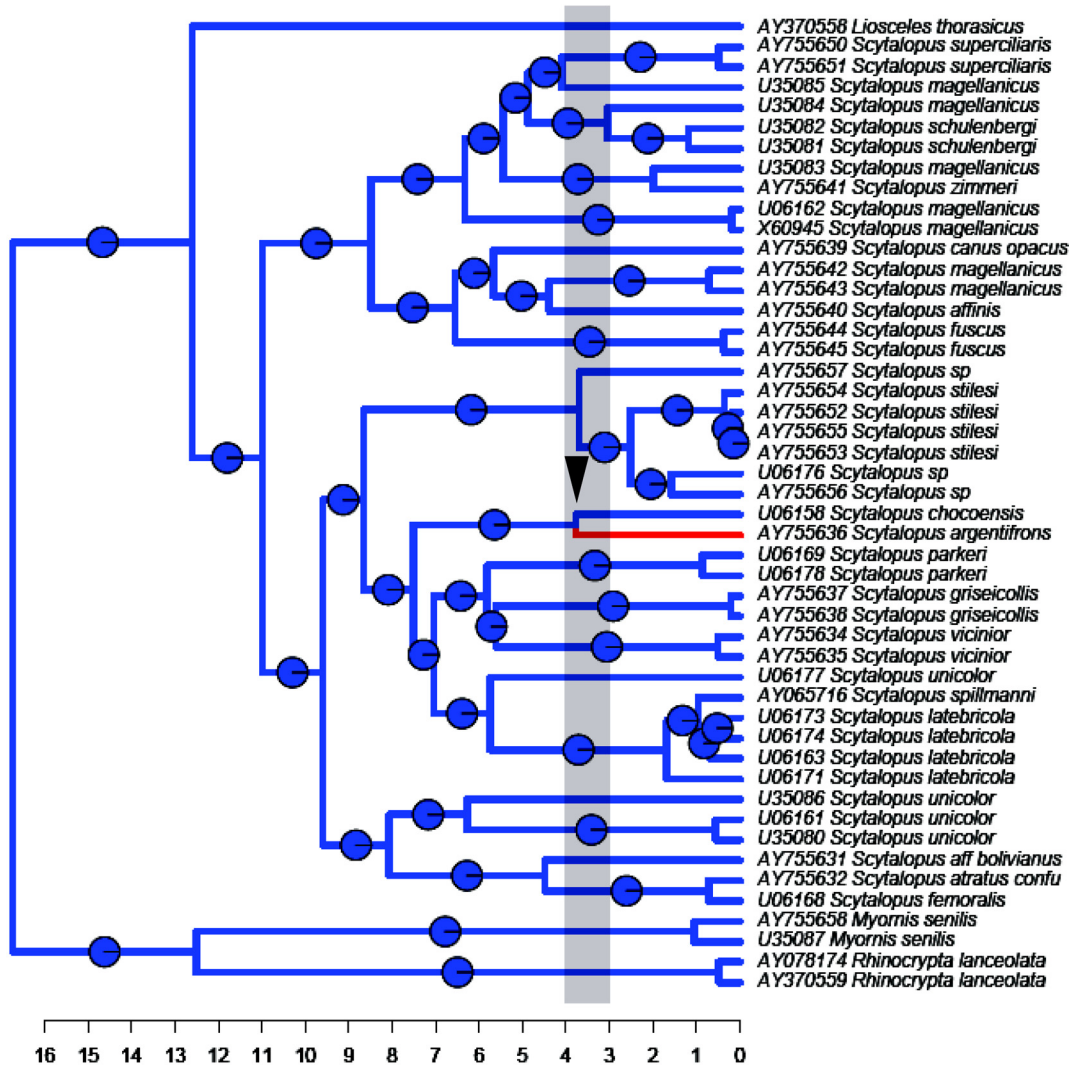
Tyrannidae parsimony reconstruction



Comments: Here we consider the Tityridae as a part of the Tyrannidae though it was recently elevated as a separate family. A published higher level analysis suggest the genera in this phylogenetic tree probably form a monophyletic group within the Tyrannidae (9), though it remains possible that a few genera not sampled could also belong to this clade (e.g. the North American *Xenotriccus*). This clade indicates that then South American derived tyrannids entered North America at least by 7.5 Ma when the first divergence event within the entirely North America *Empidonax* occurred. If this clade of Tyrannids is monophyletic, then the reconstruction indicates the family entered NA at least by 12.75 Ma. *Aphanotriccus capitalis* and several species of *Contopus* were not sampled. *Aphanotriccus capitalis* was placed as sister to the only other species in the genus, *Aphanotriccus audax*. Missing mainland species of *Contopus* were placed as a polytomy with sampled *Contopus* species. We were unable to perform a maximum likelihood reconstruction because polytomies are not permitted under this method of reconstruction.

Fig. S3. Continued [(9) Ohlson J, Fjeldsa J, Ericson PGP (2008) Tyrant flycatchers coming out in the open: Phylogeny and ecological radiation of Tyrannidae (Aves, Passeriformes). *Zoologica Scripta* 37:315–335].

Rhinocryptidae maximum likelihood and parsimony reconstruction



Comments: Only 1 species occurs in North America. The actual number of species in South America is unknown and new species are regularly discovered. The sister species to the sole Central American endemic *Scytalopus argentifrons* is *Scytalopus chocoensis* which on biogeographic grounds is geographically most proximate to *S. argentifrons*. Further sampling of South American species is unlikely to find a closer sister to *S. argentifrons*, but if it did would not change the fact that *S. argentifrons* resulted from a dispersal event at or after landbridge completion. Note that a number of cytochrome b sequences of *Scytalopus* available in Genbank formed a clade sister to all other *Scytalopus* samples. We excluded this clade because it appeared to represent amplification of a pseudogene (e.g. it's species composition overlapped broadly with the species composition of the above tree suggesting an ancient gene duplication event).

Fig. S3. Continued.

Mimidae parsimony reconstruction

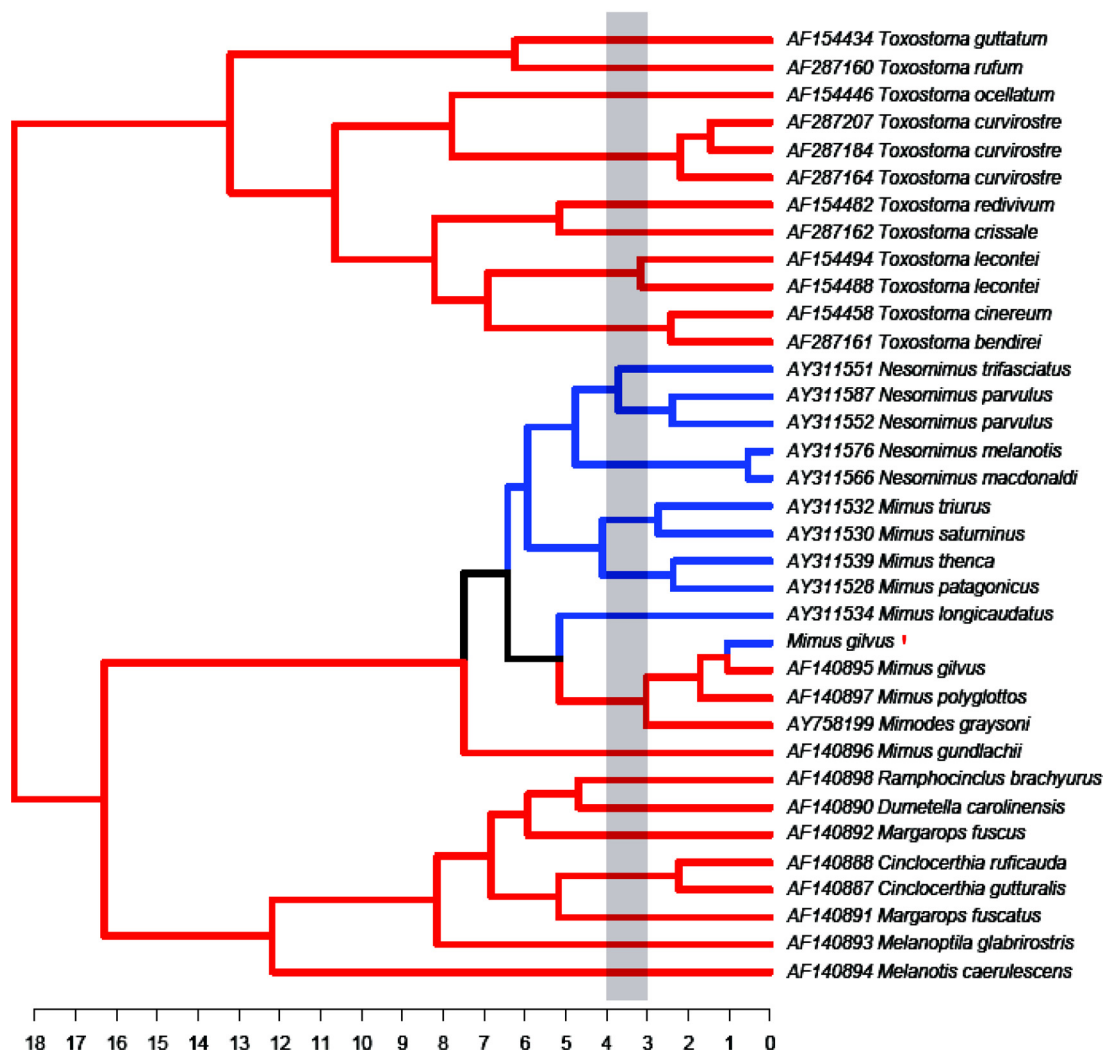
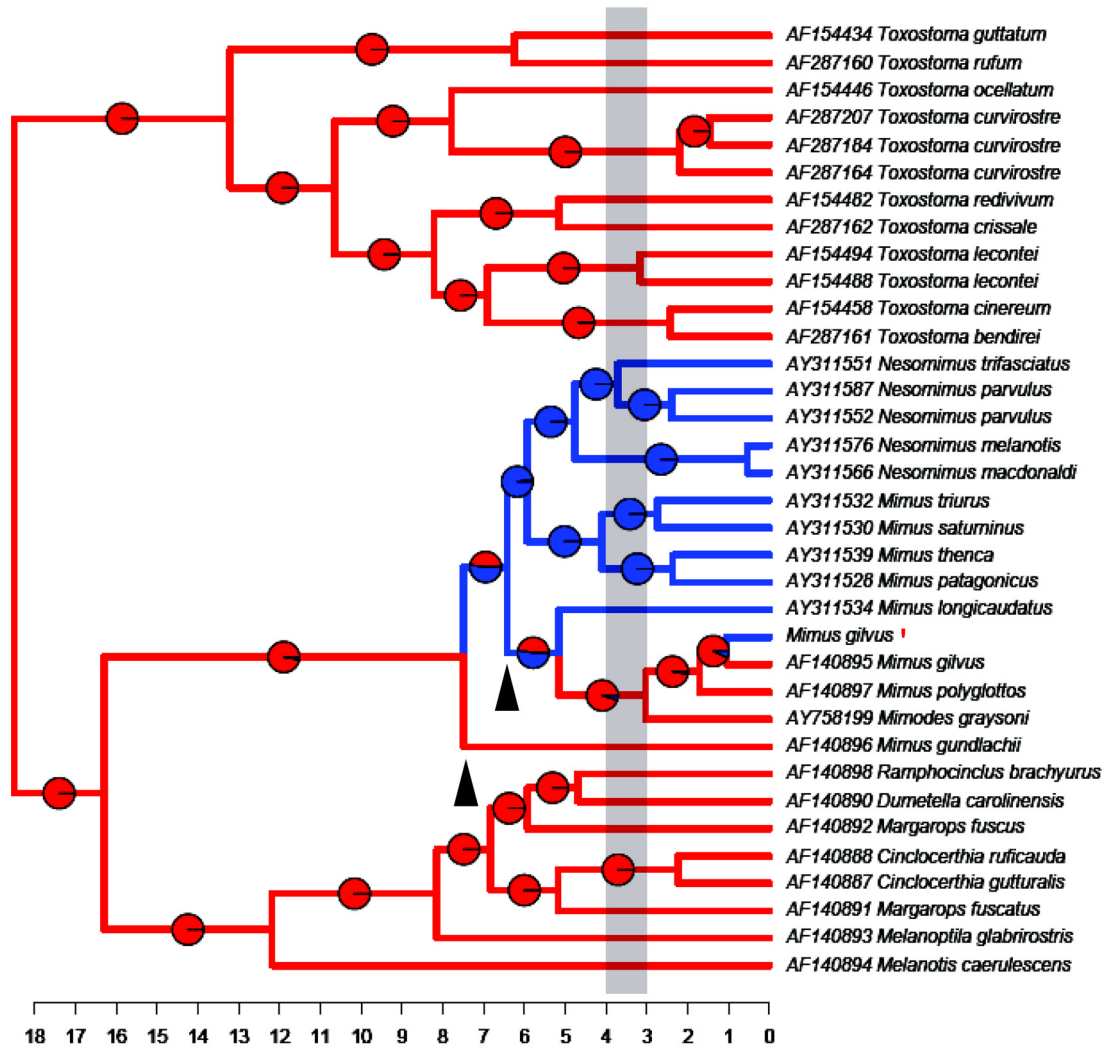


Fig. S3. Continued.

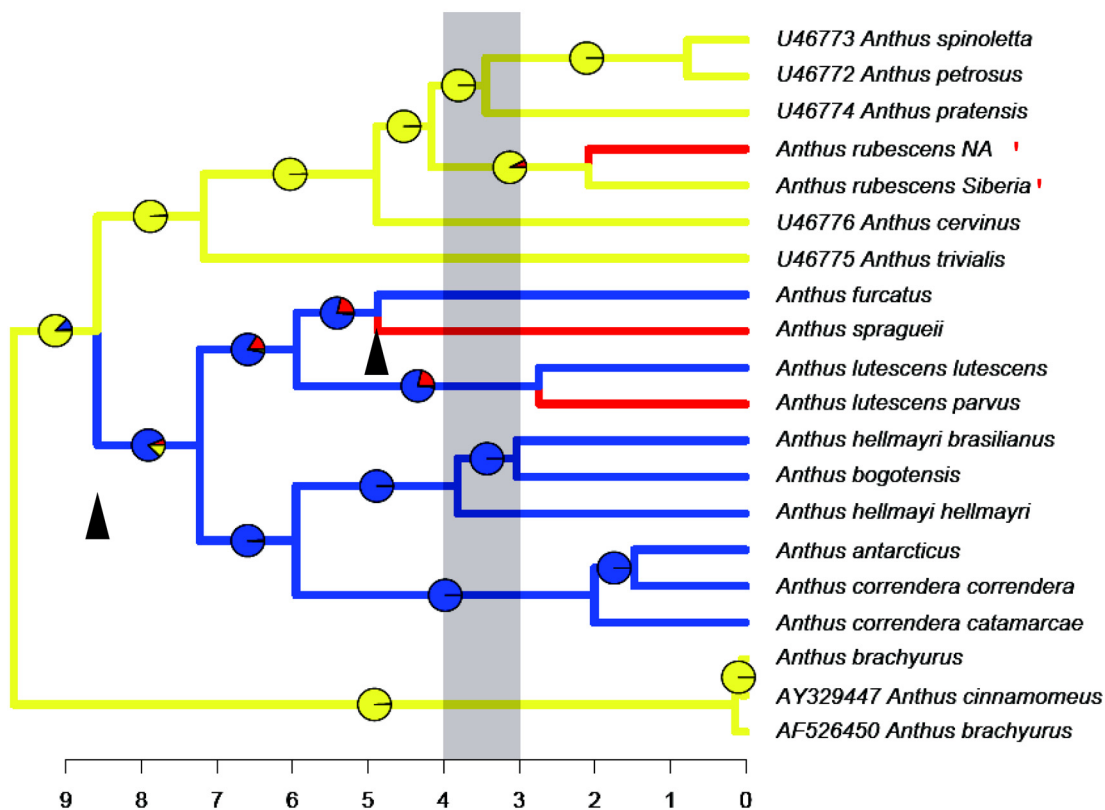
Mimidae maximum likelihood reconstruction



Comments: The date of the first crossing event into South America is uncertain in both maximum likelihood and parsimony reconstructions. The event occurred either at 6.4 Ma or 7.5 Ma. Three North America species are missing which are unlikely to alter reconstructions (*Melanotis hypoleucus*, *Toxostoma longirostris*, *Oreoscoptes montanus*). The dataset for this phylogeny was derived primarily from Lovette and Rubenstein (10).

Fig. S3. Continued [(10) Lovette IJ, Rubenstein DR (2007) A comprehensive molecular phylogeny of the starlings (Aves: Sturnidae) and mockingbirds (Aves: Mimidae): Congruent mtDNA and nuclear trees for a cosmopolitan avian radiation. *Mol Phylogenet Evol* 44:1031–1056].

Motacillidae maximum likelihood and parsimony reconstructions



Comments: The New World clade originated from the Old World at 8.6 Ma. While many Old World species are missing from this tree, a much wider sampling of Old World *Anthus* (11) demonstrated that the Old World clade composed of *Anthus trivialis*, *A. cervinus*, *A. pratensis*, *A. petrosus*, *A. spinoletta* and *A. rubescens* is the sister group to the New World clade. Both reconstruction methods suggest the New World clade originated in South America. It seems probable that South America was colonized from the Old World via North America. If true, then the earliest date of interchange would have occurred at 8.6 Ma. Alternatively, South America may have been colonized directly from the Old World (perhaps via a cross-Atlantic dispersal event). In this latter scenario, the first interchange event between North and South America would occur at 4.8 Ma. North America was colonized twice from South America. Two South American species are missing (*A. chacoensis* believed to be closely related to *A. lutescens* with which it was once considered conspecific and *A. nattereri* whose affinities are uncertain). *Anthus rubescens* was added manually to the tree in the phylogenetic position previously reported by Voelker (11) and represents a more recent invasion from the Old World. All other samples without Genbank accession numbers were provided by Gary Voelker except *A. lutescens parvus* which was collected by the lead author in Panama.

Fig. S3. Continued [(11) Voelker G (1999) Dispersal, vicariance and clocks: Historical biogeography and speciation in a cosmopolitan passerine genus (*Anthus*: Motacillidae). *Evolution* 53:1536–1552].

Troglodytidae dated phylogeny showing all species sampled.

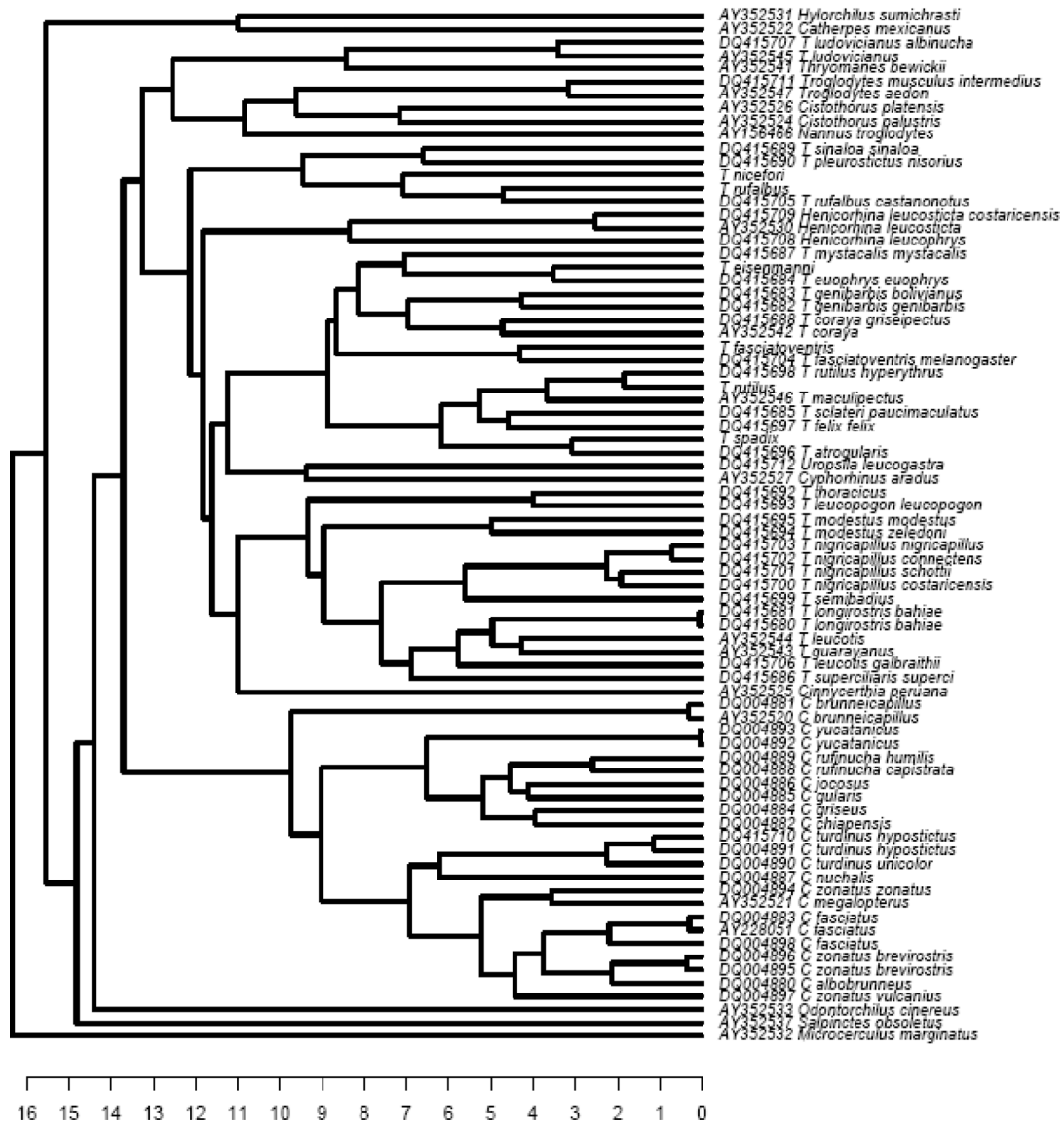


Fig. S3. Continued.

Troglodytidae parsimony reconstruction

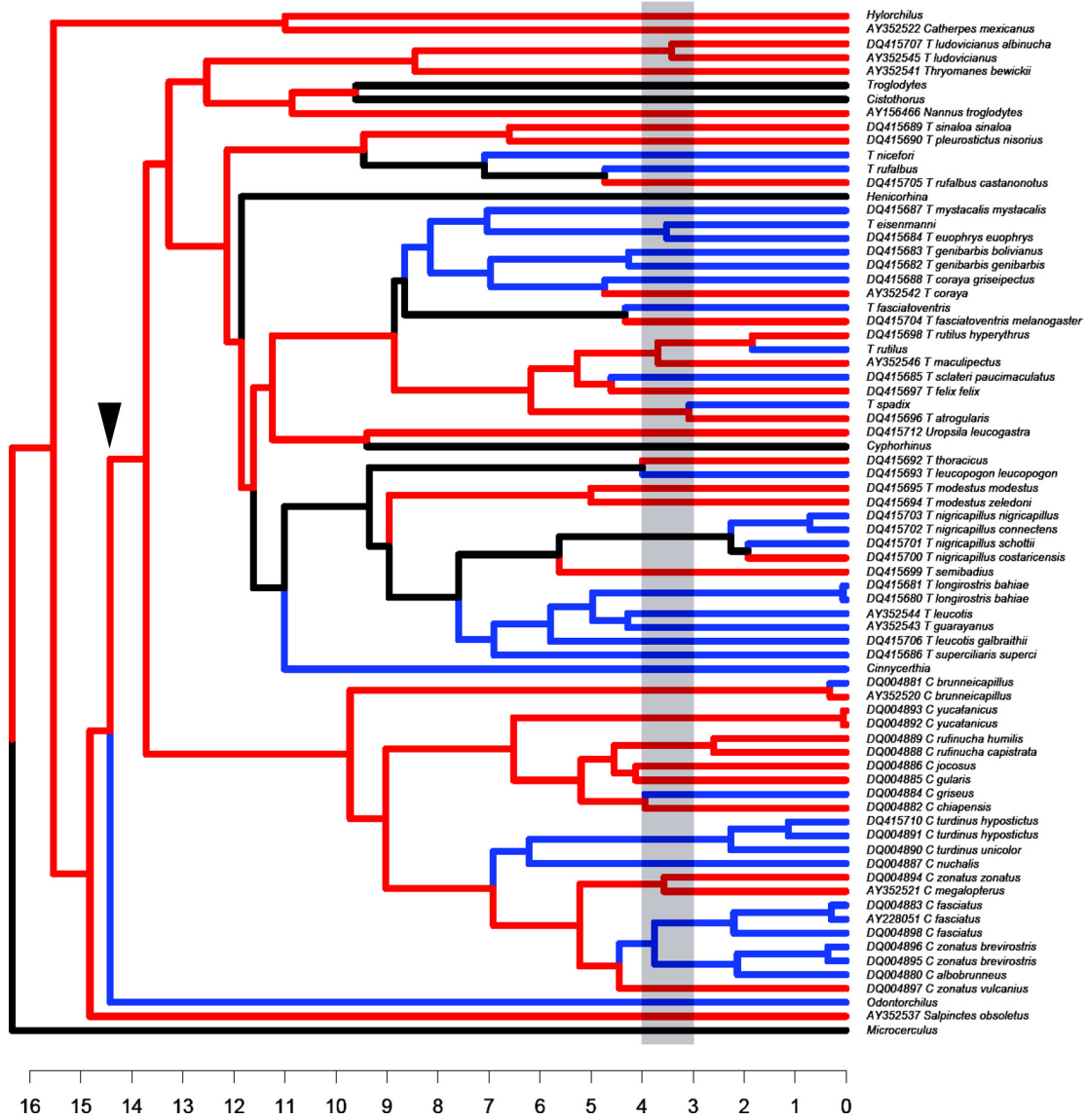


Fig. S3. Continued.

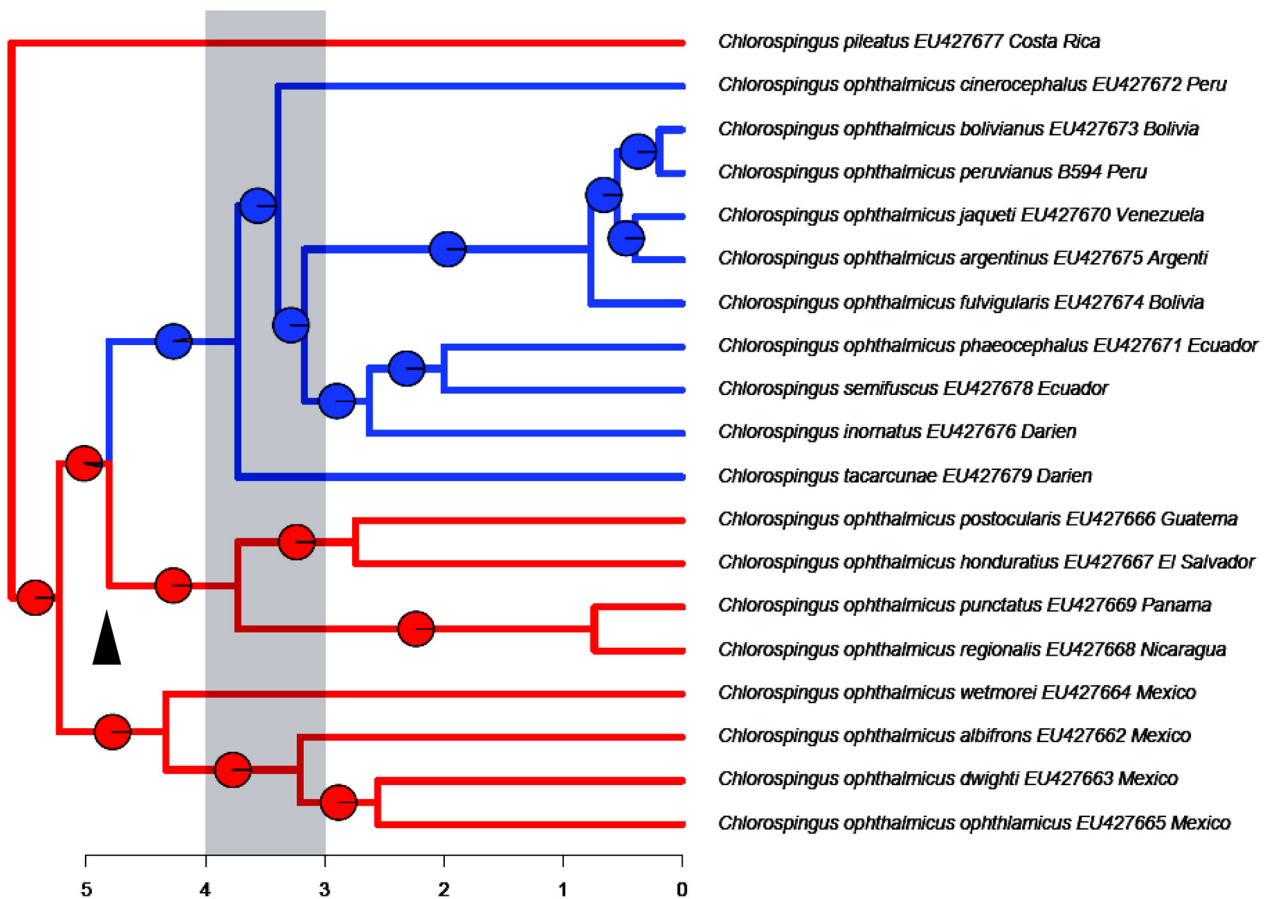
Comments for Troglodytidae: This phylogeny is almost complete at the genus level. Only two genera were not sampled (*Ferminia* and *Thryomanes*), both of which are monotypic and restricted to islands and are thus unlikely to alter interchange reconstructions. Two of the largest genera of wren are completely sampled (*Campylorhynchus*) or are missing only 4 of 27 species (*Thryothorus*; *T. spadix*, *T. eisenmanni*, *T. nicefori*, *T. griseus*). The first three of these missing species of *Thryothorus* are often not recognized as specifically distinct and were manually added to the phylogeny as sister to the species to which they are often considered to be subspecies. *T. griseus* is an enigmatic species from the Amazon that has been suggested to perhaps constitute a separate genus. Because we do not know its phylogenetic position we ignore it in the ancestor state reconstruction. The dense species sampling in *Campylorhynchus* (12) and *Thryothorus* (13) allows detailed reconstructions of interchange events in these genera. The following genera have only partial species representation on the tree: *Odontorchilus*; *Microcerculus*, *Cinnycerthia*, *Cyphorhinus*, *Cistothorus*, *Troglodytes*, *Hylorchilus* and *Henicorhina*. Of these *Microcerculus*, *Cyphorhinus*, *Cistothorus*, *Troglodytes* and *Henicorhina* occur in both continents and for purposes of ancestor state reconstruction we included only a single terminal tip for each of these genera and classified it as occurring in both continents.

We present only the parsimony reconstruction because the maximum likelihood reconstruction method does not allow tips to take on two character states (i.e. NA and SA) as implemented here for sparsely sampled genera occurring in both continents. The parsimony reconstruction nevertheless is sufficient to demonstrate that interchange occurred prior to landbridge completion. The earliest reconstructed interchange event occurred at 14.4 Ma producing the South American endemic genus *Odontorchilus*. Numerous additional colonization events occur in the remainder of the tree and are so frequent that reconstruction of exact dates of when interchange events occurred is problematic. See Barker (12) for a discussion of interchange events within *Campylorhynchus* (1 or more interchange events before and several after landbridge formation).

Campylorhynchus is abbreviated as *C.* and *Thryothorus* as *T.*

Fig. S3. Continued [(12) Barker FK (2007) Avifaunal interchange across the Panamanian Isthmus: Insights from Campylorhynchus wrens. *Biological Journal of the Linnean Society* 90:687–702 and (13) Manna NI, Keith Barker FK, Gravesa JA, Dingess-Mannn KA, Slatera PJB (2006) Molecular data delineate four genera of "Thryothorus" wrens. *Mol Phylogenet Evol* 40:750–759].

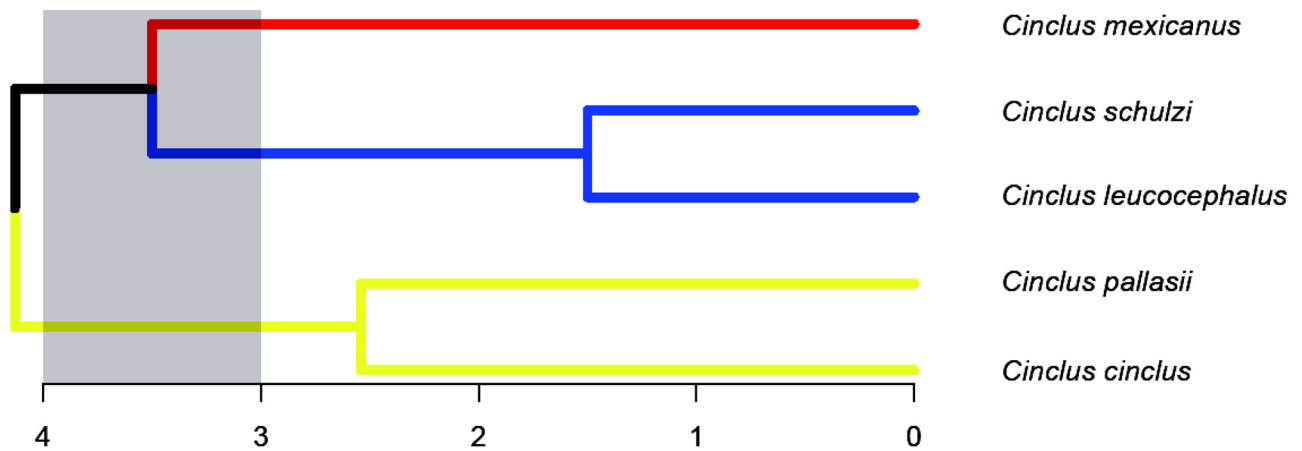
Emberizidae parsimony and maximum likelihood reconstructions



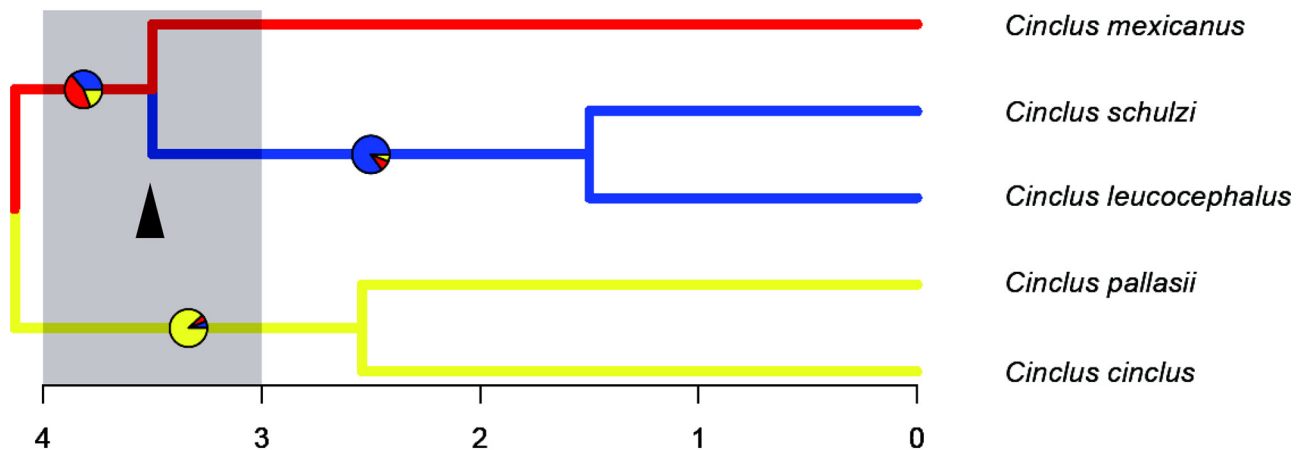
Comments: Emberizid sparrows originated in either North America or Eurasia (e.g. *Emberiza* and relatives) before spreading multiple times into South America. A detailed phylogenetic tree is not available for this family. However, detailed analysis within one Emberizid clade, *Chlorospingus*, demonstrate interchange events predating landbridge completion. Higherlevel phylogenetic studies demonstrate that *Chlorospingus* is nested within the Emberizidae rather than the Thraupidae where it has traditionally been placed (see comments in 14). The clade shown here is of a published phylogeny (14) for only the *Chlorospingus ophthalmicus* complex. *C. pileatus* is sister to the *ophthalmicus* complex and *C. tacarcunae*, *C. inornatus* and *C. semifuscus*, often recognized as separate species, are nested within *C. ophthalmicus*. The earliest date of interchange in this complex occurs prior to landbridge completion at 4.8 Ma when the Andes were colonized from Central America. Detailed analysis of interchange for the entire genus indicate additional interchange events predating 4.8 Ma (Weir unpublished data).

Fig. S3. Continued [(14) Weir JT, Bermingham E, Miller MJ, Kilcka J, González MA (2008) Phylogeography of a morphologically diverse Neotropical montane species, the Common Bush-Tanager (*Chlorospingus ophthalmicus*). *Mol Phylogenet Evol* 47:650–664].

Cinclidae parsimony reconstruction



Cinclidae maximum likelihood reconstruction



Comments: This reconstruction is based on a published phylogenetic tree (15) for which DNA sequences were not deposited in Genbank. We used the published tree topology (Figure 2 in reference 15). Dates at nodes were based on those reported in Voelker (15) using model corrected distances and a 2% clock. The first split within the family occurs only at 4.13 Ma indicating a recent expansion of this genus from the Old World where it is believed to have evolved (15) into the New World. The first colonization event of South America occurred at the time of landbridge completion. Because the family only entered the New World shortly before the landbridge formed, a pre-landbridge dispersal event would not have been likely.

Fig. S3. Continued [(15) Voelker G (2002) Molecular phylogenetics and the historical biogeography of dippers (*Cinclus*). *Ibis* 144:577–584].

Table S1. Comparison of the traditional morphology

Genus	Traditional taxonomy	Hybridization taxonomy	DNA taxonomy	Posterior probability
<i>Calcarius</i>	Emberizidae	Emberizidae	Undescribed family	1.0
<i>Plectrophenax</i>	Emberizidae	Emberizidae	Undescribed family together with <i>Calcarius</i>	1.0
<i>Saltatricula*</i>	Emberizidae	Thraupidae	Cardinalidae	1.0
<i>Habia</i>	Thraupidae	Thraupidae	Cardinalidae	1.0
<i>Chlorothraupis</i>	Thraupidae	Thraupidae	Cardinalidae	1.0
<i>Mitrospingus</i>	Thraupidae	Thraupidae	Cardinalidae	1.0
<i>Granatellus</i>	Parulidae	Parulidae	Cardinalidae	1.0
<i>Piranga</i>	Thraupidae	Thraupidae	Cardinalidae	1.0
<i>Lamprospiza</i>	Thraupidae	Thraupidae	Incertae sedis	-
<i>Paroaria</i>	Cardinalidae	Thraupidae	Thraupidae	1.0
<i>Coereba</i>	Parulidae	Parulidae	Thraupidae	1.0
<i>Tiaris</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Loxigilla</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Euneornis</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Melopyrrha</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Loxipasser</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Melanospiza</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Certhidea</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Geospiza</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Camarhynchus</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Pinaroloxias</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Saltator*</i>	Cardinalidae	Cardinalidae	Thraupidae	1.0
<i>Sporophila</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Oryzoborus</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Volatinia</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Sicalis</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Acanthidops</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Haplospiza</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Catamenia</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Coryphospingus</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Emberizoides</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Nephelornis</i>	Parulidae	?	Thraupidae	1.0
<i>Conirostrum</i>	Parulidae	Parulidae	Thraupidae	1.0
<i>Oreomanes</i>	Thraupidae	Parulidae	Thraupidae	1.0
<i>Tersina</i>	Tersinidae	Thraupidae	Thraupidae	1.0
<i>Poospiza</i>	Emberizidae	Thraupidae	Thraupidae	1.0
<i>Nesospingus</i>	Thraupidae	Thraupidae	Parulidae	0.84
<i>Spindalis</i>	Thraupidae	Thraupidae	Parulidae	0.84
<i>Phaenicophilus</i>	Thraupidae	Thraupidae	Parulidae	0.84
<i>Chlorospingus</i>	Thraupidae	Thraupidae	Emberizidae	1.0

Comparison of the traditional morphology-based (1, 2) and DNA hybridization-based taxonomies (3) of the nine-primaried oscines with the results of the analysis in Fig. S1 (DNA Taxonomy). Posterior probability is the proportion of 35,000 posterior trees in which a genus occurred within the family indicated (e.g. under DNA taxonomy).

**Saltator* and *Saltatricula*: this analysis suggests *Saltator* is a polytypic genus with *S. atricollis* and *Saltatricula* forming a clade in the Cardinalidae, and other species of *Saltator* forming a clade in the Thraupidae. This placement is contradicted by a recent analysis (4) that used a larger dataset (both cytochrome b and NADH dehydrogenase subunit 2 sequences) but less complete coverage of nine-primaried oscine genera to define monophyletic groups within the nine-primaried oscines. The Klicka et al (4) 2007 analysis placed all species of *Saltator* and *Saltatricula* within Thraupidae but otherwise agreed with our definition of the boundaries of the Thraupidae. We tentatively follow their placement of all *Saltator* and *Saltatricula* within the Thraupidae in the analysis of GABI.

1. Howard R, Moore A (1991) *A Complete Checklist of the Birds of the World*. 2nd Ed. (Academic Press, New York).
2. Peters JL (1970). *Check-List of Birds of the World*, Vol. 13. (Museum of Comparative Biology, Cambridge, Massachusetts).
3. Sibley CG, Monroe BL (1990). *Distribution and Taxonomy of the Birds of the World*. (Yale University Press, New Haven, Connecticut).
4. Klicka JK, Burns K, Spellman GM (2007) Defining a monophyletic Cardinalini: A molecular perspective. *Mol Phylogenet Evol.* 45:1014–1032.

Table S2. Maximum-likelihood support for models with branch lengths raised to the power of K and incorporating a two-rate model with best supported breakpoint (as shown in Fig. 1A)

Family	Log-likelihood when $K = 0$	Log-likelihood when $K = 1$	Best support value of K	q_a/q_b when $K = 0$	q_a/q_b when $K = 1$
Woodcreeper	-43.551	-47.28	0	35	100
Antbird	-57.709	-64.688	0	35.3	100
Blackbird	-68.672	-75.64	0	2.54	100
Tanager	-134.780	-159.072	0	99.86	75

Eleven values of K were estimated between 0 and 1 in 0.1 intervals. In all cases, $K = 0$ obtained the maximum likelihood value. Likelihoods and ratios of the rate parameter after (q_a) and before (q_b) the best fit breakpoint are shown for K values of 0 and 1. Reported values of q_a were constrained to values less than 100 times q_b . For woodcreepers, antbirds, and blackbirds, allowing q_a to exceed 100-times q_b had little further effect on log-likelihood values. Values are based on a consensus tree and as such vary slightly from values in Table 1, which are based on 100 random posterior trees.

Table S3. Estimates of extinction rates (per lineage per million years) in lineages which dispersed between continents versus those that remained in continent of origin

Family	Extinction model	Extinction SA (speciation SA/transition rates SA to NA)	Extinction NA (speciation NA/transition rates NA to SA)	Extinction both continents combined	Log-likelihood	LR (<i>P</i>)
Woodcreeper	One-rate			5.63×10^{-6}	-250.76	0.36 (<i>P</i> < 0.55)
Woodcreeper	Two-rate	1.70×10^{-5} (0.143 / 1.164)	5.85×10^{-5} (0.534 / 4.292)		-250.94	
Blackbird	One-rate			1.88×10^{-6}	-340.55	0 (<i>P</i> = 0)
Blackbird	Two-rate	8.51×10^{-6} (0.083/0.387)	9.639×10^{-5} (0.379/0.454)		-340.55	

A one-rate extinction model in which extinction rates are equal in both continents is compared to a two-rate extinction model in which extinction rates are estimated separately for North America and South America. In both the one-rate and two-rate models, per lineage speciation rates and transition rates between continents are estimated separately for each continent. Speciation rates and transition rates were almost identical in the one-rate and two-rate extinction models, and values are reported here only for the two-rate model.

Other Supporting Information Files

[Dataset S1 \(XLSX\)](#)