Article

Certhiasomus, a new genus of woodcreeper (Aves: Passeriformes: Dendrocolaptidae)

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Abstract

Phylogenetic analysis of the family Dendrocolaptidae (Aves: Passeriformes) indicates that the two species traditionally placed in the genus *Deconychura* are not sister taxa. *Certhiasomus*, a new genus of woodcreeper, is described for one of these species, *C. stictolaemus*.

Key words: *Deconychura longicauda*, *Deconychura stictolaema*, *Certhiasomus stictolaemus*, morphometric heterogeneity, phylogeny, ranking criteria

The genus *Deconychura* (Aves: Passeriformes: Dendrocolaptidae) contains two species: *D. longicauda* (Pelzeln 1868) (Long-tailed Woodcreeper), the type species (Cherrie 1891); and *D. stictolaema* (Pelzeln 1868) (Spot-throated Woodcreeper). *Deconychura longicauda* is a polytypic species (seven subspecies are currently recognized) that occurs in humid upland and floodplain forest throughout Amazonia and disjunctly in trans-Andean lowland forest from northern Colombia north to Honduras (Marantz *et al.* 2003). *Deconychura stictolaema*, three subspecies of which are currently recognized, also occurs in Amazonia but has a more limited distribution than *D. longicauda* and does not occur west of the Andes or in Central America.

Interestingly, these two species were described in different genera by the same author: Pelzeln (1868) assigned *D. longicauda* to *Dendrocincla* and *D. stictolaema* to *Sittasomus*. Pelzeln (1868) did not provide justification for placing *D. stictolaema* in *Sittasomus*, which was probably based on overall body size and proportions, but he did mention the similarity between *D. longicauda* and *Dendrocincla tyrannina*. Hellmayr (1904, 1907) noting the extreme plumage and structural similarities between *D. stictolaema* and *D. longicauda*, united them under the genus *Deconychura*, a treatment followed unanimously since then. Only Raikow's (1994) morphological phylogeny of the Dendrocolaptidae indicated that *Deconychura* might not be monophyletic. Raikow (1994) found no synapomorphies for the genus among the 36 morphological characters analyzed, and his results placed *D. longicauda* in a clade that did not include *D. stictolaema*.

As part of a project to reconstruct the species level phylogenetic relationships of the Furnariidae and Dendrocolaptidae from DNA sequences, we determined conclusively that *D. longicauda* and *D. stictolaema* are not sister taxa. Instead, *D. stictolaema* is sister to a clade composed of *D. longicauda*, *Sittasomus griseicapillus* (Vieillot 1818) (Olivaceous Woodcreeper), and the genus *Dendrocincla* (six species). We considered two taxonomic options for addressing the polyphyly of *Deconychura*: (1) merging *Dendrocincla, Sittasomus* and *Deconychura* into a single expanded genus, or (2) erecting a new genus for *D. stictolaema*. Because combining *Dendrocincla, Sittasomus*, and *Deconychura* into a single genus would result in a clade far more heterogeneous than any other genus in the Dendrocolaptidae (see below), we describe a new genus for *D. stictolaema*, as follows:

Certhiasomus, **new genus**

Type species. *Sittasomus stictolaemus* Pelzeln 1868.
Included taxa. *Certhiasomus s. stictolaemus* (Pelzeln 1868), *Certhiasomus stictolaemus secundus* (Hellmayr 1904), *Certhiasomus stictolaemus clarior* (Zimmer 1929).

Diagnosis. Small woodcreeper (13–22 g, Marantz *et al*. 2003) with relatively long tail and slender bill. *Certhiasomus* differs from *Dendrocincla* and all "strong billed woodcreeper genera (*Drymotoxeres*, *Drymornis*, *Nasica*, *Dendrexetastes*, *Hylexetastes*, *Xiphocolaptes*, *Dendrocolaptes*, *Xiphorhynchus*, *Lepidocolaptes* and *Campylorhamphus*; Feduccia 1973) by a combination of small size, operculated nostrils, and rectrices with long, strongly decurved protruding rachises covered with short stiff barbs. Distinguished from *Glyphorynchus* by its longer non-wedge-shaped bill, and from *Sittasomus* by its light throat markings and more pronounced tail graduation. Distinguished from *Deconychura* by its smaller size, absence of an apical bill hook, nearly unstreaked crown, and extensive rufous coloration on rump (restricted to upper tail coverts in *Deconychura*). Myologically, it is distinguished from *Deconychura* by the *iliotibialis lateralis pars postacetabularis* muscle, the caudal margin of which arises even with the caudal edge of the *iliofibularis* muscle in *Certhiasomus,* and cranial to it in *Deconychura* (Raikow 1994).

Etymology. From the Greek *certhia* (treecreeper) and *soma* (body), referring to the morphological similarities between this small woodcreeper and the treecreepers Certhiidae. The construction of the name parallels that of the closely related *Sittasomus*, the genus in which *C. stictolaemus* was originally described. The name is masculine in gender.

Molecular analyses. Our preliminary molecular analysis of all dendrocolaptid species found that *Certhiasomus* is sister to a clade composed of *Dendrocincla, Deconychura*, and *Sittasomus*. To demonstrate that *Deconychura* and *Certhiasomus* are not sister genera, we present an analysis of a subset of taxa from this larger study. We included in the analysis individuals of *Certhiasomus stictolaemus*, *Deconychura longicauda*, *Dendrocincla turdina* (Lichtenstein) (Plain-winged Woodcreeper)*, Sittasomus griseicapillus*, *Drymornis bridgesii* (Eyton) (Scimitar-billed Woodcreeper), *Glyphorynchus spirurus* (Vieillot) (Wedge-billed Woodcreeper), *Dendroplex picus* (Gmelin) (Straight-billed Woodcreeper), and *Lepidocolaptes lacrymiger* (Des Murs) (Montane Woodcreeper) (Table 1). We included six individuals of *C. stictolaemus*, two for each of the three described subspecies: *C. s. stictolaemus*, *C. s. secundus*, and *C. s. clarior*. We sequenced multiple individuals of *D. longicauda,* including one individual of the *typica* group from Central America. Marantz *et al*. (2003) suggested that this group might be more closely related to *C. stictolaemus* than to the Amazonian forms of *D. longicauda*. To root the tree we used as outgroups *Pygarrhichas albogularis* (King) (White-throated Treerunner, Furnariidae), *Myrmothera simplex* (Salvin & Godman) (Brown-breasted Antpitta, Grallariidae) and *Formicarius colma* Boddaert (Rufous-capped Antthrush, Formicariidae).

Total DNA was extracted from 25 mg of pectoral muscle using the Qiagen DNeasy kit, following the manufacturer's protocol. Following methods described in Chesser *et al.* (2007), we amplified and sequenced the mitochondrial genes ND3 and CO2 and the autosomal nuclear intron BF7. To amplify CO2, we used two primers newly designed for furnariids, NF3 (Sanín *et al*. 2009) and SCTRCOII (Claramunt *et al*. in press). Following the same methods, we amplified and sequenced an additional mitochondrial gene (ND2) for at least one individual per species using the primers H6313 (Johnson & Sorenson 1998) and L5215 (Hackett 1996). For at least one individual per genus, two additional nuclear protein-coding genes (RAG1 and RAG2) were used; all sequences of these genes were taken from Moyle *et al.* (2009). Following alignment and the exclusion of unique inserts from the BF7 sequences, the six-gene concatenated dataset consisted of 6,990 base pairs.

In model-based phylogenetic inference, there is a trade-off between capturing the complexity of the nucleotide substitution process and the risk of over-parameterizing the models (Posada & Buckley 2004; Sullivan & Joyce 2005; McGuire *et al*. 2007). To determine the optimal number of partitions, we tested six different partitioning regimes, ranging from unpartitioned to a maximum of sixteen different partitions (a different model for each codon position of each coding gene and the nuclear intron). Partitioned datasets were examined by performing maximum likelihood (ML) analyses using RAxML 7.0.4 on the Cipres Portal V 1.5

(www.phylo.org/sub_sections/portal/). RAxML implements the GTR+Γ model of nucleotide substitution (with or without invariants). Using the resultant likelihoods we calculated values of the Akaike Information Criterion (AIC, Sullivan & Joyce 2005) for each partitioning regime. We also investigated whether the addition of a proportion of invariant sites improved the model. We identified the GTR+ Γ+I model and a fully partitioned dataset (16 partitions) as the best model and partitioning regime. We then used RAxML to evaluate nodal support in the resulting maximum-likelihood tree by performing 1000 bootstrap replicates (Stamatakis *et al.* 2008). The analysis resulted in a single maximum-likelihood tree (log L = 20923.4) with high bootstrap support for most relationships (Fig. 1).

TABLE 1. Tissue samples used in the genetic analysis.

Taxon	Museum	Sample ID	Locality
Deconychura longicauda typica	LSUMNS	B26585	PANAMA: prov. Colón; Río Agua Salud.
D. longicauda darienensis	LSUMNS	B2084	PANAMA: prov. Darién; Cana.
D. longicauda pallida 1	LSUMNS	B905	BOLIVIA: depto. Pando; Río Beni, 600 m.
D. longicauda pallida 2	LSUMNS	B4753	PERU: depto. Loreto; S Río Amazonas, 100 m.
D. longicauda (subsp. uncertain)	LSUMNS	B27966	PERU: depto. Loreto; Contamana, 1450 m.
Certhiasomus stictolaemus stictolaemus 1	MPEG	57571	BRAZIL: Amazonas; Manicor, Rodovia do Estanho, km 126.
C. stictolaemus stictolaemus 2	MPEG	58684	BRAZIL: Amazonas; Município de Humait, T. Indígena Parintintin, Aldeia Traira-Choror.
C. stictolaemus secundus 1	LSUMNS	B27420	PERU: depto. Loreto; Contamana, 200 m.
C. stictolaemus secundus 2	LSUMNS	B2532	PERU: depto. Loreto; N Río Napo, 350 m.
C. stictolaemus clarior 1	MPEG	65378	BRAZIL: Pará; Alenquer, ESEC Grão-Par.
C. stictolaemus clarior 2	MPEG	A07970	BRAZIL: Pará; Município de Almerim, Monte Dourado, Reserva de Pacanari.
Sittasomus griseicapillus	AMNH	DOT 8415	MEXICO: Hidalgo; Molango.
Dendrocincla turdina	LSUMNS	B250	PARAGUAY: depto. Caazap; Cor. de Caaguaz, 7.5 km E. San Carlos, 250m.
Glyphorynchus spirurus	AMNH	DOT 4274	VENEZUELA: Amazonas; Sierra de Tapirapeco, Cerro Tamacuari, 1270m.
Drymornis bridgesii	LSUMNS	B25799	PARAGUAY: depto. Alto Paraguay; Madrejón, 200m.
Dendroplex picus	FMNH	334433	BOLIVIA: depto. El Beni; Laguna Suarez, 5km SW Trinidad, 230m.
Lepidocoplates lacrymiger	AMNH	DOT 7051	BOLIVIA: depto. La Paz; Parque Nacional Apolobamba, 2600m.
Pygarrhichas albogularis	AMNH	DOT 9930	ARGENTINA: depto. Bariloche; Río Negro.
Formicarius colma	AMNH	DOT 12722	VENEZUELA: Amazonas; Cerro de la Neblina Base Camp, Río Baria.
Myrmothera simplex	AMNH	DOT 4270	VENEZUELA: Amazonas; Sierra de Tapirapeco, Cerro Tamacuari, 1270m.

Tissue collections: LSUMNS—Louisiana State University Museum of Natural Science, Baton Rouge; AMNH—American Museum of Natural History, New York City; FMNH—Field Museum of Natural History, Chicago; MPEG—Museu Paraense Emílio Goeldi, Belém, Brazil

As a second method of phylogenetic inference, we performed a Bayesian analysis as implemented in MRBAYES Ver. 3.0 β3 (Huelsenbeck & Ronquist 2001; Altekar et al. 2004) on the Cornell cluster (http://cbsuapps.tc.cornell.edu/mrbayes.aspx). We used the same partitioning strategy as in the likelihood analysis, but again used model selection to determine the best substitution model for each partition. For each partition, using the tree obtained in the maximum-likelihood analysis, we used PAUP (Swofford 2003) to obtain likelihood values for all substitution models featured in Modeltest 3.7 (Posada & Crandall 1998) and then calculated values of the Bayesian Information Criterion (BIC, Posada and Buckley 2004; Sullivan & Joyce 2005) for each. BIC identified the GTR+Γ+I model as the best model for the majority of the partitions, and the HKY+Γ+I model as the best model for the first and second codon positions of RAG 1 and all three codon positions of RAG 2. The Bayesian posterior probability density was estimated by Metropolis-coupled Markov chain Monte Carlo, with four incrementally heated chains run for 25 million generations (sampled every 2500). All chains reached stationarity, and all parameters had good ESS values (>200). The analysis resulted in a topology almost identical to the best maximum-likelihood tree with high posterior support for most relationships (Fig. 2).
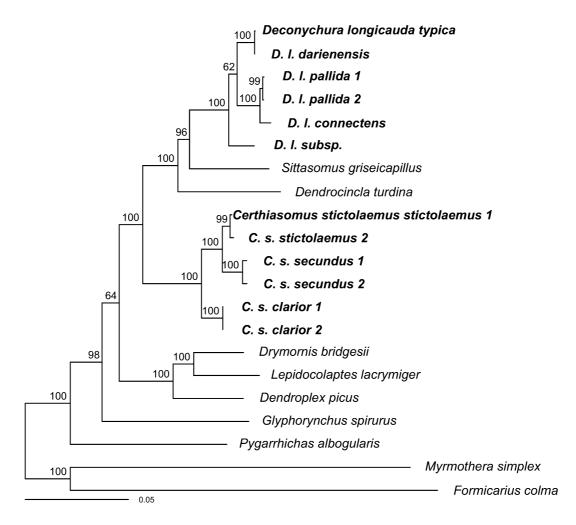

FIGURE 1. A maximum-likelihood phylogeny of the Dendrocolaptidae that highlights the lack of a sister relationship between *Certhiasomus* and *Deconychura*. Numbers above the branches indicate bootstrap support based on 1000 maximum-likelihood replicates.

In both analyses, all individuals of *D. longicauda*, including *D. l. typica*, formed a strongly supported clade (bootstrap support = 100%, posterior probability = 1.0) that was sister to *Sittasomus* and *Dendrocincla*. The (*D. longicauda, Sittasomus, Dendrocincla*) clade was sister to *Certhiasomus* with 100% bootstrap support and a posterior probability of 1.0. These results clearly demonstrate that *Certhiasomus* and *Deconychura* do not form a clade.

Phenotypic analyses. Although phenotypic differences among *Sittasomus*, *Deconychura* and *Certhiasomus* could be considered slight and not of generic significance (see diagnosis), the genus *Dendrocincla* can be distinguished by several unique characters, including the structure of their rectrices, myological synapomorphies (Raikow 1994), and foraging behavior atypical of dendrocolaptids (Skutch 1969; Willis 1972; Marantz *et al*. 2003). Therefore, uniting all these genera in a single genus (the alternative to describing a new genus) would result in a taxon that is excessively heterogeneous relative to taxa of similar rank in the Dendrocolaptidae. Traditionally, problems like this have been treated subjectively in taxonomic work. Here, we have approached the problem of taxon heterogeneity using a quantitative approach by means of a morphometric analysis of total variance (Claramunt *et al*. in press).
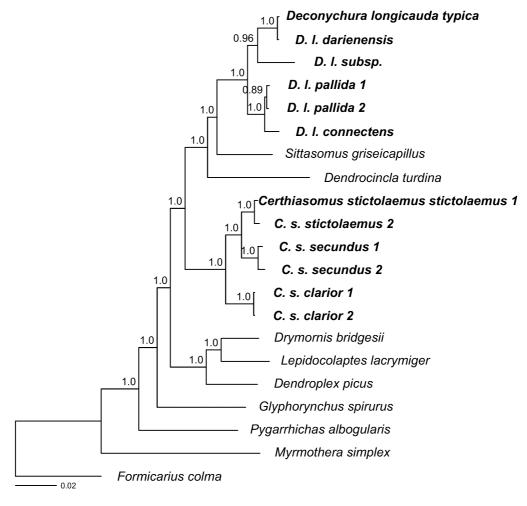

FIGURE 2. Majority-rule Bayesian consensus tree of the Dendrocolaptidae that highlights the lack of a sister relationship between *Certhiasomus* and *Deconychura*. Numbers above the branches indicate posterior probability values.

The following measurements were taken for at least three museum specimens of each of the 50 currently recognized species of Dendrocolaptidae: wing length to the longest primary, wing length to the tenth (most distal) primary, wing length to the first secondary feather, tail maximum (to the longest rectrix) and minimum (to the shortest rectrix) length, width of the innermost rectrix, bill length from naris, bill width and depth at the anterior edge of naris, tarsus length, and hallux length with claw (for further details, see Claramunt *et al*. in press). Variables were log-transformed (Gingerich 2000). To separate the effect of body size from size-free shape variation, we used Mosimann's approach (Mosimann 1970; Mosimann & James 1979). We estimated the isometric size of each species as the mean of the log-transformed variables. We then calculated size-free variables by subtracting the log(size) of the species from each variable.

Morphometric heterogeneity was quantified as the total variance (Van Valen 1974). We computed the total variance for all non-monotypic dendrocolaptid genera plus a hypothetical genus encompassing species of

Dendrocincla, *Sittasomus*, *Deconychura*, and *Certhiasomus*. We also estimated the separate contribution of size and shape to the total variance (Darroch & Mosimann 1985). Comparison of size and shape heterogeneity indicated that the morphometric variance of the hypothetical, more inclusive genus is more than twice that of the next most heterogeneous dendrocolaptid genus (Table 2). These data support our decision to create a new genus (*Certhiasomus*) rather than create an extremely heterogeneous genus by combining *Dendrocincla*, *Sittasomus* and *Deconychura* into one.

TABLE. 2. Results of the morphometric heterogeneity analysis.

Taxon	Total Variance	Size variance	Shape Variance
Dendrocincla + Deconychura[1] + *Sittasomus*	0.379	0.302	0.077
Dendrocincla	0.170	0.138	0.033
Xiphorhynchus	0.169	0.140	0.030
Campylorhamphus[2]	0.064	0.028	0.036
Lepidocolaptes	0.061	0.034	0.027
Xiphocolaptes	0.045	0.026	0.020
Dendrocolaptes	0.030	0.010	0.020
Hylexetastes	0.021	0.005	0.016
Dendroplex	0.021	0.012	0.009

[1]including both *D. longicauda* and *D. stictolaema*.
[2]excluding *C. pucherani* (Claramunt *et al.* in press).

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