



***Geocerthia*, a new genus of terrestrial ovenbird (Aves: Passeriformes: Furnariidae)**

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The avian genus *Upucerthia* was until recently considered to consist of nine species (Sibley and Monroe 1990, Dickinson 2003, Remsen 2003) of mainly terrestrial ovenbirds, commonly known as earthcreepers. Recent molecular studies of the genus (Chesser *et al.* 2007, Fjeldså *et al.* 2007) indicated that *Upucerthia*, as traditionally constituted, was highly polyphyletic, its nine species apparently belonging to four distinct lineages. Four species of *Upucerthia* – *albigula*, *jelskii*, *validirostris*, and the name-bearing species *dumetaria* – formed a well-supported clade sister to *Cinclodes* (Chesser *et al.* 2007, Fjeldså *et al.* 2007). Of the five other species of *Upucerthia*, *U. andaecola* and *U. ruficaudus* formed a clade with *Eremobius phoenicurus* and *Chilia melanura*, all of which were subsequently transferred to the genus *Ochetorhynchus* (Chesser *et al.* 2007, Fjeldså *et al.* 2007). *Upucerthia harterti* and *U. certhioides* formed a distinct clade and were placed in the newly erected genus *Tarphonomus* (Chesser and Brumfield 2007). The position of the final species, *U. serrana*, was not well resolved, although it appeared to form part of a clade including the genera *Cinclodes* and *Upucerthia sensu stricto* (Chesser *et al.* 2007, Fjeldså *et al.* 2007).

As part of a project to reconstruct the species level phylogenetic relationships of the Furnariidae from DNA sequences, we gathered additional molecular data for species in these and related genera, and determined conclusively that *U. serrana* is sister to a clade consisting of sister genera *Cinclodes* and *Upucerthia* (Fig. 1). Because *Cinclodes* and *Upucerthia* are cohesive and distinctive genera containing multiple species (*Cinclodes* consists of thirteen species, *Upucerthia* of four), we consider lumping of these well-established genera untenable. Consequently, we describe a new genus for *U. serrana* as follows:

***Geocerthia* Chesser and Claramunt, genus nov.**

Type species. *Upucerthia serrana* Taczanowski, 1875.

Included species. *Geocerthia serrana* (Taczanowski, 1875) *comb. nov.*, Striated Earthcreeper.

Diagnosis, morphology. Large earthcreeper (19–20 cm, 44–52 g, Remsen 2003). Bill longish, decurved; face grizzled brown and whitish; whitish superciliary; crown medium-dark brown with pale streaking, especially on forehead; back medium brown with faint pale streaking; wings, tail, and uppertail coverts rufous; throat whitish; underparts dull gray-brown with prominent pale streaking. *Geocerthia* differs from true *Upucerthia* earthcreepers, which have long, thin, highly decurved bills, by its comparatively shorter and stouter decurved bill and its overall darker plumage. Distinguished from all *Cinclodes* and *Upucerthia* species by its rufous wings, uppertail coverts, and tail. Lacks the wing-band typical of *Cinclodes* species.

Etymology. From the Greek *geo* (earth) and *certhia* (treecreeper), referring to the terrestrial habits of *G. serrana* and to its bill, which resembles those of the treecreepers. The construction of the name is a direct parallel to the English name earthcreeper. The name is feminine.

Molecular analyses. A molecular analysis of furnariid species revealed that *Geocerthia* is sister to a clade composed of all species of *Cinclodes* and all species of *Upucerthia sensu stricto*, which in turn are sister taxa. To demonstrate that *Geocerthia* and *Upucerthia* are not sister genera, we present an analysis of a subset of taxa from the larger study. Taxon sampling for this subset (Table 1) included representatives of *U. serrana*, all other species of the traditional genus *Upucerthia* (*Upucerthia*, *Tarphonomus*, *Ochetorhynchus*), two species of *Cinclodes*, and single species of the genera *Furnarius*, *Leptasthenura*, *Synallaxis*, *Certhiaxis*, *Pseudocolaptes*, *Philydor*, *Thripadectes*, *Automolus*, and

Lochmias. We used as outgroups the dendrocolaptines *Dendrocincla fuliginosa*, *Drymornis bridgesii*, and *Xiphorhynchus fuscus*, as well as the basal furnariid *Geositta isabellina*. As a simple test of its monophyly and phylogenetic relationships, a second individual of *Geocerthia serrana* (ZMUC [Zoological Museum, University of Copenhagen] S444; GenBank Accession #: EF635339, EF635358, EF635319) was sequenced. This individual differed from the first by only one nucleotide substitution and grouped with it in all analyses in which it was included (results not shown).

Table 1. Tissues used in the phylogenetic analysis.

Taxon	Museum	Tissue ID	Locality
<i>Geositta isabellina</i>	AMNH	12181	CHILE: Region Metropolitana, 15 km ENE Embalse El Yeso, ca. 3400m
<i>Upucerthia dumetaria</i>	AMNH	10396	ARGENTINA: Prov. Neuquén, Sierra Auca Mahuida
<i>U. albigula</i>	LSUMNS	B61491	PERU: Depto. Arequipa, 14 km E Pancarpata, 3222m
<i>U. jelskii</i>	LSUMNS	B103886	PERU: Depto. Tacna, Tacna-Ilave Road, ca 25 km NE Tarata, 4050m
<i>U. validirostris</i>	LSUMNS	B17160	ARGENTINA: Prov. Tucumán, 12 km N, 4 km W Tafi de Valle, 3060 m
<i>U. serrana</i>	LSUMNS	B49662	PERU: Depto. Lima, Santa Eulalia road, ca 86 km NE Lima
<i>Tarphonomus certhioides</i>	LSUMNS	B18872	BOLIVIA: Depto. Santa Cruz, Estancia Perforación, ca 130 km E Charagua, 520 m
<i>T. harterti</i>	LSUMNS	B34573	BOLIVIA: Depto. Santa Cruz, Tambo, 14 km SE Camarapa
<i>Ochetorhynchus andaecola</i>	LSUMNS	B1199	BOLIVIA: Depto. La Paz, 2.5 km by road S Mecapaca, ca 26 km by road S Calacoto, 3050m
<i>O. ruficaudus</i>	LSUMNS	B103908	PERU: Depto. Arequipa, km 60 on Div. Arequipa-Juliacca road, ca 10 road km W Chaguata
<i>O. phoenicurus</i>	AMNH	9943	ARGENTINA: Prov. Río Negro, 20 km E Ñorquinco, 1000 m
<i>O. melanura</i>	AMNH	12148	CHILE: Region Metropolitana, ca 4 km SSW by road from peak of Cerro de El Roble, ca 1600 m
<i>Cinclodes fuscus</i>	AMNH	12169	CHILE: Region Metropolitana, 2 km ENE Embalse El Yeso, ca. 2500 m

Taxon	Museum	Tissue ID	Locality
<i>C. nigrofumosus</i>	AMNH	12164	CHILE: Region Valparaíso, Roca Brava, ca. 2 km N Zapallar
<i>Furnarius figulus</i>	FMNH	392828	BRAZIL: Estado Alagoas, Piranhas, Fazenda Bela Vista
<i>F. rufus</i>	AMNH	10431	ARGENTINA: Prov. Neuquén, Centenario
<i>Leptasthenura aegithaloides</i>	AMNH	10306	ARGENTINA: Prov. Neuquén, Sierra Auca Mahuida
<i>Synallaxis albescens</i>	AMNH	2295	BOLIVIA: Depto. Santa Cruz, 300 m N of Rio Mercedes, 600 m
<i>Certhiaxis cinnamomeus</i>	AMNH	6190	BOLIVIA: Depto. Santa Cruz, 300 m N of Rio Mercedes, 600 m
<i>Pseudocolaptes lawrencii</i>	AMNH	3694	COSTA RICA: Prov. Heredia, 3 km N Porrosati, 2200 m
<i>Philydor pyrrhodes</i>	AMNH	8864	VENEZUELA: Estado Amazonas, Mrakapiwie
<i>Thripadectes rufobrunneus</i>	AMNH	3651	COSTA RICA: Prov. San Jose, Cerro de la Muerte, 3350 m
<i>Automolus rufipileatus</i>	LSUMNS	B1074	BOLIVIA: Depto. La Paz, Río Beni, ca 20 km by river N Puerto Linares, 600 m
<i>Lochmias nematura</i>	AMNH	12074	ARGENTINA: Prov. Misiones, Parque Provincial Urugua-i, ca.1 km W park headquarters, Ruta Provincial 19, ca 400 m
<i>Dendrocincla fuliginosa</i>	AMNH	12706	VENEZUELA: Estado Amazonas; Río Baria, Cerro de la Neblina Base Camp
<i>Drymornis bridgesii</i>	LSUMNS	B25799	PARAGUAY: Depto. Alto Paraguay, Madrejón
<i>Xiphorhynchus fuscus</i>	LSUMNS	B35576	BRAZIL: Estado Bahia, ca 16 km W Porto Seguro RPPN Vera Cruz

Tissue collections: LSUMNS – Louisiana State University Museum of Natural Science, Baton Rouge; AMNH – American Museum of Natural History, New York; FMNH – Field Museum of Natural History, Chicago.

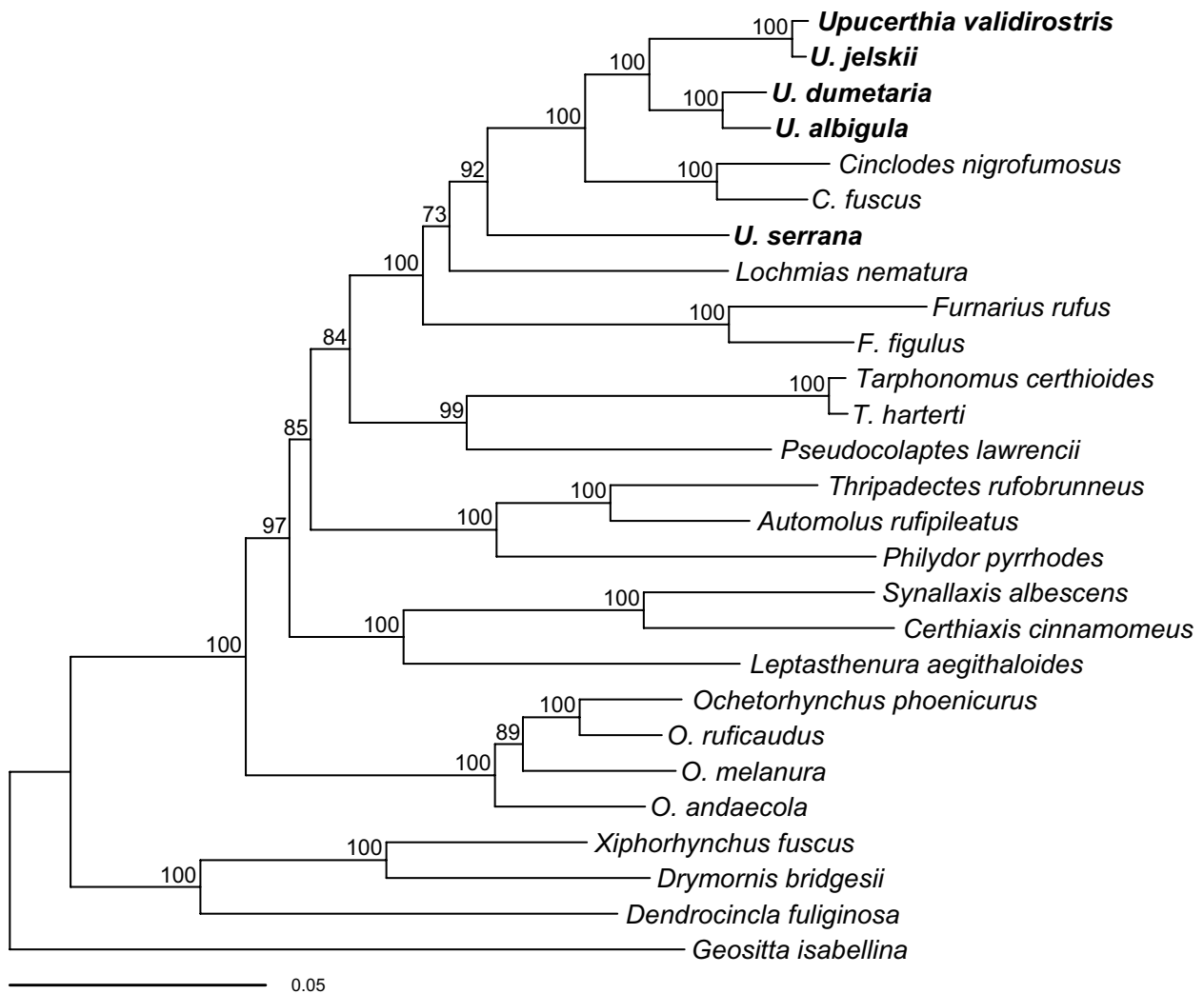


FIGURE 1. A maximum-likelihood phylogeny highlighting the lack of a sister relationship between *Upucerthia serrana* and other species of *Upucerthia sensu stricto*. Numbers above the branches indicate bootstrap support based on 150 maximum-likelihood replicates.

Total DNA was extracted from 25 mg of pectoral muscle using the DNeasy kit (Qiagen) and the standard protocol. Following methods described in Chesser *et al.* (2007), we amplified and sequenced the mitochondrial genes ND3 and CO2, and the autosomal nuclear gene beta-fibrinogen intron 7. Following the same methods, we amplified and sequenced an additional mitochondrial gene (ND2) using the primers H6313 (Johnson and Sorenson 1998) and L5215 (Hackett 1996). Two additional nuclear protein-coding genes (RAG1 and RAG2) were included for one individual from each genus. These RAG sequences were taken from Moyle *et al.* (2009) except for those of *Geocerthia serrana*, which we amplified and sequenced following the methods in Moyle *et al.* (2009). The six-gene concatenated dataset included 6,970 base pairs after alignment issues and unique inserts were excluded from BF7, the nuclear intron. An exception to a complete dataset was a partial BF7 sequence for the individual representing *Ochetorhynchus andaecola*. In addition, the ND2 gene could not be amplified for the selected individuals of *Philydor pyrrhodes* or *Lochmias nematura*; ND2 sequence from a second individual of these same species (amplified for a separate analysis) was used instead.

Because the dataset included protein-coding mitochondrial genes, a nuclear intron and protein-coding nuclear genes, it was unlikely that a single nucleotide substitution model would provide the best fit to the data. To determine the best partition of the dataset, we evaluated six different partitioning regimes ranging from unpartitioned to the maximum of sixteen partitions. Partitions were examined by performing maximum likelihood (ML) analyses using RAxML 7.0.4 on the Cipres Portal V 1.5 (http://www.phylo.org/sub_sections/portal/). RAxML implements the GTR+ Γ model and this was applied in each partition regime. We used the Akaike Information Criterion (AIC) to choose the best partitioning strategy, which was the GTR+ Γ +I model and fully partitioned dataset. We then used RAxML to evaluate nodal support

by performing 150 bootstrap replicates (Stamatakis *et al.* 2008). The analysis resulted in a single maximum-likelihood tree ($-\log L = 28529.0$) with high bootstrap support for most relationships (Fig. 1). Individuals of *Upucerthia sensu stricto* formed a strongly supported clade (100% bootstrap) that was sister to *Cinclodes*. The *Upucerthia-Cinclodes* clade was well supported (100%), and the single species *G. serrana* received strong support as sister to this clade (92%). These results clearly demonstrate that *G. serrana* is not a member of the *Upucerthia* clade.

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