Museu de Zoologia
Universidade de São Paulo

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Comparative phylogeography of Passerine birds with a circum-Amazonian distribution

Filogeografia comparada de Passeriformes com uma distribuição circum-Amazônica

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Sergio David Bolívar Leguizamón

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Original Version

Thesis submitted to the Graduate Program of the Museu de Zoologia da Universidade de São Paulo in partial fulfillment of the requirements for the degree of Doctor of Science (Systematics, Animal Taxonomy and Biodiversity).

Advisor: Prof. Dr. Luís Fábio Silveira

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A mi familia

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[...] Siguió con tanta atención las peripecias del entierro que nadie dudó de que lo estaba viendo, sobre todo porque su alzada mano de arcángel anunciador se movía con los cabeceos de la carreta.

-Adiós, Gerineldo, hijo mío -gritó-. Salúdame a mi gente y dile que nos vemos cuando escampe.

Aureliano Segundo la ayudó a volver a la cama, y con la misma informalidad con que la trataba siempre le preguntó el significado de su despedida.

-Es verdad -dijo ella-. Nada más estoy esperando que pase la lluvia para morirme.

Cien años de soledad. Gabriel García Márquez

Abstract

There are a number of common distributional patterns that have provided the foundations of our current knowledge of Neotropical biogeography. A distinctive pattern is the so-called “circum-Amazonian distribution”, which expands across the forested lowlands south and east of Amazonia, the Andean foothills, the Venezuelan Coastal Range, and the Tepuis. To date, there is no clear understanding of the processes giving rise to this distribution. To understand the evolutionary history of taxa exhibiting this pattern it is necessary to test biogeographic hypotheses offering mechanistic explanations. Comparative phylogeography allows more accurate phylogeographic hypotheses for these taxa, as well as better population genetic parameters. Comprehensive comparative studies aiming at unraveling the evolutionary and biogeographic mechanisms underlying the circum-Amazonian distribution have not been conducted yet, and only scarce descriptive information has been published. Therefore, the objective of this work was to elucidate the historical and biogeographic mechanisms underpinning circum-Amazonian distribution by performing comparative genomic analyses of a group of Suboscine passerines. Ultraconserved Elements (UCEs) were obtained for eight taxonomic groups to estimate population parameters and genealogical trees. For the *Thamnophilidae* species were inferred demographic histories with *mom2*. The best models of each taxon were analyzed in a comparative framework to relate them with previously proposed biogeographic hypotheses for the Neotropics and to propose plausible biogeographical scenarios for the circum-Amazonian pattern. The circum-Amazonian distributional pattern has two main phylogeographic units: an Andean (plus Central America region) and an eastern-forested region (Atlantic Forest ecoregion, forested areas around southeast of Amazonia), interconnected by a northern and southern corridor, allowing biotic interchanges

between them (mainly from the southern) and hybridization. Species-tree analyses recovered (a) an Andean clade with two Andean subgroups in the northern Peru and central Andes, and (b) an eastern-forested clade including northern and central/southern Atlantic Forest subgroups. The demographic histories of the Thamnophilidae taxa suggest that diversification of the circum-Amazonian taxa have a strong influence of climatic fluctuations during the Pleistocene, with interconnected refugia allowing phenotypic/genetic differentiation but maintaining a considerable level of gene flow during varying dry/cool and warm/humid periods. In addition, the results of this work opened interesting taxonomic questions about some taxa that could be covered in the future (*T. ruficapillus/torquatus* complex, *Xiphocolaptes* complex).

Resumo

Existe um número de padrões de distribuição comuns que forneceram os fundamentos do nosso atual conhecimento da Biogeografia Neotropical. Um padrão distintivo é o chamado padrão de distribuição circum-Amazônico, apresentado por grupos filogeneticamente relacionados habitando as florestas de baixada ao sul-leste da Amazônia, as encostas úmidas dos Andes, a área costeira da Venezuela e os Tepuis. Atualmente não existe um entendimento claro dos processos que deram surgimento a este padrão de distribuição. Para compreender a história evolutiva dos táxons exibindo este tipo de padrão é necessário testar hipóteses biogeográficas que ofereçam explicações mecanicistas. A Genômica comparativa permite hipóteses filogeográficas mais exatas para estes táxons, assim como melhores parâmetros demográficos. Estudos comparativos abrangentes visando em esclarecer os mecanismos evolutivos e biogeográficos relacionados a distribuição circum-Amazônica não tem sido elaborados ainda, e só informação descritiva escassa tem sido publicada. Portanto, o objetivo fundamental do projeto foi elucidar os mecanismos históricos e biogeográficos subjacentes à distribuição circum-Amazônica desenvolvendo análises genômicas comparativos de um grupo de Passeriformes Suboscines. Dados do gene ND2 e de Elementos Ultraconservados (UCEs) foram obtidos de oito grupos taxonômicos para estimar parâmetros populacionais e árvores genealógicas. Histórias demográficas foram inferidas só para as espécies da família *Thamnophilidae* usando *mom2*. Os melhores modelos de cada táxon foram analisados num marco comparativo para relaciona-los às hipóteses biogeográficas propostas para o Neotrópico e propor cenários possíveis para a distribuição circum-Amazônica. O padrão de distribuição circum-Amazônico possui duas unidades filogeográficas principais: uma unidade Andina (incluindo a região de Centro América) e uma segunda unidade incluindo as regiões florestais do

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General Introduction

Neotropical biomes and ecosystems exhibit high biodiversity and a wide range of ecological/geological characteristics (Connell, 1978; Stotz *et al.*, 1996; Myers *et al.*, 2000; Rull, 2011; Richardson & Pennington, 2016).

The Neotropics contains about 100,000 species of seed plants (37% of the world's species, Antonelli & Sanmartín, 2011), more of 3,000 species of amphibians (50% of all amphibian richness, Young *et al.*, 2004) and have high levels of richness in reptiles (Böhm *et al.*, 2013). In the same way, the Neotropical areas harbor approximately 3,800 species of birds (Stotz *et al.*, 1996) a 36% of all known landbird species and the highest level of endemism in the world (Newton & Dale, 2001), and probably these values are being underestimated.

Several theoretical and empirical approaches have been performed to identify and understand the processes involved in the evolution of such high diversity in the Neotropics (e.g. Sick, 1967; Haffer, 1969; Vuilleumier, 1971; Brown, 1979; Cracraft, 1985; Cracraft & Prum, 1988; Hooghiemstra & van der Hammen, 1998; Garzón-Orduña *et al.*, 2014; Antonelli *et al.*, 2018; Rull, 2018).

Mainly, these efforts have focused in the analysis of the Amazonian region. Thus, several hypotheses about the origin and maintenance of diversity of the Amazonia have been proposed (reviewed by Haffer, 1997 and Rull, 2018). Two of these hypotheses are based in the presence of rivers acting as barriers among populations/species. In the first one, the River Hypothesis (Sick, 1967; Capparella, 1988), the rise/presence of rivers in the Amazonian basin are the main cause in the separation of animal ancestral populations in this region (originally, the idea about rivers acting like barriers was outlined by Wallace, 1854). In the second one, the River-refuge Hypothesis

(Haffer, 1993), the isolation of ancestral populations in the Amazonia was a consequence of (a) several emerging rivers and (b) “ecologically unsuitable terrain” in the northern and southern Amazonia during the dry glacial periods in the Quaternary. Also, the Paleogeography Hypothesis (Croizat, 1976), states that geological processes (tectonic movements and level sea fluctuations) influence (indirectly) the diversity/distribution of species/subspecies allowing the isolation and re-connection of Amazonian populations. Lastly, the Refugia Hypothesis proposes that the biodiversity in Amazonia was molded by a series of climatic fluctuations during the Cenozoic, producing a reduction of the Neotropical Forests (Haffer, 1969; Vanzolini & Williams, 1970). (Cracraft, 1985) proposed other alternative to the “refugia” hypothesis; using the South American Avifauna, stated that endemism areas in these regions could be older (and, subsequently, the origin of its biodiversity) than the Pleistocene.

All these hypotheses have been subject to wide discussion, and several tests have been implemented to corroborate or refute their assumptions (Mayr & O’Hara, 1986; Salo, 1987; Nores, 1999; Loughheed *et al.*, 1999; Colinvaux *et al.*, 2000; Haffer & Prance, 2001; Haffer, 2008; FernAndes *et al.*, 2012; Maldonado-Coelho *et al.*, 2013; Garzón-Orduña *et al.*, 2015; Rocha & Kaefer, 2019, among others). For instance, Bennett *et al.*, (2012) broadly discuss about the origin of biodiversity in Neotropics and the influence of the ‘refugia’ proposed by Haffer (1969), while Ramírez-Barahona & Eguiarte (2013), Leite *et al.*, (2016) and Arruda *et al.*, (2017) tested the influence of climatic fluctuations during the Pleistocene in Neotropical regions. In the same way, Albert *et al.* (2018) review the impact of the change of course of the Amazon River in the diversification of Neotropics, and Nazareno *et al.* (2018) tested the importance of the riverine barriers (Wallace hypothesis) in some species of plants. Côrtes *et al.* and Moggi *et al.* (2015) tested the Pleistocene arcs as driver of diversification in the South American Seasonally Forests for some

species of plants. Finally, in a study based on 27 avian lineages, Smith *et al.* (2014) propose that the high diversification of Neotropical birds was not mainly affected by the changes in the South American landscape, but also due to dispersal events creating isolation and speciation.

Because of this bias in the quantity and quality of studies about Amazonia in relation to others Neotropical regions, the information about the evolutionary and biogeographic processes acting on the non-Amazonian regions is relatively scarce. However, some theoretical and empirical approaches have been performed to identify and understand the processes involved in the biodiversity of non-Amazonian areas/taxa. Initially, multiple works covered general descriptions and classifications of the different Neotropical regions (e.g. Haffer, 1969; Cabrera & Willink, 1980; Rivas-Martínez & Tovar, 1983; Cracraft, 1985; Dinerstein *et al.*, 1995; and Morrone, 2014). Others were focused in open lowlands from South America, like the Cerrado, the Caatinga and the Chaco (Prado & Gibbs, 1993; da Silva, 1995; Bridgewater *et al.*, 2004; Mayle, 2006; Roig-Juñent *et al.*, 2006; and Caetano & Naciri, 2011). In the same way, the Andean region (Fjeldså, 1992; Knapp, 2002; Doan, 2003; Brumfield & Edwards, 2007; Ribas *et al.*, 2007; Graham, 2009; Cadena *et al.*, 2016; Chazot *et al.*, 2016; Cuesta *et al.*, 2016) and the Atlantic Forest have been studied (Damasceno *et al.*, 2014; Amaral *et al.*, 2016; Dalapicolla *et al.*, 2018). Among these works, there is no consensus in the explanations about the basic evolutionary processes/patterns acting on these regions.

The circum-Amazonian distribution pattern

Despite a wide variety of proposed evolutionary and biogeographic mechanisms intended to explain Neotropical diversity, our understanding remains scarce for some of these patterns. For

instance, a considerable number of birds are distributed in those areas surrounding Amazonia but are absent from Amazonia itself (Remsen *et al.*, 1991; Bates, 1997; Lovette, 2004), and we have no clear understanding of the mechanisms responsible for those distributions. Such distributional pattern is known as the “circum-Amazonian distribution” (Figure 1) and is characterized by the presence of phylogenetically related groups mainly in “(a) *montane forested areas on the humid slopes of the Andes and the Coastal Range of Venezuela or the Tepui region; and in (b) lowland forested areas south and east of the lowland forests of Amazonia*” (Remsen *et al.*, 1991).

Figure 1. Circum-Amazonian distribution pattern sensu Remsen *et al.* (1991). Left map: Distribution of *Platyrinchus mystaceus* (modified from Remsen *et al.* (1991). Right map: Distribution of *Dysithamnus mentalis* (BirdLife International, 2016).

In the first study describing the circum-Amazonian pattern, Remsen *et al.* (1991) describe that species like *Platyrinchus mystaceus*, some *Hemitriccus*, *Dysithamnus mentalis*, *Phyllomyias burmeisteri*, and the *Elaenia* species *albiceps*, *parvirostris*, and *obscura*, among others, share this distributional pattern. Subsequent works have identified other taxa as circum-Amazonian. Bates (1997) stated that two species of *Tiaris*, *T. obscura* and *T. fuliginosa*, have a geographical

distribution congruent with the proposed by Remsen *et al.* (1991). Also, populations of *Phaeothlypis* (Lovette, 2004); and the species *Synallaxis ruficapilla* and *S. moesta* (Batalha-Filho *et al.*, 2013) share this pattern. Some species of genus *Cercomacra* (*C. melanaria*, *C. ferdinandi*, *C. carbonaria*, and *C. nigricans* complex) fit partially into this distributional pattern (see Tello *et al.*, 2014). In a recent study, Savit & Bates (2015) described the intraspecific genetic structure of the burnished-buff tanager (*Tangara cayana*), another ‘circum-Amazonian’ bird.

There are also examples in non-passerines such as the genus *Pionus*, in which the *sordidus-maximiliani* complex seem to exhibit complementary geographical ranges resulting in a circum-Amazonian distribution (see Ribas *et al.*, 2007). Moreover, the circum-Amazonian distribution pattern can also be found in other non-avian groups such as some insects and plants (e.g. Prado & Gibbs, 1993; Erwin, 2000; Canals & Johnson, 2000; Knapp, 2002; Irmeler, 2009).

Nevertheless, whereas the diversity and distribution patterns in adjacent Neotropical regions have been the focus of more studies, this complex pattern of distribution has not received enough attention, and the events and evolutionary processes behind it have not been thoroughly revealed.

Comparative Phylogeography

Phylogeography is a relatively recent and successful field that, in a broad definition, aims at studying the geographical history of a particular clade using populations as terminals instead of species (see Avise *et al.*, 1987; Zink, 2002). Phylogeography starts with the rise of mitochondrial DNA sequencing, allowing analyses to identify genealogical patterns among individuals, and link these patterns with the geographic distributions of populations (Avise, 2009). The advent of new

mathematical and molecular tools now allows comparison of genealogical patterns (based in the estimates of gene flow/divergence among species) across different lineages/taxa ('Multi-species phylogeographic' studies) co-occurring in time and space (Hickerson *et al.*, 2010). Such multi-taxon approach is known as comparative phylogeography (Arbogast & Kenagy, 2001) and its main objective is to search for concordant splits within contemporaneous, co-distributed species (Bermingham & Avise, 1986). In this way, the level of "phylogeographic congruence is a measure of the historical stability of the current species assemblage" (Zink, 2002), namely, a particular evolutionary reconstruction (a hypothesis) on co-distributed species affected by similar climatic/geological events would be more 'supported' while more individuals phylogeographic patterns being congruent. This approach would be analog to some analyses in historical biogeography that use phylogenies and "area cladograms" of several groups to identify common biogeographic patterns across space (see Nelson & Platnick, 1981; Humphries & Parenti, 1999). Among the methodologies developed to access the level of phylogeographic congruence of co-distributed taxa, the hierarchical approximate Bayesian Computational (hABC) framework proposed by Hickerson *et al.* (2006). This methodology allows to quantify the probability of simultaneous divergence among populations/taxa, estimating demographic parameters (e.g. across-species demographic variation, divergence times, inter-gene variability in coalescent times, DNA mutation rate heterogeneity, among others, see Hickerson *et al.*, 2007) from multiple phylogeographic datasets (from these populations/taxa) in a single analysis. Posteriorly, this pipeline was upgraded to test evolutionary and biogeographical scenarios (e.g. dispersal/vicariance/extinctions); to include climatic, ecological and geological (palinological) data into the prior parameters of tested model(s); and, to allow the use of multi-locus DNA sequences data (see Huang *et al.*, 2011). This method has been widely used. For instance,

Hickerson & Meyer (2008) implemented a hierarchical approximate Bayesian computation (hABC) to test vicariance/dispersal explanations of allopatric diversification across co-distributed cowrie gastropods (Cypraeidae, Mollusca), and Bell *et al.* (2011) used five species co-distributed rainforest frogs multi-locus datasets to test evidence of single/multiple vicariance events in the Australian Wet Tropics rainforests. Recently, Robinson *et al.* (2014) applied a hABC method to infer population history from genomic data, using as example populations of *Biorhiza pallida*.

Ultraconserved Elements

Initially, the empirical works in comparative phylogeography were based on the DNA information from the mitochondrial, nuclear or a few individual genes (Hickerson *et al.*, 2006). With the advent of Massively Parallel Sequencing (MPS, Shendure & Ji, 2008), the possibility to obtain multiple sets of sequences from genomes has increased (Edwards *et al.*, 2015; Edwards *et al.*, 2016).

Additionally, the use of highly conserved genomic sequences or 'ultraconserved elements' (UCEs, see Bejerano *et al.*, 2004) allows the use of a large set of universal markers to infer relationships among lineages (Faircloth *et al.*, 2012; Faircloth *et al.*, 2015). UCEs are “highly conserved regions of organismal genomes shared among evolutionary distant taxa” whose function in the genome is associated with gene regulation (Pennacchio *et al.*, 2006) and development (Sandelin *et al.*, 2004; Woolfe *et al.*, 2004). For any given UCE, levels of sequence variation increase as one moves away toward the flanking regions. Therefore, sequence data from this gradient of variation, allows sampling several levels of sequence diversity that reflect different evolutionary timescales (Faircloth *et al.*, 2012). Hence, UCEs can be used with MPS protocols to generate huge numbers of orthologous sequence data among taxonomically diverse groups. In recent reviews, Heyduk *et*

al. (2016) and Harvey *et al.* (2016) show the advantages/precautions in the use of the target enrichment methodologies, like as UCEs.

Since their application as molecular markers in phylogeny and evolution, the UCEs has been increasing recently. For instance, UCEs have proven to be useful in the reconstruction of phylogenetic relationships in Hymenoptera (Faircloth *et al.*, 2015), in New World Sparrows (Passerellidae, Bryson Jr. *et al.*, 2016), phylogeny and genetic relationships in the salamander *Plethodon serratus* (Newman & Austin, 2016). Also, the estimation of demographic and population parameters based on UCE data has been shown to improve relative to those based on mtDNA or other genomic markers (Smith *et al.*, 2013; Harvey *et al.*, 2013; Zarza *et al.*, 2016; Myers *et al.*, 2019).

Justification

Here, I implemented a comparative phylogeographic approach to study the evolutionary history of a number of passerine birds with circum-Amazonian distribution using genomic data (UCEs). First, I tested whether these circum-Amazonian distributions are the result of a congruent history across taxa or whether it is the result of lineage-specific histories. Also was possible test whether congruent topologies are associated to dispersal and vicariance events, which allow me to do inferences on the various proposed hypotheses for Neotropical diversity (e.g. paleogeography, refugia and riverine hypotheses). Additionally, it was possible to estimate the level of influence of the environmental variables on the species of these regions, and the constraints imposed by these factors. Furthermore, the genealogical/evolutionary information of each lineage was useful to determine levels of demographic structure and the dynamics among isolated populations from the

same lineages (e.g. migration rates, speciation), which generated information on the role of lineage-specific histories and idiosyncrasies in shaping circum-Amazonian populations.

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Chapter I

**Out of northeastern Brazil: demographic and evolutionary history
of the Variable Antshrike, *Thamnophilus caerulescens* (Aves,
Thamnophilidae)**

Out of northeastern Brazil: demographic and evolutionary history of the Variable Antshrike,
Thamnophilus caerulescens (Aves, Thamnophilidae)

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Abstract

The Neotropics exhibit a wealth of distributional patterns that are often shared by a number of co-distributed species. A distinctive pattern is the so-called “circum-Amazonian distribution”, which is observed in species that do not occur in Amazonia but rather in forested habitats around it forming a continuous belt that extends south and east of Amazonia, the Andean foothills, and often into the Venezuelan Coastal Range and the Tepuis. Although this pattern is widespread across a wealth of animals and plants, the historical and biogeographic mechanisms giving rise to it remain poorly understood. The Variable Antshrike (*Thamnophilus caerulescens*) is a sexually dimorphic suboscine passerine bird that is distributed along the southern portion of the circum-Amazonian belt. It comprises eight currently recognized subspecies that exhibits extreme levels of plumage variation. Our objective was to describe the phylogeographic and demographic history of *Thamnophilus caerulescens* using Ultraconserved Elements (UCEs). We inferred population structure and divergence times, as well as modeled the demographic history of the species based on comprehensive sampling across the entire distribution of the species. Structure analyses allowed to identify three genomic clusters within the species: a) northeastern Atlantic Forests; b) southeastern Cerrado, central, and southern Atlantic Forests, and c) Chacoan and Andean populations. Demographic analyses revealed a history of gene flow, mainly between birds from the central and southern Atlantic Forest, the Chacoan, and Andean populations. Differentiation took place during the Pleistocene, with a possible origin in the northern Atlantic Forest during the Pliocene. The recent diversification of the Variable Antshrike was probably affected by series of humid and dry periods throughout the Quaternary, allowing the intermittent connection between

the central-southern Atlantic Forests and the Chacoan – Andean populations, and, to a lesser extent, with the northern Atlantic Forest populations.

Introduction

The Neotropics harbor the highest levels of species diversity and endemism across multiple taxonomic groups (Halffter, 1992; Mittermeier *et al.*, 1998; Myers *et al.*, 2000; Olson *et al.*, 2001; Dinerstein *et al.*, 2017). In general, the spatial distribution of Neotropical organisms results from large-scale geological processes, such as the uplift of the Andes, that generate opportunities for allopatric differentiation and promote diversification into novel environments (Hooghiemstra *et al.*, 2002, Graham, 2009, Hoorn *et al.*, 2010, Herzog *et al.*, 2011, Prieto-Torres *et al.*, 2018). These processes are also shaped by species' ecological affinities and dispersal abilities to disperse across barriers and persist over time (Burney & Brumfield, 2009; Smith *et al.*, 2014), resulting in a complex mosaic of distributional ranges, often shared by large numbers of co-distributed species, from which some general patterns have emerged. For instance, coarse distributional limits of South American taxa have allowed us to recognize the main domains of forested areas, such as the Atlantic Forest and Amazonia, or open areas such as the Llanos and the Cerrado (Darlington, 1957; Sánchez-González *et al.*, 2008; Morrone, 2014; Prieto-Torres *et al.*, 2018). However, there is prevalent taxon-specific and scale-dependent variation in demographic and geologic histories that obfuscate our understanding of the mechanisms driving the evolutionary history of co-existing populations (Smith *et al.*, 2014).

Distributional patterns of Neotropical birds are largely bounded by the main biogeographic domains. Yet, there are numerous instances in which several widely distributed co-occurring taxa exhibit rather odd distributions that expand beyond the boundaries of these domains. One of these common patterns is known as the circum-Amazonian distribution (*sensu* Remsen *et al.*, 1991), which largely mirrors the extend of Seasonally Dry Tropical Forests – SDTF (*sensu* Mooney *et al.*, 1995) surrounding Amazonia (Chaco, Caatinga, Interandean valleys) but that expands into

neighboring forested formations in seasonal savannah environments (Cerrado, Llanos, Pampas) and humid forests (Atlantic Forest, Andean Foothills, Guiana Shield). The circum-Amazonian distribution is shared by a considerable number of species of birds, insects, and plants (Bates, 1997; Lovette, 2004; Knapp, 2002; Irmeler, 2009) but we still lack a thorough understanding of the historical events and evolutionary processes generating this pattern.

Although a wealth of hypotheses about the origin and maintenance of diversity in the Neotropics has been proposed for the Amazonia (reviewed by Haffer, 1997), they can be relevant shed light on the circum-Amazonian patterns of distribution. For example, hypotheses based in the presence of rivers acting as barriers between populations – the Riverine Hypothesis (Sick, 1967; Capparella, 1988; Wallace, 1854) – could explain the distribution of some species with an incomplete/intermittent circum-Amazonian distribution (an idea proposed for Amazonian taxa, initially by Wallace, 1854). In the same way, the Refugia Hypothesis (Haffer, 1969; Vanzolini & Williams, 1970), that proposes that the biodiversity in Amazonia was molded by a series of climatic fluctuations during the Cenozoic producing a reduction of the Neotropical Forests, could be extrapolated to explain the diversification of species of this distribution. In addition, the combined effect of these rivers and the refugia created during the dry glacial periods in the Quaternary would be another suitable explanation for circum-Amazonia taxa (River-refuge Hypothesis Haffer, 1993). Lastly, it is possible that geological processes (tectonic movements and level sea fluctuations) influence (indirectly) the diversity/distribution of species/subspecies allowing the isolation and re-connection among the different areas of the circum-Amazonian region(s) (Paleogeography Hypothesis, Croizat, 1976).

The Variable Antshrike (*Thamnophilus caerulescens*) is a suboscine passerine that exhibits circum-Amazonian distribution. It inhabits the forest understory, second-growth woodland, and

patches of thickets and trees in more open regions, and can be found in patches of degraded remnants of forest (Zimmer & Isler, 2019). The Variable Antshrike is sexually dimorphic and exhibits extreme levels of plumage variation across its range. Hence, taxonomists have recognized a number of subspecies, some of which have been recently synonymized (see Zimmer & Isler, 2019), that exhibit clinal variation in vocalizations and plumage (Brumfield, 2005; Isler *et al.*, 2005). Although this high levels of phenotypic variation lacking clear-cut geographic structure are extraordinary in the avian world, a thorough understanding of the mechanisms giving rise to the remain poorly understood.

Ultraconserved Elements (UCEs Bejerano *et al.*, 2004) are highly conserved genomic sequences that allow the use of a large set of universal markers to infer relationships among lineages (Faircloth *et al.*, 2012; Faircloth *et al.*, 2015). The estimation of demographic and population parameters based on UCE data has been shown to improve relative to those based on mtDNA or other genomic markers (Smith *et al.*, 2013). For example, Zarza *et al.* (2018) used UCEs to identify the demographic patterns in some groups of vertebrates. In the same way, Myers *et al.* (2019) infer historical demography in a species of snakes. Also, UCEs were used to delimitation of species (Ješovnik *et al.*, 2017; Pie *et al.*, 2017).

Here, we describe the large-scale phylogeographic and demographic history of *Thamnophilus caerulescens* using genome-scale. Specifically, we used ultraconserved Elements (Faircloth *et al.*, 2012; UCEs) to a) describe the populational structure and estimate divergence times, and b) identify plausible historical and evolutionary processes responsible for generating the circum-Amazonian distributional pattern of *T. caerulescens*. Specifically, we aim at testing scenarios such as a possible isolation among their populations after an initial period of expansion due to climatic fluctuations in the Cenozoic, and assess migration events between populations

during the Quaternary. To this end, we use demographic modeling to test for different scenarios contemplating different rates and directions of migration and growth rates across populations of *T. caerulea*. In addition, we describe a plausible phylogeographic scenario of the species and propose one possible change to refine the taxonomy of this polytypic taxon. The evolutionary and demographic information of the populations of *T. caerulea* will be useful to shed light on the role of lineage-specific histories and idiosyncrasies in shaping circum-Amazonian populations.

Methods

Sampling and DNA extractions

We sampled a total of 53 vouchered specimens of *T. caerulescens*, covering the total extent of its geographical distribution and including at least two individuals of each of the eight subspecies currently recognized (but see *T. c. ochraceiventer*, taxonomy *sensu* Zimmer & Isler 2019, Table S1; Fig. 1a). Additionally, following results by Brumfield and Edwards (2007), we sampled five vouchered specimens of the closely related species *T. aethiops*. We extracted total genomic DNA from muscle tissues using the PureLink® Genomic DNA Mini kit (Invitrogen Inc) and following guidelines by the manufacturer. We quantified genomic DNA concentrations using a Qubit 2.0 fluorometer with the dsDNA BR assay kit (Life Technologies, Inc).

Mitochondrial DNA

We sequenced the mitochondrial gene NADH dehydrogenase 2 (ND2) from all individuals of *T. caerulescens* and 5 individuals of the outgroup. We amplified and sequenced ND2 using standard PCR and Sanger sequencing protocols described elsewhere (Brumfield *et al.*, 2007). We edited sequences and checked that they did not include stop codons or anomalous residues using Geneious v. 11.1.4 (www.geneious.com, Kearse *et al.* 2012). We aligned sequences with the MAFFT v.7 multiple alignment plugin (Kato & Standley, 2013) implemented in Geneious. Newly obtained sequences were deposited in GenBank (Accession numbers XXXXX-XXXXXX).

We built a Median Joining Network – MJN – haplotype network (Bandelt *et al.*, 1999) implemented in POPART (Leigh & Bryant, 2015). Outgroup samples and short ingroup sequences (<700 bp) were excluded from the analysis and the matrix was trimmed to exclude any positions containing missing data (Final 1,041 bp, 53 samples).

Using the corrected Akaike Information Criterion (AICc; Hurvich and Tsai 1989) implemented in jModeltest2 (Darriba *et al.*, 2012) on the Cipres Science Gateway V 3.3 (Miller *et al.*, 2010), we selected a TrN+I+G model as the best substitution model. We estimated a time-calibrated gene tree within a Bayesian framework implemented in the program BEAST2 v2.4.4 (Bouckaert *et al.* 2014). Based on the avian mtDNA substitution rate of 2.1%/My (Weir & Schluter, 2008), we used a lognormal relaxed molecular clock with a mean rate of 0.0105 for mtDNA. We used a Coalescent Constant Population prior with no restrictions on tree shape and a randomly generated tree as a starting tree. We ran analyses for a total of 50 million generations with a sampling frequency of 1,000. We determined that replicate analyses converged (effective sample size values > 400) using Tracer 1.7.1 (Rambaut *et al.* 2018). Using TreeAnnotator v2.4.4 (Drummond *et al.* 2012, Bouckaert *et al.* 2014) and a burn-in of 30%, we estimated a posterior distribution of topologies and a 50% maximum clade credibility (MCC) tree.

Sequence capture

Based on results of the mitochondrial analyses, we selected 28 samples of *T. caerulescens* and three samples of *T. aethiops* to sequence ultraconserved elements (UCEs; Faircloth *et al.*, 2012) following a target enrichment approach. The genomic enrichment and Illumina sequencing was performed by Rapid Genomics (Gainesville, FL) using 1,000 ng of input genomic DNA for each

sample. Libraries were enriched from 2,386 UCE loci that targeted a set of 2,560 probes (Faircloth *et al.*, 2012, Tetrapods-UCE-2.5K version 1; Microarray, Ann Arbor, MI), following an open-source protocol available at www.ultraconserved.org. Samples were multiplexed at 192 samples per lane on a 125 bp paired-end Illumina HiSeq 2500 run, yielding an average coverage of 18.61X per sample.

Edition and assembly of UCEs

We followed the *Phyluce* pipeline (Faircloth, 2016, <https://github.com/faircloth-lab/phyluce>) to process the raw reads and assembly contigs corresponding to target loci. Initially, Illumiprocessor 2.0.7 (Faircloth, 2013) and Trimmomatic 0.32 (Bolger *et al.*, 2014) were used to trim adapters, barcodes and low quality regions. We used Trinity 2.0.6 (Grabherr *et al.*, 2011) to perform the assembly (script *phyluce_assembly_assembly_trinity*). To avoid including markers of different ploidy, we identified, extracted, and removed Z-linked UCEs from the assemblies using Blast 2.7.7 (see Altschul *et al.*, 1990; Camacho *et al.*, 2009). Finally, we implemented the script *phyluce_assembly_match_contigs_to_probes* to match the assembled contigs to the UCE probes (uce-2.5k-probes.fasta). The results were exported in a *fasta.

Single Nucleotide Polymorphism (SNP) calling

We extracted Single Nucleotide Polymorphisms (SNPs) from the UCE alignments using the methods described by Harvey *et al.* (2016), which are largely based on Phyluce (Faircloth, 2016). We extracted SNPs following two approaches using the script *phyluce_assembly_match_counts*.

The first one yielded a 100% complete matrix with no missing data for any individual in all loci (individuals = 28, loci = 324), and the second one yielded an incomplete matrix including all data matching the target loci (individuals = 28, loci = 2,036). When outgroups were included these matrices contained 201 and 1,954 loci, respectively. The average number of loci per individual was 2,004 and the average number of individuals per locus was 27.

To call SNPs, we first created a *fasta file with the loci extracted from each matrix (*phyluce_assembly_explode_get_fastas_file*) and we chose as reference the individual with the deepest coverage and longest mean length of recovered contigs (script *phyluce_assembly_get_trinity_coverage*, and *phyluce_assembly_get_fasta_lengths*). Then, we used bwa 0.7.7 (Li & Durbin, 2009) to map raw reads from the samples for each group with their respective reference (Li, 2013), Samtools 0.1.19 (Li *et al.*, 2009) and Picard (<http://broadinstitute.github.io/picard/>) to create *bam files, mark duplicates from the PCR and prepare the files for the next phase. We used GATK 3.8.0 (McKenna *et al.*, 2010) to extract indels, SNPs, and phase sequences. Created *vcf files were exported into other formats for downstream demographic analyzes (*nexus, *sfs.gz). Finally, we filtered loci in the complete and incomplete *vcf by selecting one random SNP per locus from the biallelic SNPs recovered in each file (script *randSnps.pl*). Before filtering, our datasets contained 324 and 2,036 SNPs in the complete and incomplete matrices, respectively. After filtering, whereas In the end, we have two SNPs dataset: one with 324 loci (from the complete matrix) and another with 2,036 loci (incomplete matrix). We implemented all the analysis in this work on the two matrices to compare the results in each of them.

Population structure

To infer population structure from the SNPs, we implemented two multivariate approaches; a Principal Components Analysis (PCA) with the R packages *adeigenet*/*ape* (Jombart, 2008 and Paradis *et al.*, 2004), and a coefficients of mixture analyses with sparse nonnegative matrix factorization for clustering (sNMF) in the R package *LEA* (Frichot *et al.*, 2014, Frichot & François, 2015) with the following parameters; five α values (10, 50, 100, 500, 1000), K values of 1 to 10 (K = 1:10), and 100 runs per K value, and the minimum cross entropy as TRUE to estimate the best number of K. Additionally, we implemented a Discriminant Analysis of Principal Components (DAPC; Jombart *et al.*, 2010) within the *adeigenet* package recovering PCs with 80% of variance, and a maximum of 10 groups.

Species trees and gene trees

We ran two million iterations in SNAPP (Bryant *et al.*, 2012) to identify the relationships among the clusters recovered in the PCA and sNMF analyzes using the SNPs extracted from the UCEs. Therefore, we tested three possible scenarios. The first one considered all the samples from *T. caerulescens* and *T. aethiops* (outgroup) to test the monophily of *T. caerulescens*. The second one considered *T. caerulescens* divided into three clusters: a) northern Atlantic Forest; b) the remaining samples of *T. caerulescens*; and c) *T. aethiops*. The third scenario included five clusters: a) northern Atlantic Forest; b) southeastern Cerrado, central and southern Atlantic Forest; c) Chaco; d) Andes; and e) *T. aethiops*. We used Tracer 1.7.1 (Rambaut *et al.*, 2018) and Figtree 1.4.4 (Rambaut, 2009) to evaluate and visualize the results.

Demographic history

We used the software *momi2* (<https://github.com/popgenmethods/momi2>) to infer possible demographic scenarios in *T. caerulescens*. *momi2* used a SFS file that can be obtained from the SNPs extracted from the UCEs to infer demographic histories by fitting the observed value of the SFS to its expected value in a composite likelihood framework (Kamm *et al.*, 2018). In this way, multiple demographic models were tested and the most informative was selected using the Akaike Information Criterion (AIC, Akaike, 1973). We tested multiple models with different demographic scenarios for the populations in *T. caerulescens*, based on the results of PCA, DAPC, and sNMF analyzes. Thus, we tested three main types of models (Fig. 2, all models in Figure S1a-S1b) on a scenario with three clusters: a) northern Atlantic Forest; b) southeastern Cerrado, central and southern Atlantic Forests; and c; the Andean and Chacoan populations. The first group of models infer possible events of migration and divergence times among the three clusters (Fig. 2a); the second group includes the parameters of the first group plus possible events of expansion of the *caerulescens* and Andean clusters (Fig. 2b). Finally, the third group of models includes a bottleneck event in the northern Atlantic Forest cluster after the split from the remaining populations (Fig 2c).

For each model, we implemented 100 runs to avoid suboptimal results. Based on the run with the highest likelihood for each model, we evaluated the relative weight of the best model using the Akaike Information Criterion (AIC, Akaike, 1973). Finally, we ran 100 bootstrap simulations to estimate confidence intervals of the parameters of the best selected model.

Results

Time calibration based on mtDNA

Preliminary analyses of the 53 ND2 sequences identified 30 unique haplotypes and a considerable levels of admixture among the individuals of populations collected (Fig. 1b). Maximum-likelihood and Bayesian phylogenetic reconstructions showed four strongly supported groups: a) northern Atlantic Forest; b) southeastern Cerrado, central and southern Atlantic Forest; c) Chaco; and d) Andes (see Supplementary information, Fig. S2a-S2b).

Analyses of divergence times estimated that *T. caerulescens* diverged from its closest relatives close to 5 Mya [6.5 – 3.6 Mya] in the Zanclean period of the early Pliocene. The primary divergence between the population of the northern Atlantic Forest and the others populations took place around 1.2 Mya [1.7 – 0.8 Mya] during the Calabrian stage of the Pleistocene. The diversification of the remaining clusters took place during the Middle Pleistocene [0.8 – 0.3 Mya], showing that *T. caerulescens* has deversified primarily during the last million years (Fig. 3a).

Genomic data quality

We recovered 5,702,659 reads per sample (N = 28; min=1,904,001 and max=10,284,782) after trimming. The assembly produced 17,803 contigs per sample (total=498,503, min= 4,888, max=143,662) with an average length of 464.53 bp, for a total of 185,331,752 bp. Were recovered a total of 4,697 contigs with more of 1 kb of length (2,385 from 2,560 loci in the Tetrapods-UCE-2.5K probe). We built two SNPs datasets one with 324 and another with 2,036 loci with the

samples of *T. caerulescens* (see Methods: SNP calling). Here we show unified results, but when results differed between the two datasets, we will show both.

Population structure

Principal component analyses support the existence of three genetic clusters within *T. caerulescens* (Fig. 3b). One group represented the northernmost region of the Atlantic Forest (subspecies *cearensis*), the second one included individuals from the southeastern Cerrado and the central and southern Atlantic Forest (subspecies *caerulescens*, *gilvigaster*, and *ochraceiventer*), and the third one comprised populations in the Andean and Chacoan regions (remaining subspecies). Analyses based on the incomplete matrix showed further structure within this last group: one Andean cluster (subspecies *aspersiventer* and *melanochrous*) and one Chacoan cluster (subspecies *dinellii* and *paraguayensis*; Fig. S3). In addition, structure in this third group reflected a pattern of continuous or clinal variation running from north to south (*melanochrous* – *aspersiventer* – *dinellii/paraguayensis*; Fig. S4a-S4b), consistent with previous description of phenotypic and genetic variation in Bolivia (Brumfield, 2005; Isler *et al.*, 2005).

The sNMF analyses also infer the three main clusters described above (Fig. 3c). However, the use of different values of the α regularization parameter and the use of either the complete or the incomplete matrix, could alter the number of identified clusters (see Table S2 and Fig. S5). With the complete matrix the number of inferred groups varied from two to five, whereas the incomplete matrix led to defining two or three clusters. Most importantly, the main pattern that emerged from these results is that highest levels of admixture were primarily observed in those individuals in the Andean and Chacoan populations (see Tables S3 – S4 from DAPC).

Species trees and gene trees

Under the scenarios analyzed, SNAPP consistently showed that *T. caerulescens*, as currently defined, is monophyletic and is composed of three well-supported groups (Fig. 4a). The first one corresponds to the northern Atlantic Forest group (hereafter *cearensis* group), the second one to the the Andes and Chaco populations (hereafter Andean group), and the third one to the eastern Cerrado, central and southern Atlantic Forest (hereafter *caerulescens* group). Support levels using both complete and incomplete matrices varied, but groupings and topologies were congruent.

Demographic history

The demographic history of the *cearensis*, *caerulescens*, and Andean groups was best explained by models considering asymmetrical gene flow. For the complete matrix (Fig. 5a), the most informative model proposed unidirectional asymmetrical migration (*cearensis* → *caerulescens* → Andean, log-lik = -1229.45, AIC = 2476.91 $\omega_i = 1$; Table 1). In this model, the events of migration took place after the LGM (*cearensis* → *caerulescens* 19,228 year; *caerulescens* → Andean 10,000 years). Additionally, the percentage of migrations was higher from the *caerulescens* → Andean populations than the *cearensis* → *caerulescens*, congruent with the patterns of admixture showed in the sNMF analyses. After bootstrapping, we dated the divergence of the *cearensis* from the others groups approximately 743,054 years ago (95% CI 700,975 – 785,133), whereas the Andean – *caerulescens* divergence took place 385,122 years ago (95% CI 361,096 – 409,149).

For the incomplete matrix (Fig. 5b), a model with bidirectional and asymmetrical migration was identified as the best (*cearensis* $\leftrightarrow$ *caerulescens* $\leftrightarrow$ Andean, log-lik = -7274.51, AIC = 14,575.02; $\omega_i = 1$, Table 2). After bootstrapping, we dated the divergence of the *cearensis* from the others groups approximately 630,469 years ago (95% CI 616,307 – 644,631), whereas the Andean – *caerulescens* divergence occurred 377,685 years ago (95% CI 367,612 – 387,758). In this model, the events of migration took place before and after the LGM. The migration from *cearensis* $\rightarrow$ *caerulescens* occurred 25,526 year ago. The *caerulescens* $\rightarrow$ Andean migration occurred 365,700 years ago, and the Andean $\rightarrow$ *caerulescens* migration 13,857 years ago). Additionally, the percentage of migrations was higher in the *caerulescens* $\leftrightarrow$ Andean populations than in the *cearensis* $\rightarrow$ *caerulescens*, congruent with the patterns of admixture identified. In general, the divergence events between populations of *T. caerulescens* occurred during the Middle Pleistocene (0.78 – 0.12 Myr), consistent with the results obtained with mitochondrial phylogenetic analyses. However, the divergence between the northern Atlantic Forest (the *cearensis* group) and the other populations were older in the ND2 analysis (835,592 years, Calabrian). Similarly, incomplete and complete matrices differed in the time of divergence of *cearensis* group from all other populations and in the time of the events of migration. However, there is a consistent signal of the idea that *cearensis* is the most divergent and isolated population in *T. caerulescens* and that the percentage of migration between *caerulescens* and the Andean group is higher than that between *cearensis* and *caerulescens*.

Discussion

*Population structure in *Thamnophilus caerulescens**

This is the first phylogeographic study about the Variable Antshrike (*T. caerulescens*) using genomic data. Previous research focused on specific populations and mitochondrial DNA only (Brumfield, 2005; Isler *et al.*, 2005) or as part of analyses at a higher taxonomic level (Brumfield & Edwards, 2007). Here, we identified three main genetic clusters in the Variable Antshrike: *cearensis* in the northern Atlantic Forest, *caerulescens* in the southeastern Cerradao, central, and southern Atlantic forest, and an Andean – Chacoan group. These results are congruent across phylogenetic, structure, and demographic analyses and they provide a good starting point toward the understanding of the demographic history of this species, as well as the mechanisms underlying circum-Amazonian distributions.

Moreover, these results highlight the high levels of admixture in the Andean and Chacoan populations, all of which are phenotypically distinct and that seem to be varying clinally, as previously suggested based on mitochondrial, plumage, and vocal data (Brumfield, 2005; Isler *et al.*, 2005). Clinal variation has been described in a number of Andean birds (Graves, 1991; Areta & Pearman, 2013; Doren *et al.*, 2018; Seeholzer & Brumfield, 2018) and other taxa (Premoli, 2003), but mechanisms driving this pattern remain to be studied in greater detail. Some of the most likely explanations largely fall within the realm of local adaptation in response to latitudinal and environmental gradients, geological events, climatic variation during the Pleistocene, secondary contact between isolated populations, and hybridization (Miller *et al.*, 2010b; Herzog & Kattan, 2011; Luebert & Weigend, 2014; Chattopadhyay *et al.*, 2017; Polato *et al.*, 2018). For *T.*

caerulescens, a larger sampling effort and others methodological approaches will be necessary to clarify this phenomenon in specific.

In addition, it seems that there is an effect of the amount of data used on the ability to detect population structure. The level of resolution of PCA and sNMF analyses was affected possibly because the number of loci was dramatically reduced (324 loci from the 2,036 in the incomplete matrix), likely representing information loss. Frichot *et al.* (2014) warns about the influence of the α parameter (regularization parameter α) in the results in the sNMF program, especially in the complete matrix dataset. It could be a factor that allowed discordant results (multiple K values for different α values). The level of admixture among the clusters varies between the two matrices and is affected for α parameter, but it is clear that there was a considerable genic flow among the clusters, mainly between the *caerulescens* and Andean groups.

Demography and biogeographical remarks

Mitochondrial estimates indicated that *T. caerulescens* diverged from its closest relative between 6.5 and 3.6 Mya, a time older than estimated by Brumfield & Edwards (2007) for the ‘montane *T. caerulescens* clade’ (1.6 Myr), whereas the most recent divergences within the *T. caerulescens* started to take place close to 1.2 Mya during the Pleistocene. These values are older than those inferred in demographic analyses (0.75/0.63 and 0.38/0.37 Myr, complete/incomplete matrices), but a direct comparison between these two analyses could be difficult, given that they are based on different methodological approaches. The mitochondrial gene ND2 is thought to evolve at a unique clock-like substitution rate, whereas UCEs represent a wider spectrum of the heterogeneous history of the genome comprising hundreds of loci with hundreds of possible different rates.

Demographic analyses identified as the best models those scenarios with migration from *cearensis* $\rightarrow$ *caerulescens* $\rightarrow$ Andean and bidirectional migrations among all them (complete and incomplete matrix, respectively), without expansion or bottleneck effects affecting their populational size. In addition, the migration rate between the *caerulescens* $\leftrightarrow$ Andean groups is higher than that with *cearensis*. The underlying explanation of these models can be grounded on various hypotheses proposed for the diversification of Neotropical organisms. For example, climatic fluctuations leading to forest retractions and expansions (i.e., Refuge Hypothesis; Haffer, 1969; Vanzolini & Williams, 1970) during the Cenozoic have been a recurrent explanation for diversification of lineages of multiple taxonomic groups (see Richardson *et al.*, 2001; Thomaz *et al.*, 2015; Pérez-Escobar *et al.*, 2017; García-Vázquez *et al.*, 2017; Leal *et al.*, 2018). The formation of refuges during cycles of humid and dry periods in the Quaternary has been described as one of the main mechanisms driving the proliferation of new lineages. For non-Amazonian regions, refuges has been proposed as drivers of differentiation and speciation in some species (Carnaval & Moritz, 2008; Campagna *et al.*, 2012; Ramos *et al.*, 2018; de Oliveira Miranda *et al.*, 2019). Following this reasoning, the early divergence and the high level of differentiation of *cearensis* from the others could be a consequence of the persistence of a refuge in the northeastern Brazil (the Pernambuco refuge, see Carnaval & Moritz, 2008; Carnaval *et al.*, 2009) during the Pliocene-Pleistocene, and the barrier effect of Rio São Francisco (i.e., Riverine Hypothesis; Sick, 1967; Capparella, 1988; Wallace, 1854). This region has been also considered a center of endemism for passerine birds (Silveira *et al.*, 2003; da Silva *et al.*, 2004) and has been represented as a unit separated from the central-southern Atlantic Forest in subsequent works (Batalha-Filho *et al.*, 2013; DaSilva *et al.*, 2015). On the other hand, Carvalho *et al.* (2017) and Maldonado-Coelho *et al.* (2013) showed that in the Atlantic Forests rivers are not efficient primary barriers to

break the migration among populations, with climatic fluctuations ('bioclimatic units' based in altitudinal gradients) having a greater impact on these regions (Carnaval & Moritz, 2008). In the *T. caerulescens* case, it is possible that the São Francisco River currently acts as a secondary barrier, preventing gene flow between the northern and the central/southern Atlantic Forest populations (D'horta *et al.*, 2011; Werneck *et al.*, 2012).

The level of admixture and the migration rate between the *caerulescens* and Andean clusters suggest a recent expansion and a possible incipient differentiation of these populations. It is plausible that, after an expansion period (late Miocene – early Pleistocene, see Prates *et al.*, 2017), these two clusters began to separate due the isolation during the Quaternary, but maintaining considerable amounts of intrapopulational gene flow, and, to a lesser extent, along an Atlantic Forest – Cerrado – Chaco corridor. There are some examples about the connections between the eastern forests in Brazil and the Andes. For example, Batalha-Filho *et al.* (2013) suggests a plausible connection between some species of *Synallaxis* from the central-south Atlantic Forest and the Andes during the Pleistocene. In addition, Trujillo-Arias *et al.* (2017, 2018) shows that there were possible connections between the Atlantic Forest and central Andes during the Pleistocene, possibly through Cerrado and Chaco ecoregions (see Cabanne *et al.*, 2019).

The existence of these corridors are consistent with the Pleistocene Arch Hypothesis (PAH, Prado & Gibbs, 1993; Moggi *et al.*, 2015). The PAH could be invoked to explain these demographic scenarios, wherein a continuum of relatively stable areas of non-Amazonian forests (Seasonally Dry Tropical Forests – SDTFs –) allows the migration and colonization of taxa during the Cenozoic. Under this scenario, *T. caerulescens* could have migrated southward from the territory currently comprised by northeastern Brazil colonizing the Chacoan and central Andean regions during the Quaternary. Climatic cycles during this same period could also have allowed

the posterior isolation of different populations. For example, Florentín *et al.* (2018) suggest that the existence of these connections between areas of SDTFs from the eastern Brazil and the Chacoan region was an important force in the diversification of the plant genus *Galianthe*. However, Arruda *et al.* (2018) concluded that the presence of refugia had a greater effect on the diversification of organisms than the presence of a continuum of forested areas, at least during the last 21 ka. Similarly, Werneck *et al.* (2011) reject the idea of a stable PAH connecting patches of SDTF in those areas known today as the Caatinga, Cerrado and Chaco and proposed an alternative scenario in which such an arch might have existed earlier, either during the Lower Pleistocene or the Tertiary) followed by cycles of fragmentation and secondary expansion during the Holocene. Although our results are inconclusive as to whether such SDTF corridor was present during the Pleistocene or the late Tertiary, they are consistent with the idea of a once continuous population that underwent divergence and subsequent secondary contact during the Pleistocene. In that sense, the idea of refugia in northeastern Brazil (*cearensis*), the forested areas of the Cerrado and the central and southern Atlantic Forest (*caerulescens*) and the Andean-Chacoan regions are consistent with the demographic parameters and population structure of *T. caerulescens*. Further expansion, was possibly affected by the Rio São Francisco and the Rio Paraná, which seem to be playing an a role in maintaining, to some extent, the separation between *cearensis* and *caerulescens* and *caerulescens* and Andean populations, respectively.

A likely scenario for the demographic history of T.caerulescens

The results of our analyses suggests that the history of *T. caerulescens* began in the Late Miocene-Pliocene, with an initial population that originated in the northern Atlantic Forest (Pernambuco

refuge *sensu* Carnaval & Moritz, 2008) and expanded southward during the Pleistocene, thereby colonizing the Cerrado, central and southern Atlantic Forests, the Chaco and the central Andes (Fig. 5b). In this way, while the northern Atlantic Forest populations remained isolated via climatic and geological secondary barriers, the two last groups of populations have maintained intermittent contact due to cycles of retractions and expansions of their habitat during the Pleistocene-Holocene, with a considerable grade of hybridization and polymorphism (phenotypic/genetic clinal variation). This scenario is partially congruent with that proposed by Brumfield & Edwards (2007) for the Variable Antshrike, in which the geographical origin of the species was placed in the ‘lowlands of eastern Brazil’. However, the authors did not have enough power to infer whether those ‘lowlands’ were located in northern, central, or southern portions of eastern Brazil (see Brumfield, 2005). On the other hand, Thomé *et al.* (2010) refute the idea of taxa diverged initially in northern Atlantic Forest with posterior expansion via southward in the Pleistocene using data from some endemic species of toads, with simultaneous presence of central-southern refugia in the Atlantic Forest in the same period of time.

The most intriguing situation regarding the evolutionary history of *T. caerulescens* is related to the patterns and processes driving the outstanding phenotypic differentiation within the the Andean and Chacoan regions. These populations represent an extremely heterogeneous cluster of phenotypically distinct individuals with relatively shallow, albeit somewhat structured, genetic diverences. There is robust evidence of clinal plumage, vocal, and mitochondrial variation (Brumfield, 2005; Isler *et al.*, 2005), but a most intense sampling effort, both geographic and genetic, will be necessary to elucidate the causes of this variation.

Taxonomic considerations

Although this work does not aim at conducting a taxonomic revision of *T. caerulescens*, here we have sufficient information to propose one modification in the taxonomy of the species. The considerable genetic differentiation and geographical isolation of the northern Atlantic forest populations in the species would be sufficient evidence to elevate the subspecies *T. caerulescens cearensis* to species-level status. In addition, the plumage pattern of *cearensis* is diagnosable from that of nominal form, with a ‘*male with less black on crown and upperparts, while the female have a crown rufous, wing-coverts ochraceous olive-brown (edges brightest), tail tinged clay colour, throat pale ochraceous*’ (Zimmer & Isler, 2019). We observed this plumage differentiation in specimens analyzed from the MZUSP (Museu de Zoologia da Universidade de São Paulo, Brazil). A formal taxonomic revision on *Thamnophilus caerulescens* has not been elaborated until now, and we believe that our study represents a starting point for a more in-depth taxonomic analysis on this species.

Final remarks

The lineages identified here for *Thamnophilus caeruleescens* are congruent with the geographical distribution of the species; having an isolate clade from northeastern Atlantic Forests, and other two with high level of admixture, plumage and vocal variation in the central-southern Atlantic Forests (plus eastern Cerrado) and Andes + Chaco. The level of admixture, times of divergence and demographic history support a scenario of recent diversification in the taxon, with climatic fluctuations during the Quaternary as its main influence. Specifically, the isolation of *cearensis* group could be increased by the presence of São Francisco River as a secondary barrier, illustrate an actual process of speciation. In this way, we think that the *cearensis* group (northern Atlantic Forest) has the potential to be considered a full taxonomic species. Finally, the species *T. caeruleescens* needs a complete taxonomic review to corroborate this affirmation.

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Figure 1. (a) Map showing the samples collected of *T. caerulescens* (codes of samples in Table S1.). (b) median-joining network depicting relationships among the haplotypes in *T. caerulescens*.

Figure 2. Demographic models tested in momi2 for the clusters identified for *T. caerulescens*.

Figure 3. (a) Bayesian reconstruction and divergence times for *T. caerulescens*. (b) Clusters identified by DAPC in *T. caerulescens*. (c) Graphical representation of admixture estimates of three clusters in *T. caerulescens*. Estimated admixture coefficients using sNMF using $K = 3$ and $\alpha = 100$ (cross-entropy=0,379352).

Figure 4. (a) Species trees inferred by SNAPP for the *T. caerulea* data. (b) Demographic reconstruction with the best model for the complete matrix of SNPs (324 loci). (c) Demographic reconstruction with the best model for the incomplete matrix of SNPs (2,036 loci).

Figure 5. Plausible scenarios of diversification of *T. caerulescens*, with the migration pulses inferred by momi2. **(a)** Best model in the complete matrix of SNPs (324 loci). **(b)** Best model in the incomplete matrix of SNPs (2,036 loci).

Figure S1a. Graphical representation of all models tested in momi2 (part 1).

Figure S1b. Graphical representation of all models tested in momi2 (part 2).

Figure S2. Topologies reconstructed for the mtDNA data of *T. caeruleus*. (a) Maximum Likelihood in RAxML. (b) Bayesian inference with BEAST.

Figure S3. Clusters identified with the incomplete matrix for *T. caerulescens*. The central Andean samples can be separated in a southern Peru-Bolivia and a central Peru subgroups.

Figure S4. DAPC depicting a clinal pattern in the central Andean samples of *T. caerulescens*. **(a)** Complete matrix. **(b)** Incomplete matrix.

Figure S5. Values of cross-entropy for six values of α (1, 10, 50, 100, 500, 1000). (a) Complete matrix. (b) Incomplete matrix.

Table 1. List of tested models for the complete matrix in *T. caerulescens*.

Model number	Log likelihood	Number parameters model	AICs	Delta AIC	Weight AICs
Model 1	-1258.51153	2	2521.023061	44.1059732	2.65E-10
Model 2	-1249.760663	5	2509.521326	32.60423837	8.32E-08
Model 3	-1252.647448	5	2515.294896	38.37780816	4.64E-09
Model 4*	-1229.458544	9	2476.917088	0	1
Model 5	-1240.297117	9	2498.594234	21.67714629	1.96E-05
Model 6	-1235.112871	9	2488.225743	11.30865505	0.003502328
Model 7	-1225.937369	13	2477.874737	0.957649748	0.619510968
Model 8	-1252.889427	11	2527.778853	50.86176583	9.03E-12
Model 9	-1266.947654	11	2555.895309	78.97822097	7.08E-18
Model 10	-1243.957441	16	2519.914881	42.99779359	4.60E-10
Model 11	-1247.822782	16	2527.645565	50.72847734	9.65E-12
Model 12	-1273.973514	11	2569.947027	93.02993993	6.29E-21
Model 13	-1255.509493	16	2543.018986	66.10189838	4.43E-15
Model 14	-1284.761711	11	2591.523422	114.6063348	1.30E-25
Model 15	-1293.999998	11	2609.732288	132.8152009	1.44E-29
Model 16	-1293.866144	11	2609.732288	132.8152009	1.44E-29

* Chosen model.

Table 2. List of tested models for the incomplete matrix in *T. caerulescens*.

Model number	Log likelihood	Number parameters model	AICs	Delta AIC	Weight AICs
Model 1	-7481.577811	2	14967.15562	392.1354344	7.06E-86
Model 2	-7383.252541	5	14776.50508	201.4848944	1.77E-44
Model 3	-7386.643388	5	14783.28678	208.2665891	5.96E-46
Model 4	-7323.523233	9	14665.04647	90.02627891	2.83E-20
Model 5	-7345.247239	9	14708.49448	133.4742895	1.04E-29
Model 6	-7299.864124	9	14617.72825	42.70805956	5.32E-10
Model 7*	-7274.510094	13	14575.02019	0	1
Model 8	-7574.598842	11	15171.19768	596.1774969	3.48E-130
Model 9	-7528.523218	11	15079.04644	504.026249	3.57E-110
Model 10	-7388.482618	16	14808.96524	233.9450474	1.58E-51
Model 11	-7394.500327	16	14821.00065	245.9804667	3.85E-54
Model 12	-7522.21469	11	15066.42938	491.4091924	1.96E-107
Model 13	-7394.482314	16	14820.96463	245.9444395	3.93E-54
Model 14	-7807.853685	11	15637.70737	1062.687182	1.74E-231
Model 15	-7621.885811	19	15281.77162	706.7514342	3.40E-154
Model 16	-7724.954811	11	15471.90962	896.8894352	1.75E-195

Table S1. Samples collected of *T. caerulescens* for this study.

Code in Graphics	Voucher	Taxon	State	Country	Locality	UCEs
1	ALG-014	<i>Thamnophilus caerulescens</i>	Alagoas	Brazil	AL, São José da Lage, Usina Serra Grande	
2	ALG-020	<i>Thamnophilus caerulescens</i>	Alagoas	Brazil	AL, São José da Lage, Usina Serra Grande	YES
3	ALG-053	<i>Thamnophilus caerulescens</i>	Alagoas	Brazil	AL, São José da Lage, Usina Serra Grande	
4	ALG-080	<i>Thamnophilus caerulescens</i>	Alagoas	Brazil	AL, São José da Lage, Usina Serra Grande	YES
5	ALG-085	<i>Thamnophilus caerulescens</i>	Alagoas	Brazil	AL, São José da Lage, Usina Serra Grande	YES
6	ALG-086	<i>Thamnophilus caerulescens</i>	Alagoas	Brazil	AL, São José da Lage, Usina Serra Grande	YES
7	ALG-102	<i>Thamnophilus caerulescens</i>	Alagoas	Brazil	AL, São José da Lage, Usina Serra Grande	YES
8	MZ 82619	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	Cunha, estrada para o Parque Estadual	
9	MZ 82637	<i>Thamnophilus caerulescens</i>	Minas Gerais	Brazil	Itamonte	YES
10	MZ 91196	<i>Thamnophilus caerulescens</i> <i>gilvigaster</i>	Santa Catarina	Brazil	Nova Trento	YES
11	MZ 91197	<i>Thamnophilus caerulescens</i> <i>gilvigaster</i>	Santa Catarina	Brazil	Nova Trento	YES
12	MZ 91661	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	Angatuba, Fazenda Entre Rios	YES
13	MZ 91755	<i>Thamnophilus caerulescens</i>	Minas Gerais	Brazil	Passa Tempo, Fazenda Ribeirão das Cachoeiras	
14	MZ 93176	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	Estação Biológica de Boracéia, Salesópolis	YES
15	MZ 96752	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	Campos do Jordão, Fazenda Prana	
16	MZ 96753	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	Campos do Jordão, Fazenda Prana	
17	MZ 96754	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	Campos do Jordão, Fazenda Prana	
18	MZ 96755	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	Campos do Jordão, Fazenda Prana	
19	FRA 258*	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	Delfim Moreira (8 Km SE)	

Code in Graphics	Voucher	Taxon	State	Country	Locality	UCEs
20	KU 3195	<i>Thamnophilus caerulescens</i>	Alto Paraguay	Paraguay	Bahia Negra, 14 km W, Estancia Triunfo	YES
21	KU 3700	<i>Thamnophilus caerulescens</i>	Itapua	Paraguay	San Rafael N.P., San Pedro Mi	YES
22	KU 3721	<i>Thamnophilus caerulescens</i>	Caazapa/Itapua	Paraguay	San Rafael N.P., Parabel	YES
23	KU 21634	<i>Thamnophilus caerulescens</i>	Puno	Peru	above San Juan del Oro	
24	KU 21654	<i>Thamnophilus caerulescens</i>	Puno	Peru	above San Juan del Oro	YES
25	ML 2030*	<i>Thamnophilus caerulescens</i>	Minas Gerais	Brazil	Patrocinio	YES
26	ML 2031*	<i>Thamnophilus caerulescens</i>	Goiás	Brazil	Cristalina	YES
27	BOR-14-32	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	Estação Biológica de Boracéia	
28	ML 2032*	<i>Thamnophilus caerulescens</i>	Minas Gerais	Brazil	Patrocinio	
29	MCP 3306	<i>Thamnophilus caerulescens</i>	Rio Grande do Sul	Brazil	São Gabriel	YES
30	MCP 4053	<i>Thamnophilus caerulescens</i>	Rio Grande do Sul	Brazil	Jaquirana	
31	MCP 4843	<i>Thamnophilus caerulescens</i>	Santa Catarina	Brazil	São Bonifácio	YES
32	MPEG T14940	<i>Thamnophilus caerulescens</i>	Santa Catarina	Brazil	Pomerode, Morro da Turquia	YES
33	MPEG T14991	<i>Thamnophilus caerulescens</i>	Santa Catarina	Brazil	Caçador, Linha São Francisco	
34	MPEG T15207	<i>Thamnophilus caerulescens</i>	Pernambuco	Brazil	Barreiros, Engenho Cachoeira Linda (08o48'S;35o19'W)	
35	MPEG T15691	<i>Thamnophilus caerulescens</i>	Minas Gerais	Brazil	Fazenda Princesa da Serra, Córrego do Mota, Serra Azul, Itatiaiuçu	YES
36	MPEG T15720	<i>Thamnophilus caerulescens</i>	Minas Gerais	Brazil	Barragem de rejeito da USIMINAS, Serra Azul, Itatiaiuçu	
37	MPEG T15783	<i>Thamnophilus caerulescens</i>	Minas Gerais	Brazil	Barragem de rejeito da USIMINAS, Serra Azul, Itatiaiuçu	
38	BO513 EU295759**	<i>Thamnophilus caerulescens</i>	Minas Gerais	Brazil	Araponga	
39	FMNH 395426	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	Boraceia	
40	LSUB 1684	<i>Thamnophilus caerulescens</i>	Pasco	Peru	Santa Cruz; about 9 km SSE Oxapampa	

Code in Graphics	Voucher	Taxon	State	Country	Locality	UCEs
41	LSU 38284	<i>Thamnophilus caerulescens</i>	Santa Cruz	Bolivia	La Pajcha, 28 km S Samaipata;	
42	MPEG CPEII037	<i>Thamnophilus caerulescens</i>	Pernambuco	Brazil	Barreiros, Engenho Cachoeira Linda (08o48'S;35o19'W)	YES
43	MZ 81155	<i>Thamnophilus caerulescens</i>	São Paulo	Brazil	E. E. Bananal, Bananal	
44	MZ 84352	<i>Thamnophilus caerulescens</i>	Santa Catarina	Brazil	SC-407, Rancho Queimado	
45	UWBM 77213	<i>Thamnophilus caerulescens</i>	Tarija	Bolivia	Entre Rios, O'connor	YES
46	UWBMRTB 407	<i>Thamnophilus caerulescens</i>	Cochabamba	Bolivia	Provincia de Chapare, San Onofre	
47	YPM 10106 KJ 810434	<i>Thamnophilus caerulescens</i>	Artigas	Argentina	Artigas	
48	LSUMZ 105988	<i>Thamnophilus caerulescens melanochrous</i>	Pasco	Peru	Santa Cruz; about 9 km SSE Oxapampa	YES
49	LSUMZ 171295	<i>Thamnophilus caerulescens paraguayensis</i>	Santa Cruz	Bolivia	Santa Cruz, Prov. Cordillera, 38.4 km E Abapo, 18 degrees 44' 48" S, 63 degrees 04' 06" W	YES
50	LSUMZ 168944	<i>Thamnophilus caerulescens connectens</i>	Santa Cruz	Bolivia	Santa Cruz, La Chuchial	YES
51	LSUMZ 170871	<i>Thamnophilus caerulescens subandinus</i>	Loreto	Peru	Ca. 80 km SE Juanjui on E. bank upper Río Pauya	YES
52	LSUMZ 179678	<i>Thamnophilus caerulescens aspersiventer</i>	Puno	Peru	Abra de Maruncunea, 14 degrees 12' S, 69 degrees 13' W	YES
53	MZUSP 81155	<i>Thamnophilus caerulescens caerulescens</i>	São Paulo	Brazil	E. E. de Bananal, Bananal	YES
54	MZ 81269	<i>Thamnophilus aethiops incertus</i>	Maranhão	Brazil	Açailândia, Fazenda Itabaiana	YES
55	MZ 93741	<i>Thamnophilus aethiops polionotus</i>	Roraima	Brazil	Caracará, rio Jufari, Igarapé Caicubi, Trilha Paraguai, Sitio do Valdir	YES
56	J 1799*	<i>Thamnophilus aethiops injunctus</i>	Rondônia	Brazil	JIRAU, margen esquerda Rio Madeira, Caiçara T1P2	YES
57	FMNH 399223	<i>Thamnophilus aethiops</i>	Alagoas	Brazil	Ibateguara, Engenho Coimbra, Usina Serra Grande	
58	MPEG 62216	<i>Thamnophilus aethiops</i>	Amazonas	Brazil	Juruti, Base Capiiranga	

* Field number

** Genebank code access

Table S2. Cross-entropy values for *T. caeruleus* ($\alpha=1, 10, 50, 100, 500, 1000$).

Alpha=1	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.41463	0.37810	0.37439	0.38679	0.40498	0.40998	0.42651	0.43924	0.46538	0.46480	0.488458	0.5041613	0.37439	0.37810	0.00370
mean	0.46818	0.43040	0.42527	0.43747	0.45027	0.46680	0.48686	0.50796	0.52824	0.54831	0.5722283	0.5980912	0.42527	0.43040	0.00513
max	0.51230	0.47448	0.47385	0.49359	0.50404	0.52809	0.56818	0.57198	0.62220	0.63828	0.660845	0.6886311	0.47385	0.47448	0.00063
Alpha=10	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.42668	0.38206	0.37474	0.39066	0.38981	0.41915	0.41590	0.43532	0.45610	0.49724	0.5225096	0.5146925	0.37474	0.38206	0.00732
mean	0.46730	0.42947	0.42333	0.43588	0.44978	0.46952	0.48733	0.50797	0.53013	0.54987	0.5744045	0.5983819	0.42333	0.42947	0.00614
max	0.51302	0.47696	0.50495	0.50696	0.51499	0.53598	0.53778	0.57670	0.62257	0.63576	0.7052284	0.6887136	0.47696	0.50495	0.02799
Alpha=50	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.42023	0.38590	0.37785	0.38267	0.38716	0.42027	0.41344	0.45151	0.46307	0.49679	0.4992932	0.5330865	0.37785	0.38267	0.00482
mean	0.46999	0.43371	0.42788	0.44203	0.45580	0.47623	0.49685	0.51848	0.53777	0.56201	0.5846736	0.6082007	0.42788	0.43371	0.00583
max	0.51047	0.46892	0.49179	0.49246	0.52463	0.53898	0.54475	0.59322	0.59113	0.65335	0.6883291	0.7150304	0.46892	0.49179	0.02287
Alpha=100	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.41976	0.38379	0.37935	0.38487	0.39180	0.40879	0.43221	0.46163	0.48039	0.49214	0.5288857	0.5362145	0.37935	0.38379	0.00443
mean	0.46993	0.43360	0.42808	0.44140	0.45668	0.47602	0.49718	0.52316	0.53976	0.56591	0.5922528	0.6147111	0.42808	0.43360	0.00552
max	0.51528	0.48304	0.48267	0.50933	0.50896	0.54028	0.55194	0.59271	0.62097	0.65933	0.7248343	0.6998336	0.48267	0.48304	0.00037
Alpha=500	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.41880	0.38092	0.38137	0.39765	0.40557	0.44746	0.44972	0.50243	0.50964	0.53512	0.5661571	0.5901958	0.38092	0.38137	0.00045
mean	0.46720	0.43245	0.43261	0.44980	0.47214	0.49230	0.52136	0.54960	0.57662	0.60627	0.6349305	0.6638951	0.43245	0.43261	0.00016
max	0.53756	0.50182	0.50858	0.52420	0.54205	0.57109	0.62757	0.60047	0.65621	0.68353	0.7254975	0.7601563	0.50182	0.50858	0.00675
Alpha=1000	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.43014	0.39367	0.39913	0.40786	0.43649	0.45183	0.48806	0.50107	0.50813	0.55429	0.5805905	0.596142	0.39367	0.39913	0.00546
mean	0.46897	0.43501	0.43493	0.45501	0.47874	0.51062	0.53522	0.56459	0.59446	0.62411	0.6530534	0.6837274	0.43493	0.43501	0.00008
max	0.52614	0.48990	0.48405	0.52469	0.54719	0.60167	0.60715	0.64636	0.66495	0.73103	0.7408487	0.7669721	0.48405	0.48990	0.00586

Table S3. Group membership in samples of UCEs of *T. caerulea* (complete matrix).

Clusters	<i>cearensis</i>	<i>caerulea</i>			Andean			
Samples/Subspecies*	<i>cearensis</i>	<i>caerulea</i>	<i>gilviger</i>	<i>ochraceiventer</i>	<i>paraguayensis</i>	<i>dinellii</i>	<i>aspersiventer</i>	<i>melanochrous</i>
O002_Tha_cae_ALG_020_BR_AL	1	0	0	0	0	0	0	0
O006_Tha_cae_ALG_080_BR_AL	1	0	0	0	0	0	0	0
O007_Tha_cae_ALG_085_BR_AL	1	0	0	0	0	0	0	0
O008_Tha_cae_ALG_086_BR_AL	1	0	0	0	0	0	0	0
O010_Tha_cae_ALG_102_BR_AL	1	0	0	0	0	0	0	0
O032_Tha_cae_MZ_82637_BR_MG	0	0.452	0.547	0	0	0	0	0
O078_Tha_cae_MZ_91196_BR_SC	0	0.591	0.397	0.012	0	0	0	0
O079_Tha_cae_MZ_91197_BR_SC	0	0.311	0.689	0	0	0	0	0
O097_Tha_cae_MZ_91661_BR_SP	0	0.67	0.295	0.035	0	0	0	0
O134_Tha_cae_MZ_93176_BR_SP	0	0.76	0.226	0.014	0	0	0	0
O214_Tha_cae_KU_3195_PA_ALT	0	0	0	0	0.869	0.13	0	0
O216_Tha_cae_KU_3700_PA_ITA	0	0.752	0.242	0.006	0	0	0	0
O217_Tha_cae_KU_3721_PA_CAA_ITA	0	0.691	0.221	0.088	0	0	0	0
O230_Tha_cae_KU_21654_PE_PU	0	0	0	0	0	0	0.708	0.292
O272_Tha_cae_ML_2030_BR_MG	0	0.693	0.303	0.005	0	0	0	0
O273_Tha_cae_ML_2031_BR_G0	0	0.332	0.109	0.56	0	0	0	0
O288_Tha_cae_MCP_3306_BR_RS	0	0.695	0.304	0.001	0	0	0	0
O299_Tha_cae_MCP_4843_BR_SC	0	0.721	0.215	0.064	0	0	0	0
O349_Tha_cae_MPEG_T14940_BR_SC	0	0.343	0.653	0.005	0	0	0	0
O390_Tha_cae_MPEG_T15691_BR_MG	0	0.71	0.29	0	0	0	0	0
O450_Tha_cae_MPEG_CPEII037_BR_PE	1	0	0	0	0	0	0	0
O453_Tha_cae_UWBM_77213_B0_TJ	0	0	0	0	0.046	0.954	0	0
O603_Tha_cae_LSUMZ_105988_PE_PAS	0	0	0	0	0	0	0.328	0.672
O604_Tha_cae_LSUMZ_171295_B0_SaC	0	0	0	0	0.897	0.103	0	0
O605_Tha_cae_LSUMZ_168944_B0_SaC	0	0	0	0	0.024	0.976	0	0
O606_Tha_cae_LSUMZ_170871_PE_L0	0	0	0	0	0	0	0	1
O607_Tha_cae_LSUMZ_179678_PE_PU	0	0	0	0	0	0	0.964	0.036
O608_Tha_cae_MZUSP_81155_BR_SP	0	0.51	0.471	0.018	0	0	0	0

Table S4. Group membership in samples of UCEs of *T. caeruleascens* (incomplete matrix).

Clusters	<i>cearensis</i>	<i>caeruleascens</i>			Andean			
Samples/Subspecies*	<i>cearensis</i>	<i>caeruleascens</i>	<i>gilvigaster</i>	<i>ochraceiventer</i>	<i>paraguayensis</i>	<i>dinellii</i>	<i>aspersiventer</i>	<i>melanochrous</i>
O002_Tha_cae_ALG_020_BR_AL	1	0	0	0	0	0	0	0
O006_Tha_cae_ALG_080_BR_AL	1	0	0	0	0	0	0	0
O007_Tha_cae_ALG_085_BR_AL	1	0	0	0	0	0	0	0
O008_Tha_cae_ALG_086_BR_AL	1	0	0	0	0	0	0	0
O010_Tha_cae_ALG_102_BR_AL	1	0	0	0	0	0	0	0
O032_Tha_cae_MZ_82637_BR_MG	0	0.934	0.065	0	0	0	0	0
O078_Tha_cae_MZ_91196_BR_SC	0	0.732	0.239	0.028	0	0	0	0
O079_Tha_cae_MZ_91197_BR_SC	0	0.038	0.962	0	0	0	0	0
O097_Tha_cae_MZ_91661_BR_SP	0	0.742	0.257	0.001	0	0	0	0
O134_Tha_cae_MZ_93176_BR_SP	0	0.98	0.017	0.002	0	0	0	0
O214_Tha_cae_KU_3195_PA_ALT	0	0	0	0	0.923	0.077	0	0
O216_Tha_cae_KU_3700_PA_ITA	0	0.288	0.709	0.003	0	0	0	0
O217_Tha_cae_KU_3721_PA_CAA_ITA	0	0.429	0.57	0.001	0	0	0	0
O230_Tha_cae_KU_21654_PE_PU	0	0	0	0	0	0	1	0
O272_Tha_cae_ML_2030_BR_MG	0	0.345	0.011	0.644	0	0	0	0
O273_Tha_cae_ML_2031_BR_GO	0	0.346	0.019	0.635	0	0	0	0
O288_Tha_cae_MCP_3306_BR_RS	0	0.38	0.62	0	0	0	0	0
O299_Tha_cae_MCP_4843_BR_SC	0	0.281	0.715	0.004	0	0	0	0
O349_Tha_cae_MPEG_T14940_BR_SC	0	0.368	0.629	0.003	0	0	0	0
O390_Tha_cae_MPEG_T15691_BR_MG	0	0.949	0.01	0.042	0	0	0	0
O450_Tha_cae_MPEG_CPEH037_BR_PE	1	0	0	0	0	0	0	0
O453_Tha_cae_UWBM_77213_B0_TJ	0	0	0	0	0.238	0.762	0	0
O603_Tha_cae_LSUMZ_105988_PE_PAS	0	0	0	0	0	0	0	1
O604_Tha_cae_LSUMZ_171295_B0_SaC	0	0	0	0	0.932	0.068	0	0
O605_Tha_cae_LSUMZ_168944_B0_SaC	0	0	0	0	0	1	0	0
O606_Tha_cae_LSUMZ_170871_PE_L0	0	0	0	0	0	0	0	1
O607_Tha_cae_LSUMZ_179678_PE_PU	0	0	0	0	0	0	1	0
O608_Tha_cae_MZUSP_81155_BR_SP	0	0.364	0.631	0.005	0	0	0	0

Chapter II

Comparative phylogeography of passerine birds with a circum- Amazonian distribution

Comparative phylogeography of passerine birds with a circum-Amazonian distribution

Abstract

There are a number of common distributional patterns that have provided the foundations of our current knowledge of Neotropical biogeography. A distinctive pattern is the so-called “circum-Amazonian distribution”, which expands across the forested lowlands south and east of Amazonia, the Andean foothills, the Venezuelan Coastal Range, and the Tepuis. To date, there is no clear understanding of the processes giving rise to this distribution. To understand the evolutionary history of taxa exhibiting this pattern it is necessary to test biogeographic hypotheses offering mechanistic explanations. Comparative phylogeography allows more accurate phylogeographic hypotheses for these taxa, as well as better population genetic parameters. Comprehensive comparative studies aiming at unraveling the evolutionary and biogeographic mechanisms underlying the circum-Amazonian distribution have not been conducted yet, and only scarce descriptive information has been published. Therefore, the objective of this work was to elucidate the historical and biogeographic mechanisms underpinning circum-Amazonian distribution by performing comparative genomic analyses of a group of Suboscine passerines. Ultraconserved Elements (UCEs) were obtained for eight taxonomic groups to estimate population parameters and genealogical trees. For the *Thamnophilidae* species were inferred demographic histories with *moments*. The best models of each taxon were analyzed in a comparative framework to relate them with previously proposed biogeographic hypotheses for the Neotropics and to propose plausible biogeographical scenarios for the circum-Amazonian pattern. The circum-Amazonian distributional pattern has two main phylogeographic units: an Andean (plus Central America

region) and an eastern-forested region (Atlantic Forest ecoregion, forested areas around southeast of Amazonia), interconnected by a northern and southern corridor, allowing biotic interchanges between them (mainly from the southern) and hybridization. Species-tree analyses recovered (a) an Andean clade with two Andean subgroups in the northern Peru and central Andes, and (b) an eastern-forested clade including northern and central/southern Atlantic Forest subgroups. The demographic histories of the *Thamnophilidae* taxa suggest that diversification of the circum-Amazonian taxa have a strong influence of climatic fluctuations during the Pleistocene, with interconnected refugia allowing phenotypic/genetic differentiation but maintaining a considerable level of gene flow during varying dry/cool and warm/humid periods. In addition, the results of this work opened interesting taxonomic questions about some taxa that could be covered in the future (*T. ruficapillus/torquatus* complex, *Xiphocolaptes* complex).

Introduction

A major breakthrough in the understanding of earth's biodiversity is the different evolutionary, biogeographical, and environmental processes affecting the distribution of the species and the response to these processes (Darlington, 1959). In this sense, it is expected that species with similar geographical distributions would have also common history of processes/events molding their habitats (Humphries & Parenti, 1999). Relatively new groups of analysis were developed in order to identify and understand the relationship between co-distributed species and the biogeographical/evolutionary processes affecting them, called as Comparative Phylogeography (CP) (Arbogast & Kenagy, 2001; Hickerson *et al.*, 2010). The main objective of CP is to search for concordant splits within contemporaneous, co-distributed species (Bermingham & Avise, 1986). In this framework, the level of "phylogeographic congruence is a measure of the historical stability of the current species assemblage" (Zink, 2002), namely, a particular evolutionary reconstruction (a hypothesis) on co-distributed species affected by similar climatic/geological events would be more 'supported' while more individuals phylogeographic patterns being congruent. The CP has been applied in the study of multiple co-distributed taxa (Barker *et al.*, 2015; Potter *et al.*, 2017), mainly in areas of interest as the Neotropics (Françoso *et al.*, 2016; Rincon-Sandoval *et al.*, 2019; Sartorato Zanchetta *et al.*, 2019).

As proved by several studies, the Neotropical biomes and ecosystems exhibit high biodiversity and a wide range of ecological/geological characteristics (Myers *et al.*, 2000; Rull, 2011; Richardson & Pennington, 2016; Dinerstein *et al.*, 2017). In this way, extensive work has been developed to explain and understand this high diversity in the Neotropics, as the processes involved in that phenomenon, arising a varying number of hypotheses, based in both theoretical

and empirical approaches (e.g. Sick, 1967; Haffer, 1969; Vuilleumier, 1971; Brown, 1979; Cracraft, 1985; Hooghiemstra & van der Hammen, 1998; Garzón-Orduña *et al.*, 2014). These hypotheses cover proposals from ecological perspectives like the Gradient Hypothesis (Endler, 1982) to those based on geographical isolation as Refuges (Haffer, 1969; Vanzolini & Williams, 1970) and Rivers (see Wallace, 1854; Sick, 1967), and Paleogeographic ones as the Arch and the Lagoon Hypotheses (Patton & Silva, 1997; Marroig & Cerqueira, 1997). All these hypotheses have been subject to wide discussion, and several tests have been implemented to corroborate or refute their assumptions (Mayr & O'Hara, 1986; Salo, 1987; Nores, 1999; Loughheed *et al.*, 1999; Colinvaux *et al.*, 2000; Haffer, 2008; FernAndes *et al.*, 2012; Maldonado-Coelho *et al.*, 2013; Garzón-Orduña *et al.*, 2015; Rocha & Kaefer, 2019, among others).

Despite the large variety of proposed evolutionary and biogeographic mechanisms intended to explain Neotropical diversity, our understanding remains scarce for some of these patterns. For instance, a considerable number of birds are distributed in the surroundings of the Amazonia but they are absent in the Amazonia itself (Remsen *et al.*, 1991; Bates, 1997; Lovette, 2004), and there is no clear understanding of the mechanisms involved in that kind of distributions. Such distributional pattern is known as “circum-Amazonian distribution” (Figure 1) and is characterized by the presence of phylogenetically related groups mainly in “(a) montane forested areas on the humid slopes of the Andes and the Coastal Range of Venezuela or the Tepui region; and in (b) lowland forested areas south and east of the lowland forests of Amazonia” (Remsen *et al.*, 1991). Remsen *et al.* (1991), in the first study describing the circum-Amazonian pattern, described that species as *Platyrinchus mystaceus*, *Hemitriccus* spp., *Dysithamnus mentalis*, *Phyllomyias burmeisteri*, and *Elaenia albiceps*, *E. parvirostris*, and *E. obscura*, among others, share this distributional pattern. Subsequent works have identified other taxa as circum-

Amazonian. Bates (1997) stated that two species of *Tiaris*, *T. obscura* and *T. fuliginosa*, have a geographical distribution congruent with the proposed by Remsen *et al.* (1991). More examples of species exhibiting this circum-Amazonian pattern were presented by Lovette (2004) in the case of *Phaeothlypis* and by Batalha-Filho *et al.* (2013) in *Synallaxis ruficapilla* and *S. moesta*. Additionally, some species of *Cercomacra* (*C. melanaria*, *C. ferdinandi*, *C. carbonaria*, and the *C. nigricans* complex) and *Tangara cayana* fit partially into this distributional pattern (see Tello *et al.*, 2014; Savit & Bates, 2015). There are also examples in non-passerines such as the genus *Pionus*, in which the *sordidus-maximiliani* complex seem to exhibit complementary geographical ranges resulting in a circum-Amazonian distribution (see Ribas *et al.*, 2007). Moreover, the circum-Amazonian distribution pattern was identified in other non-avian groups such as some insects (references related to insects) and plants (references related to plants) (e.g. Prado & Gibbs, 1993; Erwin, 2000; Canals & Johnson, 2000; Knapp, 2002; Irmeler, 2009). Nevertheless, whereas the diversity and distribution patterns in adjacent Neotropical regions have been the focus of several studies, this complex pattern of distribution has not received enough attention, and the events and evolutionary processes behind it have not been thoroughly revealed.

Here, we implemented a comparative phylogeographic approach to infer common evolutionary histories from eight taxa of Passeriformes with circum-Amazonian distribution, using genomic information from Ultraconserved Elements (UCEs, Bejerano *et al.*, 2004). The UCEs are highly conserved genomic sequences that allow the use of a large set of universal markers to infer relationships among lineages (Faircloth *et al.*, 2012; Faircloth *et al.*, 2015), and they can be used to estimate demographic and population parameters (Smith *et al.*, 2013; Zarza *et al.*, 2018; Myers *et al.*, 2019; Oswald *et al.*, 2019). We estimated the populational parameters and demographic history for each species, followed by the comparative analysis of their evolutionary histories.

Lastly, we proposed plausible scenarios in order to explain the formation of this distributional pattern based mainly in the proposed hypotheses of diversification for the Neotropics.

Methods

Analyzed taxa and sampling efforts

We used samples from eight taxonomic groups with a circum-Amazonian distributional pattern (see Table 1). These were: 1) *Platyrinchus mystaceus* (Tyrannidae); 2) the complex *Xiphocolaptes albicollis*, *X. falcistrostris*, *X. promeropirhynchus* and *X. major* (Dendrocolaptidae) 3) *Philydor rufum* and 4) *Lochmias nematura* (Furnariidae); 5) the complexes *Thamnophilus palliatus*/*T. tenuepunctatus*; and 6) *Thamnophilus ruficapillus*/*T. torquatus*, 7) *Dysithamnus mentalis* and 8) *Thamnophilus caerulescens* (Thamnophilidae).

We gathered samples from ornithological collections in Brazil and the USA (see Table 2). In total, we included 602 vouchered tissue samples. Our sampling covered the majority of the species geographic ranges, but samples from the northernmost region of the Northern Andes (the montane-forested areas of the Colombian Andes and the Coastal Range of Venezuela and the Tepuis) were missing for some species (see Table S1).

DNA extraction

We extracted total genomic DNA from muscle tissues using the PureLink® Genomic DNA Mini kit (Invitrogen Inc.). We quantified genomic DNA concentrations using a Qubit 2.0 fluorometer (Life Technologies, Inc.). We sent at least 1,000 ng of genomic DNA for each sample (301 samples) to Rapid Genomics (Gainesville, FL). Libraries were enriched from 2,386 UCE loci that targeted a set of 2,560 probes (Faircloth *et al.*, 2012, Tetrapods-UCE-2.5K version 1; Microarray,

Ann Arbor, MI), following an open-source protocol (available at www.ultraconserved.org). Samples were multiplexed at 192 samples per lane on a 125 bp paired-end Illumina HiSeq 2500 run, yielding an average coverage of 18.66X per sample.

Mitochondrial DNA

As a preliminary assessment of population structure for each complex, we sequenced the mitochondrial gene NADH dehydrogenase 2 (ND2) for all individuals of each species and at least three individuals of their respective outgroups (see Table S2). We amplified and sequenced ND2 using standard PCR and Sanger sequencing protocols described elsewhere (Brumfield *et al.*, 2007). We edited sequences and checked that they did not include stop codons or anomalous residues using Geneious v. 11.1.4 (www.geneious.com, Kearse *et al.* 2012). We aligned sequences with the MAFFT v.7 multiple alignment plugin (Katoh & Standley, 2013) implemented in Geneious. We will be deposited the newly obtained sequences in GenBank (Accession numbers XXXXX-XXXXXX).

We built a Median Joining Network – MJN – haplotype network (Bandelt *et al.*, 1999) implemented in POPART (Leigh & Bryant, 2015). Outgroup samples and short ingroup sequences (<700 bp) were excluded from the analysis and the matrix was trimmed to exclude any positions containing missing data (see Supplementary Material, Table S1). We selected the best substitution model for each species (see Table 3) using the corrected Akaike Information Criterion (AICc; Hurvich and Tsai 1989) implemented in jModeltest2 (Darriba *et al.*, 2012) on the Cipres Science Gateway V 3.3 (Miller *et al.*, 2010). We estimated a time-calibrated gene tree within a Bayesian framework implemented in the program BEAST2 v2.4.4 (Bouckaert *et al.* 2014). Based on the

avian mtDNA substitution rate of 2.1%/My (Weir & Schluter, 2008), we used a lognormal relaxed molecular clock with a mean rate of 0.0105 for mtDNA. We used a Coalescent Constant Population prior with no restrictions on tree shape and a randomly generated tree as a starting tree. We ran analyses for a total of 50 million generations with a sampling frequency of 1,000. We determined that replicate analyses converged (effective sample size values > 400) using Tracer 1.7.1 (Rambaut *et al.* 2018). Using TreeAnnotator v2.4.4 (Drummond *et al.* 2012, Bouckaert *et al.* 2014) and a burn-in of 30%, we estimated a posterior distribution of topologies and the maximum clade credibility (MCC) tree.

Edition and assembly of UCEs

We followed the Phyluce pipeline (Faircloth, 2016, <https://github.com/faircloth-lab/phyluce>) to process the raw sequences of the UCEs sequenced. Initially, Illumiprocessor 2.0.7 (Faircloth, 2013) and Trimmomatic 0.32 (Bolger *et al.*, 2014) were implemented to trim adapters, barcodes and low quality regions. We used Trinity 2.0.6 (Grabherr *et al.*, 2011) to perform the assembly (script *phyluce_assembly_assemblo_trinity*). To avoid including markers of different ploidy, we identified, extracted, and removed Z-linked UCEs from the assemblies using Blast 2.7.7 (see Altschul *et al.*, 1990; Camacho *et al.*, 2009). Finally, we implemented the script *phyluce_assembly_match_contigs_to_probes* to match the assembled contigs to the UCE probes (uce-2.5k-probes.fasta). The results were exported in a *fasta format.

SNP calling

For each species, we extracted Single Nucleotide Polymorphisms (SNPs) from the UCE alignments using the methods described by Harvey *et al.* (2016), which are largely based on Phyluce (Faircloth, 2016). We extracted SNPs following two approaches using the script *phyluce_assembly_match_counts*. The first one yielded a 100% complete matrix with no missing data for any individual in all loci, and the second one yielded an incomplete matrix including all data matching the target loci.

First, we created a *fasta file with the loci extracted from the complete matrix of each species (*phyluce_assembly_explode_get_fastas_file*), and we chose a reference from the sequences analyzed; estimating the coverage and the mean length of recovered contigs (script *phyluce_assembly_get_trinity_coverage*, and *phyluce_assembly_get_fasta_lengths*). Secondly, we used bwa 0.7.7 (Li & Durbin, 2009) to map raw reads from the samples for each species with their respective reference (Li, 2013), Samtools 0.1.19 (Li *et al.*, 2009) and Picard (<http://broadinstitute.github.io/picard/>) to create *bam files, mark duplicates from the PCRf and prepare the files to the next phase. We used the GATK 3.8.0 (McKenna *et al.*, 2010) to extract the indels, SNPs, and do the phasing of sequences. The *vcf files created were exported in other formats to posterior demographic analyzes. Finally, we filter the loci in the complete and incomplete *vcf selecting one random SNP per locus from the biallelic SNPs recovered in each file (script *randSnps.pl*). In the end, we have two SNPs datasets (matrices), one complete and incomplete by each species. We implemented all the analysis in this work on the two matrices to compare the results in each of them. The complete matrices with few (<300 loci by matrix) or zero loci extracted were excluded from the demographic analyses (see Table 4).

Population structure

We inferred population structure from the SNPs matrices for each species using two multivariate approaches; a Principal Components Analysis – PCA – with the R packages *adeigenet*/*ape* (Jombart, 2008 and Paradis *et al.*, 2004), and a coefficients of mixture analyses with sNMF in the R package *LEA* (Frichot *et al.*, 2014, Frichot & François, 2015). The sNMF analyses were implemented with the following parameters; five α values (10, 50, 100, 500, 1000), K values of 1 to 10 (K = 1:10), and 100 runs per K value, and the minimum cross-entropy as TRUE to estimate the best number of K. In the same way, we implemented a Discriminant Analysis of Principal Components – DAPC – (Jombart *et al.*, 2010) within *adeigenet* package recovering PCs with 80% of variance, and a maximum of 10 groups.

Species trees and gene trees

We ran three million iterations in SNAPP (Bryant *et al.*, 2012) in two runs to identify the relationships among the clusters recovered in the PCA/sNMF analyzes using the SNPs extracted from the UCEs for each species. We evaluated the ESS values of the runs with Tracer 1.7.1 (Rambaut *et al.*, 2018), merges the runs with *logcombiner*, and visualizes the topology with *densitree* to (programs from BEAST).

Demographic history

For the species with an optimal sampling effort, we used the software *mom2* to infer possible demographic scenarios for each species. *mom2* used an SFS file that can be obtained from the SNPs extracted from the UCEs to infer demographic histories by fitting the observed value of the SFS to its expected value in a composite likelihood framework (Kamm *et al.*, 2018).

We tested multiple models with different demographic scenarios for the populations of each species based on the results of PCA/DAPC/sNMF and SNAPP analyzes (see Figure 2), and the most informative were selected using the Akaike Information Criterion (AIC, Akaike, 1973). In general, we tested models that (a) are framed into the main hypothesis of diversification proposed (e.g. Refuge, Rivers hypotheses), models depicting (b) events of migration among the populations proposed for the taxa, (c) the effects glacial periods during the Pleistocene (Last Glacial Maximum, LGM), and (d) levels of population expansion. For each model (in each series of runs), we implemented 100 runs to avoid suboptimal results. With the run with the highest likelihood for each model, we evaluate the relative weight of the best model the Akaike Information Criterion (AIC, Akaike, 1973). In the same way, we run 100 bootstraps simulations to estimate confidence intervals of the parameters in the best model chosen in the AIC. Finally, based in the most informative models for each species, we looked for common scenarios across taxa that could explain a common history underlying circum-Amazonian distributions.

Results

mtDNA preliminary analyses and times of divergence

In general, we found evidence of considerable intraspecific genetic variation across taxa with signatures of recent population expansions (but see *L. nematura* and *T. ruficapillus/torquatus* complex). Haplotype networks are congruent with this signal in depicting geographical structure (see Figure S1 – S3) and Tables S3-S22 for a summary of these results).

Maximum likelihood and Bayesian gene tree estimation approaches (from this point, called ML and BI analyses, respectively, see Figures 3a – 3c and S4 – S7) recovered all species as monophyletic, except for the *T. palliatus/tenuepunctatus* and *T. ruficapillus/torquatus* complexes, wherein current taxonomy is not in agreement with our results. In the first case, *T. tenuepunctatus* is embedded within the Andean clade of *T. palliatus* (northernmost individuals in the central Andes). In the second case, the *T. ruficapillus* from southern Atlantic Forest is more closely-related to the *T. torquatus* than it is to other *T. ruficapillus* Andean and Chacoan (see Figures 3a – S5).

In general, the ML and BI topologies across taxa give rise to some commonalities across taxa. First, there is a deep division between the Andean and Atlantic Forest populations (*L. nematura*, *P. rufum*, *T. caerulescens* and *T. ruficapillus/torquatus* complex) and persistent and well-supported clades restricted to the central and southern Atlantic Forest (*D. mentalis*, *L. nematura*, *P. mystaceus*, *P. rufum* and *T. caerulescens*). Furthermore, we were able to identify isolated and divergent populations restricted to the northern Atlantic Forest (*P. mystaceus* and *T. caerulescens*).

Divergence times of Thamnophilid species (*D. mentalis*, *T. caerulescens*, *T. palliatus/tenuepunctatus* and *T. ruficapillus/torquatus*) from their outgroups varied from the Late Miocene to the Middle Pleistocene, with posterior divergences occurred since the early Pleistocene. For the Furnariid species (*L. nematura* and *P. rufum*) and *P. mystaceus* divergence starts in the Miocene/Pliocene, while the *Xiphocolaptes* complex have a most recent and rapid diversification, starting in the Calabrian (from *X. ocellatus*) and the Middle Pleistocene. A common pattern is a high rate of diversification from the early/middle Pleistocene in all taxa (see Figure 3a – 3c).

UCE statistics and sequencing

UCEs sequencing, considering the samples from the 8 species complexes, resulted in an average of 4,139,618 (min=72,929, max=13,782,612) read pairs per sample after trimming with Illumiprocessor; after assembling the reads we gathered an average of 12,441.86 UCEs contigs with a mean coverage (x) of 18.66 (see Tables 5 – 6). In the end, we processed and analyzed 302 UCEs samples.

Population Structure in circum-Amazonian Passerines

Based on the geographical distributions and population structure of each species analyzed here, we identified three common demographical units (Figures 4 – 5). Maybe the most persistent unit is the central-southern Atlantic Forest cluster(s), shared by populations of almost all species analyzed (*D. mentalis*, *T. caerulescens*, the *T. ruficapillus/torquatus* complex, *P. mystaceus*, *L.*

nematura, *P. rufum*, the species *albicollis* in the *Xiphocolaptes* complex). In these species, all analyses recovered this cluster (PCA/DAPC, sNMF), with a considerable level of admixture in some species with populations of adjacent areas like the northern Atlantic Forest (e.g. *T. ruficapillus/torquatus* complex) and the central Andean regions (*P. mystaceus*, *T. caerulescens*). In addition, for *D. mentalis* and *P. mystaceus*, sNMF runs showed admixture between the central-southern Atlantic Forest and individuals of the Tepuis region (see Figures 5a and 5g).

A second main unit, recovered in *T. caerulescens* and *P. mystaceus*, was a northern Atlantic Forest cluster from the forested remnants of the Atlantic Forest ecoregion in the states of Alagoas and Pernambuco in Brazil ('Pernambuco Endemism Centre', see Figures 4b/5g – 4b/5g). In this area we observe signatures of admixture between the central-southern Atlantic Forest and central Andean populations in *T. caerulescens*, and with populations from the eastern Amazonian, Bolivia, and the Tepuis in *P. mystaceus*.

We also identified a complex of 'Andean' cluster across all taxa not as geographically delimited as in the previous two clusters. We identified a 'complete' Andean cluster that covers the northern/central Andes including the Tepuis and Central America regions (see maps of *D. mentalis* and *P. mystaceus*, and *P. rufum* in Figures 4a/5a – 4f/5f – 4g/5g). In the same way, populations from *T. caerulescens* and the *T. ruficapillus/torquatus* complex shared a central Andean cluster from northern Argentina/Bolivia to central Peru (Figures 4b/5b – 4d/5d). Finally, a northern Peru cluster was recovered by *Lochmias nematura* *T. palliatus/tenuipunctatus* complex populations (Figures 4c/5c – 4e/5e).

sNMF analyses inferred a substantial level of admixture in the Andean clusters, mainly in individuals from two areas (Figures 5a – 5c – 5g – 5h). A first area from Bolivia to southern Peru as result of the contact between the southern Atlantic Forest and the Central Andean populations

of species with a continuous distribution like *D. mentalis*, *T. caerulescens*, and *P. mystaceus*. A second contact zone is that between the northern and the central Andes (maybe influenced by the Huancabamba depression) that showed considerable admixture with forested areas of Brazil (*D. mentalis*) or with adjacent regions like central Andes, Central America and the Tepuis (*L. nematura*, *P. mystaceus*, *Xiphocolaptes* and *T. palliatus/tenuepunctatus* complexes. In some species, the number of optimal clusters inferred by sNMF was ambiguous due to very close values of cross-entropy estimates (see Tables S23-S30). In this case, we used the results from PCA/DAPC analyses and identified common results among all them (PCA/DAPC + sNMF). We summarized the results of the admixture analyses performed in sNMF the Figure 6a-6b.

Species trees

In general, the topologies recovered by SNAPP showed high support for all scenarios/species analyzed (>60%). We identified an Andean – forested Brazilian regions sister relationship, except for *D. mentalis*, *T. caerulescens*, and *Xiphocolaptes* complex (Figures 7a – 7b). For *D. mentalis*, a northern Brazilian clade (subspecies *emiliae*) and its closest relative (subspecies *affinis*) are sisters to a comprehensive Andean clade (northern/central Andes + Tepuis + Central America). In turn, this clade is sister to the *mentalis* from the central-southern Atlantic Forest region (Figure 7a). In the *Xiphocolaptes* complex, the four scenarios tested (three to six clusters), showed mixed results, but it is clear that *X. albicollis* is monophyletic (see Figures 7b and S9). For *T. caerulescens*, the central Andean and the southern Atlantic Forest clades formed a clade, related to a third group from the northern Atlantic Forest region (see Figure 7a).

The phylogenetic relationships of clades from the eastern part of the circum-Amazonia distributional pattern (here ‘*the lowland forested areas south and east of the lowland forests of Amazonia*’ sensu Remsen *et al.*, 1991) present some commonalities. A first pattern identified for the *P. mystaceus* and *T. ruficapillus/torquatus* complexes showed the sister relationship between the clades from the northeastern and the central/southern forested regions in Brazil. Also a second sister relationship between the Atlantic Forest populations of *L. nematura* and *T. palliatus/tenuepunctatus* with clades from forested areas of eastern Amazonia and Tepuis (a northern connection, see Figures S8 – S9).

Similarly, we identified common patterns in the western portion of the circum-Amazonian region. First, a central Andean group with two sub-clades, a north central and a south-central Andean clades, from northern to central Peru and from here to northern Argentina (south Bolivia), present in the *L. nematura* and *T. palliatus/tenuepunctatus* complex. Secondly, a most ‘extended’ clade, covering the Andes plus adjacent areas like the Tepuis and individuals from Central America in *D. mentalis*, *P. mystaceus*, *Xiphocolaptes* complex (Figures 7a – 7b).

Demographic modelling

Due to the scarce sampling effort for some species analyzed (see Fig. S2a – S2h), we only conducted the demographic analyses of the antbird taxa (*D. mentalis*, *T. caerulescens*, the *T. palliatus/tenuepunctatus* and *T. ruficapillus/torquatus* complexes from *Thamnophilidae*), each with a three population scheme (based on the populational structure analyses).

We identified commons patterns among the best models inferred by *mom2* for each species (Figure 8). Detailed results for each species complex with AIC and parameters values can be found

on table (see Tables 7 – 10). In general, the models presented bidirectional migration among their populations, but with relatively low rates of migration (maximum values 25% - 36% in *T. palliatus/tenuepunctatus* complex model). For *T. palliatus/tenuepunctatus* complex and *D. mentalis*, the rate of migration is higher from the populations of forested areas in Brazil to the Andean region than in the opposite direction. In *T. caerulescens* and the *T. ruficapillus/torquatus* complex, the higher migration rates seem to occur between the southern Atlantic Forest and Andean populations, congruent some results of the admixture analyses of sNMF, where populations from the connection between the regions have a ‘high’ levels of admixture (Figure 5). Mean divergence times also were inferred in these models, the populations of the four antbird species seem to have a starting point of divergence in the Pleistocene, from early Gelasian (*T. ruficapillus/torquatus* complex) to Middle Pleistocene (*T. caerulescens*), similar to the found by BEAST in the ND2 analyses. Finally, the time of the events of migration among the populations also were estimated, and for three species (less *T. caerulescens*) these ‘pulses’ happened prior the Last Glacial Maximum (LGM) (Figure 8).

Discussion

Population structure of circum-Amazonian Passerines

In this first phylogeographic approach to the circum-Amazonian distributional pattern, we found considerable level of populational structure in the species cohabiting this distribution, well-supported phylogroups and certain geographical congruence. In general, the identified clusters fit with biogeographical units proposed in diverse type of studies and taxonomic groups (Bates *et al.*, 1998; Morrone, 2001; Silva *et al.*, 2004; Dinerstein *et al.*, 2017), and the phylogenetic relationships among the populations of almost all species showed a ‘common’ pattern.

First, we identified two main regions in the circum-Amazonian distributional pattern, the Andean and the Brazilian forested populations. This division can be ‘strict’ like *P. rufum*, *L. nematura* or *T. ruficapillus/torquatus* complex, with a clear separation between the two units with no admixture, or a relaxed like *T. caerulescens*, *D. mentalis*, and *P. mystaceus*, with intermediate clusters, contact zones and a considerable level of gene flow. Hybridization and clinal variation have been documented for these regions for *T. caerulescens* and *D. mentalis* (Todd, 1916; Brumfield, 2005; Isler *et al.*, 2005; Zimmer & Isler, 2019a), species with a continuous distribution along of a **southern arch** of the circum-Amazonian distribution (central Andes $\leftrightarrow$ southern Atlantic Forest/SDTFs connections). In turn, the presence of geographical variation/hybrid zones seems be influenced by latitudinal gradients, geological events, climatic variations during the Pleistocene, and secondary contact among isolated populations (Miller *et al.*, 2010b; Herzog & Kattan, 2011; Luebert & Weigend, 2014; Chattopadhyay *et al.*, 2017; Polato *et al.*, 2018).

Within the Brazilian forested regions, our analyses inferred other phylogeographic subunits, mainly related to the Atlantic Forest ecoregion. This forested areas have been continuously proposed as a region with high-levels of biodiversity, endemism, and a priority hotspot for conservation efforts (Myers *et al.*, 2000). In addition, the populational analyses defined the northern portion of the Atlantic Forest as an independent cluster from the central-southern regions (see *T. caerulescens*, *P. mystaceus*). A refuge in this region during the Quaternary (Pernambuco refuge, see Carnaval & Moritz, 2008; Carnaval *et al.*, 2009), and the presence of the Rio São Francisco as barrier can have potential effect in the isolation of this region from the central/southern Atlantic Forest (but see Carnaval & Moritz, 2008; Carvalho *et al.*, 2017).

The demographic patterns in the Andean unit of the circum-Amazonia distribution is more complex, and the sampling effort did not allow us to make solid inferences about its populational structure and phylogenetic relationships (samples from Colombia, Venezuela, Ecuador and Tepuis were scarce). However, the clusters identified in this region present similarities to the identified by previous works. Morrone & Utrubey (1997) identified a northern Peru area of endemism (our cluster from northern to central Peru) in a cladistics analysis about the historical biogeography of the northern Andes (see also Morrone, 1994). In addition, several authors considered this area as a ‘*transitional zone*’ between the northern and Central Andes (see Berry, 1982; Weigend, 2002). In this zone, the presence of the Huancabamba Depression is considered as a geographical barrier that prevents the passage of organisms through the mountainous chain. However, the isolation effect of this barrier does not seem relevant for certain groups as some amphibians and reptiles as the same species have a continuous distribution at both sides of the depression (Duellman, 1979). In the same way, similar analyses identified our central Andes cluster (central Peru to northern

Argentina/Bolivia) as part of a biogeographical unit and possibly an important center of speciation (Cracraft, 1985; Morrone, 2014; Perez-Escobar *et al.*, 2017).

Species trees and phylogenetics patterns

Similar to the populational structure results, the phylogenetic relationship of the circum-Amazonian taxa analyzed here suggest certain level of geographical congruence. In the Brazilian forested populations were identified two clades, the northern and the central – southern Atlantic Forest groups, previously identified in phylogenetic reconstructions using toads and birds (Thomé *et al.*, 2010; Batalha-Filho *et al.*, 2013). However, we found that the species with a complete distribution in the Atlantic Forests regions (and adjacent forested areas) do not have a sister relationship between the two clades (see D’Horta *et al.*, 2011; Franco *et al.*, 2017 for examples with sister relationship between these two areas). In *P. mystaceus*, the central – southern clade is closest to the eastern-forested area of Amazonia (subspecies *cancromus*) that to the *niveigularis* clade (northern Atlantic Forest clade). In similar way, SNAPP inferred that in *D. mentalis*, the *emiliae* clade (northern Atlantic Forest + eastern Amazonia) as most related to the *affinis* clade (SDTFs south of Amazonia) that with the central – southern Atlantic Forest group. These results are congruent with studies of taxa with Atlantic Forest distribution (Carvalho *et al.*, 2017; Lima *et al.*, 2018; Machado *et al.*, 2018).

The phylogenetic relationship within the Andean clusters seems defined in SNAPP, with the northern Peru and the central Andes clusters being monophyletic and related to the eastern-forested areas (but see ND2 results). In the same way, previous analyses showed that these two areas are part of a central Andean subunit (Berry, 1982; Morrone & Utrubey, 1997). However, the

relationships of the Andean unit with adjacent areas are not clear, maybe due to the missing samples in the northern Andes or the evolutionary complexity of the region. The reviewed literature identified the Tropical Andes as a complex geological/biogeographical unit, including areas the mountainous region of Venezuela but not the Tepuis (Gansser, 1973; Rivas-Martinez, 1983; Graham, 2009). Borges *et al.* (2018) concluded that the Pantepui region a biogeographic unit separated from the Andes, with probable past interconnections with the northern Andes (Bonaccorso & Guayasamin, 2013). On the other hand, Dal Vechio *et al.* (2018) found a highly supported sister relationship between Atlantic Forest and Tepuis populations of *Bothrops bilineatus*, with a diversification from the Guiana shield to the northern Atlantic Forest via a forest corridor in the northeastern South America, also in concordance with the inferred by Lovette (2004) for *Phaeothlypis* populations. In relation to the Andes – Central American regions, the species covers this distribution showed two results, in *D. mentalis* the Andes + Central American samples forms a unique cluster, while *P. mystaceus* and the *Xiphocolaptes* complex presented a Central American and north Andean clusters.

Demographic modeling and the rise of the circum-Amazonian distribution

Summarizing the populational structure and modelling analyses, the formation of a circum-Amazonian distributional pattern can be explained by two not exclusive types of expansion/diversification: a diversification via forested areas north to the Amazon forested lowlands (***northern diversification***, via Tepuis), and a ***southern diversification***, via forested lowlands of east/southern Brazil joining to the Andes.

Using as reference the models inferred for the thamnophilid species and their geographical distribution, a southern diversification seems more probable, with initial populations from forested regions from Brazil – e.g. Atlantic Forest ecoregion – expanding to southwest to central Andes (in *T. caerulescens*, *D. mentalis*, and the *T. palliatus/tenuepunctatus* complex), congruent with the proposed by Chapman (1926). Brumfield & Edwards (2007) also suggested that the Andean populations (at least for *T. caerulescens*) represents a secondary invasion of the species via a ‘forest bridge’ between the southeastern Brazil and the central Andes. Multiple authors studied these possible connections between Andes and Atlantic Forest (Batalha-Filho *et al.*, 2013; Trujillo-Arias *et al.*, 2017; Cabanne *et al.*, 2019). In a work about the biotic interchange between the Amazonian and the Atlantic Forest regions, Ledo & Colli (2017) concluded that a southern route (southeastern forested $\leftrightarrow$ western Amazonian areas) were the most probable scenario to explain the connection between these regions, this same scenario can be framed into the central Andes $\leftrightarrow$ southern Atlantic Forest connection(s).

Among the hypotheses proposed to explain the diversification in the Neotropics summarized in the introduction, these models seems fit with the presence of refuges/forested spots interconnected during the climatic fluctuations in the Pliocene – Pleistocene (Refugia Hypothesis, Haffer, 1969, Vanzolini & Williams, 1970), allowing partial isolations and intermittent gene flow among their populations, and proliferation of new lineages (see Figures 9 – 11). From this proposal in 1969, several authors used the climatic fluctuations during the Cenozoic as explanation for diversification of lineages of multiple groups for the Amazonian (Richardson *et al.*, 2001; Silva *et al.*, 2018; Pupim *et al.*, 2019), and non-Amazonian biotas (Madriñan *et al.*, 2013; Thomaz *et al.*, 2015; Pérez-Escobar *et al.*, 2017; García-Vázquez *et al.*, 2017).

Another hypothesis, the Pleistocene Arch Hypothesis, can to explain the diversification of the species modelled (PAH, Prado & Gibbs, 1993; ‘PAT’ in Moggi *et al.*, 2015). In PAH, a continuum of relatively stable areas of non-Amazonian forests (Seasonally Dry Tropical Forests – SDTFs) allows the migration and colonization of taxa during the Cenozoic. For instance, in the phylogeographic pattern of *D. mentalis* and the *T. palliatus/tenuepunctatus* complex, the SDTFs to south of the Amazonian forests could be serve as a corridor between the northeastern forested areas of Brazil and the central Andes during the Pleistocene (see Figure 9a – 9b). SNAPP/sNMF supported this configuration, with continuous populations forming an ‘arch’ around of the Amazonian rainforest region. Despite the lack of widespread support of this hypothesis (see Moggi *et al.*, 2015), some authors have supported PAH as a driver in the diversification in the Neotropics (Collevatti *et al.*, 2012; Florentín *et al.*, 2018), mainly using species of plants. On the other hand, the presence of refuges has more theoretical/empirical support in the reviewed literature (see Werneck *et al.*, 2011; Arruda *et al.*, 2018). For the species of Thamnophilidae analyzed here, the models fit better a refugia scenario, and for species like *D. mentalis* and the *T. palliatus/tenuepunctatus* complex, further methodological approaches are yet needed to elucidate this question.

Regarding divergence times, the four species of Thamnophilidae analyzed by momi2 showed events of diversification in the Pleistocene (but see *T. ruficapillus/torquatus*). These results were congruent with the BEATS analyses (mtDNA) and in general with the divergence times for others Thamnophilidae (e.g. Choueri *et al.*, 2017; Ribas *et al.*, 2018). In momi2, the estimation of divergence times seems very dependent of other parameters in the models (specially the populational size, N_e), and it is necessary to be careful in the construction of the initial models. Additionally, due to the fact that UCEs do not have just one rate of substitution like the ND2 gene

(a UCE contains hundreds of loci with hundreds of possible rates) a comparison of the times of divergence between mtDNA and UCEs analyses could be difficult. We tried to minimize these problems by testing multiple N_e values for the initial models, and used the substitution rate proposed by Nadachowska-Brzyska *et al.* (2015).

Some taxonomic and phylogenetic considerations of circum-Amazonian Passerines

The *T. ruficapillus/torquatus* complex was challenging to frame in the patterns explained so far. This taxonomic complex is a not monophyletic group, with the southern populations of *T. ruficapillus* being closest to *T. torquatus* (sNMF identified hybrid individuals between these two clusters) that with the Andean populations of the same taxon, result supported by mtDNA and UCEs information. In the reviewed literature, there are not studies specifically about this complex. In their work about the genus *Thamnophilus*, Brumfield & Edwards (2007) found that in the group called the ‘*barred clade*’, the *ruficapillus/torquatus* complex was indeed a monophyletic group, with a common ancestor that could be a highland-restricted or a lowlands-to-highlands taxon. A possible scenario is that of “lowlands-to-highlands” origin from the southern Atlantic Forest region moving west to the central Andes (Andean *ruficapillus* populations) and north to the forested areas in central/northern Brazil, with posterior isolation of the morphologically differentiated *T. torquatus*. A recent secondary contact could explain the hybrid zone between the southern *T. ruficapillus* and the *T. torquatus* populations. A deeper analysis of this complex that include taxonomy, ecology and evolutionary will be important to elucidate what is going on in these species.

In the *Thamnophilus palliatus/tenuepunctatus* complex, the populational analyses presented not recognizable differences between the two species (but see the ND2 topologies). The only two samples of *T. tenuepunctatus* (extreme northern Peru and southern Ecuador) fall into the northern Peru cluster of *T. palliatus*, but with high levels of admixture (sNMF analysis). In the same way, the sample collected in eastern Colombia (department of Vichada), a locality outside of the species distributions, seems to be part of the Amazonian cluster, possibly representing an undescribed taxon. Based on the handbook of the Birds of the World (HBW, Zimmer & Isler, 2019b), the species have adjoining ranges with no apparent barriers and no intergradation. However, our results imply a possible contact zone and hybridization at a genetic level. A better sampling effort help to clarify this complex.

In the *Xiphocolaptes* complex, all structural analyses support the existence of a *X. albicollis* cluster/clade (from Atlantic Forest ecoregion), being the only taxon recovered as an independent unit within the complex. In the same way, *X. falcistrostris* seems be an independent cluster, but fails in the DAPC analyses and one scenario of sNMF, doing part of a cluster including the *promeropirhynchus* samples from the Tepuis and lowland samples of Central America.

The phylogenetic relationships in *Xiphocolaptes* are obscure. Nevertheless, we recovered *X. albicollis* as a well-supported clade consistent in all scenarios tested by SNAPP (see Figures 7b – S7). In addition, we recovered a well-supported clade formed by the Andean cluster of *X. promeropirhynchus* (*promeropirhynchus* group of Marantz *et al.* 2019) and *X. major*, in concordance with the found by Raikow (1994) and Derryberry *et al.* (2011). *X. falcistrostris* was also recovered by the analysis. Finally, *T. promeropirhynchus* is not monophyletic, but, like proposed by Marantz *et al.* (2019), this species can be divided in three groups, an Andean clade (including montane individuals of Central America + *X. major*), a Amazonian, and a lowlands of

central America (plus Tepuis) clade. Like the two anterior complexes, other type of information will be useful to resolve the taxonomy/systematics of this group of species.

Conclusions

In this first phylogeographic comparative approach to the understanding of the circum-Amazonian distributional pattern using genomic data of Passerines, we found general congruence among the populational structure, phylogenetic relationships, and demographic histories of the taxa analyzed. We defined two main units: the Andean and the Brazilian forested phylogeographic region(s), disjointed complete or partially via a **northern** (northern Andes $\leftrightarrow$ Tepuis $\leftrightarrow$ Atlantic Forest) or **southern interconnection** (southern Atlantic Forest $\leftrightarrow$ central Andes). Contact zones among clusters included individuals with considerable levels of admixture, supports the possibility of events of hybridization among populations, mainly in the northern – southern interconnections. Species trees analyses inferred well-supported clades from central/southern and northern Atlantic Forest populations. In the same way, we identified central Andean clades (northern Peru and central Peru - Bolivia), but a bigger sampling effort will be necessary in the north Andean region. Demographic histories of the *Thamnophilidae* taxa seems to be product of a recent diversification with climatic fluctuations throughout the Quaternary as its main influence, fitting into a Refugia context previously proposed by other authors. However, at least to *D. mentalis* and the *Thamnophilus palliatus/tenuepunctatus* complex, alternative hypotheses (like corridors of STDs vegetation during the Pleistocene) could not be discarded. In addition, our results raise new question about the taxonomy and systematics of the circum-Amazonian species (the *T. ruficapillus/torquatus*, *T. palliatus/tenuepunctatus*, and the *Xiphocolaptes* complexes). Future

studies about the circum-Amazonian distribution have to cover other taxonomic groups outside Aves, phenotypic and ecological data, and the implementation of comparative methodologies that can include all those parameters for estimation of demographic/evolutionary scenarios that explain in deep the past and current dynamics of the circum-Amazonian distributional pattern.

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Appendix (Chapter II)

Figure 1. Distribution of *Dysithamnus mentalis* (BirdLife International, 2019), a circum-Amazonian species (*sensu* Remsem et al., 1991).

Figure 2. Basic models tested for the four species of Thamnophilidae. Divergence times (red square). Events of migration (blue arrows). Bottleneck events (green circles). All models tested were variations of these basic models, these variations consisted in change number of events and direction of the migrations..

Figure 3a. Divergence times among intraspecific lineages for the four species of Thamnophilidae. Blue bars are confidence intervals of divergence time estimates. Collapsed clades indicate geographical clusters identified by DAPC/sNMF: Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean); Brown-Yellow: forests southeast of the Amazon; Pale-Blue: southern Peru-Bolivia region; Blue: Outgroups.

Figure 3b. Divergence times among intraspecific lineages for *L. nematura*, *P. rufum*, and the *Xiphocolaptes* complex. Blue bars are confidence intervals of divergence time estimates. Collapsed clades indicate geographical clusters identified by DAPC/sNMF: Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean); Brown-Yellow: forests southeast of the Amazon; Pale-Blue: southern Peru-Bolivia region; Gray: Tepuis-Central America; Yellow: Amazonian region; Blue: Outgroups.

Figure 3c. Divergence times among intraspecific lineages for *P. mystaceus*. Blue bars are confidence intervals of divergence time estimates. Collapsed clades indicate geographical clusters identified by DAPC/sNMF: Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean); Brown-Yellow: forests southeast of the Amazon; Blue: Outgroups.

Figure 4. Results of DAPC and find.cluster() analyses for the genomic data (UCEs) of the Thamnophilid species. **(a)** *D. mentalis*. **(b)** *T. caeruleus*. **(c)** *T. palliatus/tenuepunctatus* complex. **(d)** *T. ruficapillus/torquatus* complex.

4e

P. rufum

4f

P. mystaceus

4g

4h

Figure 4. Results of DAPC and find.cluster() analyses for the genomic data (UCEs). (e) *L. nematura*. (f) *P. rufum*. (g) *P. mystaceus*. (h) *Xiphocolaptes* complex.

Figure 5. Results of sNMF analysis for the genomic data (UCEs) of the Thamnophilid species. (e) *D. mentalis*. (f) *T. caeruleus*. (g) *T. palliatus/tenuepunctatus*. (h) *T. ruficapillus/torquatus*.

Figure 5. Results of sNMF analysis for the genomic data (UCEs). (e) *L. nematura*. (f) *P. rufum*. (g) *P. mystaceus*.

Figure 5. Results of sNMF analysis for the genomic data (UCEs). **(h)** *Xiphocolaptes* complex.

Figure 6a. Values of the cross-entropy criterion for the sNMF runs (six α values). Green: $\alpha=1$; Red: $\alpha=10$; Brown-Yellow: $\alpha=50$; Pink: $\alpha=100$; Gray: $\alpha=500$; Blue: $\alpha=1000$.

Figure 6b. Values of the cross-entropy criterion for the sNMF runs (six α values). Green: $\alpha=1$; Red: $\alpha=10$; Brown-Yellow: $\alpha=50$; Pink: $\alpha=100$; Gray: $\alpha=500$; Blue: $\alpha=1000$.

Figure 7a. Species trees inferred by SNAPP for the thamnophilid taxa data. Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean); Brown-Yellow: forests southeast of the Amazon; Pale-Blue: southern Peru-Bolivia region; Blue: Outgroups.

Figure 7b. Species trees inferred by SNAPP for the thamnophilid taxa data. Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean); Brown-Yellow: forests southeast of the Amazon; Pale-Blue: southern Peru-Bolivia region; Blue: Outgroups. Numbers in the figures represents the species in the *Xiphocolaptes* complex.

Figure 8. Best models inferred by momi2 for the four thamnophilid taxa. Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean); Brown-Yellow: forests southeast of the Amazon; Pale-Blue: southern Peru-Bolivia region.

Figure 9. Plausible scenarios of diversification and migration pulses inferred by momi2 for the *D. mentalis* and the *T. palliatus/teunuepunctatus* complex. Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean); Brown-Yellow: forests southeast of the Amazon; Pale-Blue: southern Peru-Bolivia region.

Figure 10. Plausible scenarios of diversification and migration pulses inferred by momi2 for *T. caerulescens*. (a) Complete matrix of SNPs (324 loci). (b) Incomplete matrix of SNPs (2,036 loci). Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean) region.

Figure 11. Plausible scenarios of diversification and migration pulses inferred by momi2 for *T. ruficapillus/tenuepunctatus* complex. Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean) region.

Figure S1. median-joining network depicting relationships among the haplotypes in the thamnophilid taxa. (a) *D. mentalis*. (b) *T. caeruleus*. (c) *T. palliatus/tenuepunctatus* complex. (d) *T. ruficapillus/torquatus* complex. Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean); Brown-Yellow: forests southeast of the Amazon; Pale-Blue: southern Peru-Bolivia region; Gray: Tepuis-Central America; Yellow: Amazonian region.

Figure S2. median-joining network depicting relationships among the haplotypes in (a) *L. nematura*. (b) *P. rufum*. (c) *P. mystaceus*. Red: northern Atlantic Forest; Green: central-southern Atlantic Forest; Pink: Andean (or central Andean); Brown-Yellow: forests southeast of the Amazon; Pale-Blue: southern Peru-Bolivia region; Gray: Tepuis-Central America; Yellow: Amazonian region.

Figure S3. median-joining network depicting relationships among the haplotypes in *Xiphocolaptes* complex.

Figure S4. Phylogenetic reconstruction for *D. mentalis* (Maximum Likelihood).

Figure S5. Phylogenetic reconstruction for (a) *T. caerulescens*. (b) *T. palliatus/tenuepunctatus*. (c) *T. ruficapillus/torquatus* (Maximum Likelihood).

Figure S6. Phylogenetic reconstruction for (a) *L. nematura*. (b) *P. rufum*. (c) *P. mystaceus* (Maximum Likelihood).

Xiphocolaptes complex

Figure S7. Phylogenetic reconstruction for *Xiphocolaptes* complex (Maximum Likelihood).

Figure S8. Alternative scenarios tested in SNAPP for (a) *T. palliatus/tenuepunctatus*. (b) *T. ruficapillus/torquatus*. (c) *L. nematura*. (d) *P. mystaceus*.

Figure S9. Alternative scenarios tested in SNAPP for *Xiphocolaptes* complex.

Chapter II: Comparative phylogeography of passerine birds with a circum-Amazonian distribution (Main Tables).

Table 1.

Portuguese	Species	Common name (English/Portuguese)
Thamnophilidae	<i>Dysithamnus mentalis</i>	Plain Antvireo/Choquinha-lisa
Thamnophilidae	<i>Thamnophilus caeruleus</i>	Variable Antshrike/Choca-da-mata
Thamnophilidae	<i>Thamnophilus palliatus</i>	Chestnut-backed Antshrike/Choca-listrada
Thamnophilidae	<i>Thamnophilus tenuipunctatus</i>	‘Lined Antshrike’ (inglês)
Thamnophilidae	<i>Thamnophilus ruficapillus</i>	Southern Rufous-capped Antshrike/Choca-de-chapéu-vermelho
Thamnophilidae	<i>Thamnophilus torquatus</i>	Rufous-winged Antshrike/Choca-de-asa-vermelha
Furnariidae	<i>Lochmias nematura</i>	Streamcreeper/João-porca
Furnariidae	<i>Philydor rufum</i>	Buff-fronted Foliage-gleaner/Limpa-folha-de-testa-baia
Platyrinchidae	<i>Platyrinchus mystaceus</i>	White-throated Spadebill/Patinho
Dendrocolaptidae	<i>Xiphocolaptes albicollis</i>	White-throated Woodcreeper/Arapaçu-de-garganta-branca
Dendrocolaptidae	<i>Xiphocolaptes falcirostris</i>	Moustached Woodcreeper/Arapaçu-do-nordeste
Dendrocolaptidae	<i>Xiphocolaptes major</i>	Great Rufous Woodcreeper/Arapaçu-do-campo
Dendrocolaptidae	<i>Xiphocolaptes promeropirhynchus</i>	Strong-billed Woodcreeper/Arapaçu-do-campo

Table 2. List of ornithological collections used in this study.

Museum/Collection	Samples
MZUSP ¹	217
MPEG ²	131
PUC-RS ³	16
KU ⁴	25
FMNH ⁵	34
LSU ⁶	50
NMNH ⁷	6
Fabio Raposo Amaral	7
Total	486

Collections: (1) Museu de Zoologia da Universidade de São Paulo, (2) Museu Paraense Emílio Goeldi, (3) Pontifícia Universidade Católica do Rio Grande do Sul, (4) University of Kansas, (5) Field Museum of Natural History, (6) LSU Museum of Natural Science, (7) National Museum of Natural History of the Smithsonian Institute

Table 3. Best substitution model for the ND2 samples of each species (jModeltest2).

Species	Model AICc	Model BIC
<i>Dysithamnus mentalis</i>	TIM3+I+G	TIM3+I+G
<i>Lochmias nematura</i>	TVM+G	TPM2uf+G
<i>Philydor rufum</i>	TIM2+G	TPM2uf+I
<i>Platyrrhinus mystaceus</i>	TIM1+I+G	TIM1+G
<i>Thamnophilus caeruleus</i>	TrN+I+G	TrN+G
<i>Thamnophilus palliatus/tenuipunctatus</i> complex	TIM1+G	HKY+G
<i>Thamnophilus ruficapillus/torquatus</i> complex	TPM1uf+G	HKY+G
<i>Xiphocolaptes</i> complex	TIM2+I	TPM2uf+I

Table 4. Number of loci recovered in the complete and incomplete matrices for each species.

Species	Complete	Incomplete
<i>Dysithamnus mentalis</i>	6	1848
<i>Lochmias nematura</i>	0	1950
<i>Philydor rufum</i>	209	1901
<i>Platyrrhinus mystaceus</i>	9	1843
<i>Thamnophilus caeruleus</i>	324	2,036
<i>Thamnophilus palliatus/tenuipunctatus</i> complex	65	1855
<i>Thamnophilus ruficapillus/torquatus</i> complex	74	1845
<i>Xiphocolaptes</i> complex	18	1887

* Matrix with few loci, not used for analyses.

Table 5. Statistics of UCEs after the Illumiprocessor trimming.

Species	Mean of reads*	Minimum	Maximum
<i>Dysithamnus mentalis</i>	4,097,390.07	712,910	11,636,996
<i>Lochmias nematura</i>	3,476,554.27	1,214,882	9,107,376
<i>Philydor rufum</i>	4,114,619.60	72,929	9,687,756
<i>Platyrinchus mystaceus</i>	3,381,776.76	1,463,758	6,144,094
<i>Thamnophilus caeruleus</i>	5,702,659.25	1,904,001	10,284,782
<i>Thamnophilus palliatus/tenuepunctatus</i> complex	3,884,606.87	1,149,098	8,008,501
<i>Thamnophilus ruficapillus/torquatus</i> complex	3,890,676.52	1,380,904	8,066,334
<i>Xiphocolaptes</i> complex	3,147,543.00	948,950	13,782,612

*After trimming

Table 6. Statistics of UCEs after the assemble process.

Species	Mean of reads*	Minimum	Maximum	Total contigs	Mean length	Total bp	Contigs >1K
<i>Dysithamnus mentalis</i>	13,737.31	4,896	157,428	810,501	500.72	337,268,803	18,608
<i>Lochmias nematura</i>	10,836.91	3,595	29,696	238,412	646.91	132,156,469	21,910
<i>Philydor rufum</i>	9,145.31	1,642	25,486	539,573	516.59	262,997,817	18,393
<i>Platyrinchus mystaceus</i>	13,086.41	2,961	29,403	222,469	535.97	107,686,462	15,323
<i>Thamnophilus caeruleus</i>	17,803.68	4,888	143,662	498,503	464.53	185,331,752	4,697
<i>T. palliatus/tenuepunctatus</i> complex	13,747.19	5,743	75,200	426,163	521.32	191,133,806	14,929
<i>T. ruficapillus/torquatus</i> complex	10,998.04	5,517	21,193	252,955	530.60	121,822,170	6,347
<i>Xiphocolaptes</i> complex	10,551.93	2,825	32,323	453,733	566.11	235,914,712	30,777

*After Trinity

Table 7. Values of AIC and Δ AIC for *D. mentalis* (incomplete matrix).

Model	Log_likelihood	n_parameters	AICs	Delta_AIC	weight_AICs
Model 1	-5309.276383	8	10634.55277	81.76809762	1.76E-18
Model 2	-5275.603138	12	10575.20628	22.42160665	1.35E-05
Model 3*	-5262.392335	14	10552.78467	0	1
Model 4	-5261.258098	16	10554.5162	1.731526292	0.420730351
Model 5	-5480.279081	18	10996.55816	443.7734919	4.32E-97
Model 6	-5407.541805	18	10851.08361	298.2989407	1.68E-65
Model 7	-5486.576572	18	11009.15314	456.3684745	7.96E-100
Model 8	-5491.428656	22	11026.85731	474.0726424	1.14E-103
Model 9	-7152.90404	22	14349.80808	3797.023411	0
Model 10	-18294.94633	22	36633.89266	26081.10799	0
Model 11	-5279.918669	16	10591.83734	39.05266805	3.31E-09
Model 12	-5262.817181	16	10557.63436	4.84969321	0.088491692
Model 13	-9709.965268	22	19463.93054	8911.145868	0

* Best model for *D. mentalis*.

Table 8. Values of AIC and Δ AIC for *T. caerulescens* (incomplete matrix).

Model	Log_likelihood	n_parameters	AICs	Delta_AIC	weight_AICs
Model 1	-7481.577811	2	14967.15562	392.1354344	7.06E-86
Model 2	-7383.252541	5	14776.50508	201.4848944	1.77E-44
Model 3	-7386.643388	5	14783.28678	208.2665891	5.96E-46
Model 4	-7323.523233	9	14665.04647	90.02627891	2.83E-20
Model 5	-7345.247239	9	14708.49448	133.4742895	1.04E-29
Model 6	-7299.864124	9	14617.72825	42.70805956	5.32E-10
Model 7*	-7274.510094	13	14575.02019	0	1
Model 8	-7574.598842	11	15171.19768	596.1774969	3.48E-130
Model 9	-7528.523218	11	15079.04644	504.026249	3.57E-110
Model 10	-7388.482618	16	14808.96524	233.9450474	1.58E-51
Model 11	-7394.500327	16	14821.00065	245.9804667	3.85E-54
Model 12	-7522.21469	11	15066.42938	491.4091924	1.96E-107
Model 13	-7394.482314	16	14820.96463	245.9444395	3.93E-54
Model 14	-7807.853685	11	15637.70737	1062.687182	1.74E-231
Model 15	-7621.885811	19	15281.77162	706.7514342	3.40E-154
Model 16	-7724.954811	11	15471.90962	896.8894352	1.75E-195

* Best model for *T. caerulescens*.

Table 9. Values of AIC and Δ AIC for *T. palliatus/tenuepunctatus* complex.

Model	Log_likelihood	n_parameters	AICs	Delta_AIC	weight_AICs
Model 1	-6488.079556	7	12990.15911	29.50880915	3.91E-07
Model 2*	-6465.325151	15	12960.6503	0	1
Model 3	-6468.525541	17	12971.05108	10.4007799	0.005514414
Model 4	-6469.110862	18	12974.22172	13.57142202	0.001129804
Model 5	-6473.793174	18	12983.58635	22.93604613	1.05E-05
Model 6	-6470.946603	18	12977.89321	17.24290411	0.000180198
Model 7	-6477.629595	18	12991.25919	30.60888845	2.26E-07
Model 8	-6477.486628	18	12990.97326	30.3229544	2.60E-07
Model 9	-6470.352923	15	12970.70585	10.05554331	0.006553398
Model 10	-6473.685497	17	12981.37099	20.72069164	3.17E-05
Model 11	-6568.463888	18	13172.92778	212.277474	8.03E-47
Model 12	-6555.799502	0	13111.599	150.9487024	1.67E-33
Model 13	-6602.795104	20	13245.59021	284.9399062	1.34E-62
Model 14	-6626.392417	20	13292.78483	332.1345312	7.55E-73
Model 15	-6563.466586	28	13182.93317	222.282869	5.39E-49
Model 16	-7937.080681	23	15920.16136	2959.511059	0
Model 17	-7814.284258	21	15670.56852	2709.918214	0
Model 18	-6469.870035	20	12979.74007	19.0897677	7.16E-05
Model 19	-6605.452577	21	13252.90515	292.2548514	3.45E-64

* Best model for *T. palliatus/tenuepunctatus* complex.

Table 10. Values of AIC and Δ AIC for *T. ruficapillus/torquatus* complex.

Model	Log_likelihood	n_parameters	AICs	Delta_AIC	weight_AICs
Model 1	-6774.176937	7	13562.35387	173.1198488	2.56E-38
Model 2*	-6675.617013	19	13389.23403	0	1
Model 3	-6676.236177	19	13390.47235	1.238327941	0.538394363
Model 4	-6693.848291	19	13425.69658	36.46255731	1.21E-08
Model 5	-6687.52161	19	13413.04322	23.80919384	6.76E-06
Model 6	-7569.224441	23	15184.44888	1795.214857	0
Model 7*	-7582.263814	23	15210.52763	1821.293602	0
Model 8	-7683.624616	23	15413.24923	2024.015207	0

* Best model for *T. ruficapillus/torquatus* complex.

Chapter II: Comparative phylogeography of passerine birds with a circum-Amazonian distribution (Supplementary material).

Table S1. List summarized of all samples gathered for this study.

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0001	ALG-014	<i>Thamnophilus caerulescens</i>	Alagoas		YES
0002	ALG-020	<i>Thamnophilus caerulescens</i>	Alagoas	YES	YES
0003	ALG-021	<i>Dysithamnus mentalis</i>	Alagoas		YES
0004	ALG-046	<i>Dysithamnus mentalis</i>	Alagoas	YES	YES
0005	ALG-053	<i>Thamnophilus caerulescens</i>	Alagoas		
0006	ALG-080	<i>Thamnophilus caerulescens</i>	Alagoas	YES	YES
0007	ALG-085	<i>Thamnophilus caerulescens</i>	Alagoas	YES	YES
0008	ALG-086	<i>Thamnophilus caerulescens</i>	Alagoas	YES	YES
0009	ALG-087	<i>Dysithamnus mentalis</i>	Alagoas	YES	YES
0010	ALG-102	<i>Thamnophilus caerulescens</i>	Alagoas	YES	YES
0011	ALG-110	<i>Dysithamnus mentalis</i>	Alagoas		
0012	ALG-111	<i>Dysithamnus mentalis</i>	Alagoas		YES
0013	ALG-116	<i>Platyrinchus mystaceus</i>	Alagoas		YES
0014	ALG-117	<i>Platyrinchus mystaceus</i>	Alagoas		YES
0015	ALG-135	<i>Dysithamnus mentalis</i>	Alagoas		YES
0016	ALG-136	<i>Dysithamnus mentalis</i>	Alagoas		YES
0017	J_2216	<i>Thamnophilus palliatus puncticeps</i>	Rondônia	YES	YES
0018	J_2217	<i>Thamnophilus palliatus puncticeps</i>	Rondônia	YES	YES
0019	MZ_79194	<i>Dysithamnus mentalis</i>	Minas Gerais	YES	YES
0021	MZ_79195	<i>Dysithamnus mentalis</i>	Minas Gerais	YES	YES
0023	MZ_79196	<i>Dysithamnus mentalis</i>	Minas Gerais	YES	YES
0026	MZ_79203	<i>Dysithamnus mentalis</i>	Minas Gerais		YES
0027	MZ_81479	<i>Dysithamnus mentalis</i>	São Paulo		YES
0028	MZ_81480	<i>Dysithamnus mentalis</i>	São Paulo		YES
0030	MZ_82619	<i>Thamnophilus caerulescens caerulescens</i>	São Paulo		YES
0032	MZ_82637	<i>Thamnophilus caerulescens caerulescens</i>	Minas Gerais	YES	YES
0033	MZ_85427	<i>Thamnophilus ruficapillus</i>	Minas Gerais	YES	YES
0034	MZ_85660	<i>Platyrinchus mystaceus</i>	São Paulo		YES
0035	MZ_85740	<i>Dysithamnus mentalis</i>	Alagoas	YES	YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0037	MZ_85741	<i>Dysithamnus mentalis</i>	Alagoas	YES	YES
0038	MZ_85745	<i>Platyrrhinus mystaceus</i>	Alagoas	YES	YES
0039	MZ_85759	<i>Platyrrhinus mystaceus</i>	Alagoas		
0040	MZ_85760	<i>Platyrrhinus mystaceus</i>	Alagoas	YES	YES
0042	MZ_85805	<i>Platyrrhinus mystaceus</i>	Pernambuco	YES	YES
0043	MZ_85806	<i>Platyrrhinus mystaceus</i>	Pernambuco		YES
0044	MZ_85832	<i>Platyrrhinus mystaceus</i>	Alagoas		YES
0046	MZ_85833	<i>Platyrrhinus mystaceus</i>	Alagoas	YES	YES
0047	MZ_86001	<i>Thamnophilus palliatus</i>	Minas Gerais	YES	YES
0049	MZ_86016	<i>Thamnophilus palliatus</i>	Bahia	YES	YES
0051	MZ_86384	<i>Dysithamnus mentalis</i>	Tocantins	YES	YES
0052	MZ_87826	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0053	MZ_87827	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0054	MZ_87828	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0055	MZ_87829	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0056	MZ_87833	<i>Dysithamnus mentalis</i>	São Paulo		YES
0057	MZ_87834	<i>Dysithamnus mentalis</i>	São Paulo	YES	YES
0058	MZ_88334	<i>Platyrrhinus mystaceus</i>	Rio de Janeiro	YES	YES
0059	MZ_88399	<i>Dysithamnus mentalis</i>	São Paulo		YES
0066	MZ_90916	<i>Thamnophilus palliatus</i>	Bahia	YES	YES
0067	MZ_90917	<i>Thamnophilus palliatus</i>	Bahia	YES	YES
0068	MZ_90946	<i>Xiphocolaptes albicollis</i>	Bahia		YES
0069	MZ_90947	<i>Xiphocolaptes albicollis</i>	Bahia	YES	YES
0070	MZ_90971	<i>Platyrrhinus mystaceus</i>	Bahia		YES
0071	MZ_90972	<i>Platyrrhinus mystaceus</i>	Bahia		YES
0072	MZ_90973	<i>Platyrrhinus mystaceus</i>	Bahia		YES
0073	MZ_90974	<i>Platyrrhinus mystaceus</i>	Bahia	YES	YES
0074	MZ_90975	<i>Platyrrhinus mystaceus</i>	Bahia	YES	YES
0075	MZ_90976	<i>Platyrrhinus mystaceus</i>	Bahia		YES
0076	MZ_90977	<i>Platyrrhinus mystaceus</i>	Bahia		YES
0077	MZ_90978	<i>Platyrrhinus mystaceus</i>	Bahia	YES	YES
0078	MZ_91196	<i>Thamnophilus caeruleus</i> <i>gilviger</i>	Santa Catarina	YES	YES
0079	MZ_91197	<i>Thamnophilus caeruleus</i> <i>gilviger</i>	Santa Catarina	YES	
0080	MZ_91201	<i>Dysithamnus mentalis</i>	Santa Catarina	YES	YES
0084	MZ_91246	<i>Lochmias nematura</i>	Santa Catarina	YES	YES
0085	MZ_91254	<i>Philydor rufum</i>	Santa Catarina	YES	YES
0086	MZ_91267	<i>Platyrrhinus mystaceus</i>	Santa Catarina		YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0087	MZ_91268	<i>Platyrrhinus mystaceus</i>	Santa Catarina	YES	YES
0088	MZ_91269	<i>Platyrrhinus mystaceus</i>	Santa Catarina	YES	YES
0089	MZ_91380	<i>Thamnophilus palliatus</i>	Bahia		YES
0090	MZ_91465	<i>Platyrrhinus mystaceus</i>	Bahia	YES	YES
0091	MZ_91466	<i>Platyrrhinus mystaceus</i>	Bahia	YES	YES
0092	MZ_91467	<i>Platyrrhinus mystaceus</i>	Bahia		YES
0097	MZ_91661	<i>Thamnophilus caeruleus</i> <i>caeruleus</i>	São Paulo	YES	YES
0098	MZ_91681	<i>Platyrrhinus mystaceus</i>	São Paulo	YES	YES
0099	MZ_91682	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0100	MZ_91683	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0101	MZ_91684	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0102	MZ_91685	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0103	MZ_91755	<i>Thamnophilus caeruleus</i> <i>caeruleus</i>	Minas Gerais		YES
0104	MZ_91759	<i>Dysithamnus mentalis</i>	Minas Gerais	YES	YES
0105	MZ_91760	<i>Dysithamnus mentalis</i>	Minas Gerais	YES	YES
0107	MZ_92136	<i>Xiphocolaptes albicollis</i>	São Paulo		YES
0108	MZ_92160	<i>Dysithamnus mentalis</i>	São Paulo		YES
0109	MZ_92161	<i>Dysithamnus mentalis</i>	São Paulo		YES
0110	MZ_92162	<i>Dysithamnus mentalis</i>	São Paulo		YES
0111	MZ_92163	<i>Dysithamnus mentalis</i>	São Paulo		YES
0112	MZ_92164	<i>Dysithamnus mentalis</i>	São Paulo		YES
0113	MZ_92165	<i>Dysithamnus mentalis</i>	São Paulo		YES
0116	MZ_92168	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0117	MZ_92169	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0118	MZ_92170	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0119	MZ_92171	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0120	MZ_92172	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0121	MZ_92173	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0123	MZ_92478	<i>Lochmias nematura</i>	São Paulo	YES	YES
0127	MZ_92487	<i>Platyrrhinus mystaceus</i>	São Paulo	YES	YES
0128	MZ_92488	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0129	MZ_92489	<i>Platyrrhinus mystaceus</i>	São Paulo		YES
0130	MZ_92490	<i>Platyrrhinus mystaceus</i>	São Paulo		
0131	MZ_93101	<i>Dysithamnus mentalis</i>	São Paulo		YES
0133	MZ_93175	<i>Dysithamnus mentalis</i>	São Paulo	YES	YES
0134	MZ_93176	<i>Thamnophilus caeruleus</i> <i>caeruleus</i>	São Paulo	YES	YES
0135	MZ_93203	<i>Xiphocolaptes albicollis</i>	São Paulo	YES	YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0136	MZ_93204	<i>Xiphocolaptes albicollis</i>	São Paulo	YES	YES
0137	MZ_93208	<i>Lochmias nematura</i>	São Paulo		YES
0138	MZ_93226	<i>Platyrrhynchus mystaceus</i>	São Paulo		YES
0139	MZ_93227	<i>Platyrrhynchus mystaceus</i>	São Paulo		YES
0140	MZ_93228	<i>Platyrrhynchus mystaceus</i>	São Paulo		YES
0141	MZ_93229	<i>Platyrrhynchus mystaceus</i>	São Paulo		YES
0142	MZ_93230	<i>Platyrrhynchus mystaceus</i>	São Paulo		YES
0143	MZ_93231	<i>Platyrrhynchus mystaceus</i>	São Paulo		YES
0144	MZ_93232	<i>Platyrrhynchus mystaceus</i>	São Paulo		YES
0145	MZ_93233	<i>Platyrrhynchus mystaceus</i>	São Paulo		YES
0146	MZ_93234	<i>Platyrrhynchus mystaceus</i>	São Paulo	YES	YES
0147	MZ_93408	<i>Thamnophilus palliatus</i>	Pará	YES	YES
0148	MZ_93501	<i>Dysithamnus mentalis</i>	São Paulo		YES
0149	MZ_93502	<i>Dysithamnus mentalis</i>	São Paulo		YES
0150	MZ_93511	<i>Xiphocolaptes albicollis</i>	São Paulo	YES	YES
0151	MZ_93512	<i>Xiphocolaptes albicollis</i>	São Paulo		YES
0152	MZ_93513	<i>Xiphocolaptes albicollis</i>	São Paulo		YES
0153	MZ_93514	<i>Philydor rufum</i>	São Paulo	YES	YES
0161	MZ_94441	<i>Platyrrhynchus mystaceus</i>	Minas Gerais		YES
0163	MZ_94637	<i>Dysithamnus mentalis</i>	Goiás	YES	YES
0164	MZ_94638	<i>Dysithamnus mentalis</i>	Goiás	YES	YES
0165	MZ_95594	<i>Thamnophilus palliatus</i>	Pará		YES
0166	MZ_96752	<i>Thamnophilus caerulescens caerulescens</i>	São Paulo		YES
0167	MZ_96753	<i>Thamnophilus caerulescens caerulescens</i>	São Paulo		
0168	MZ_96754	<i>Thamnophilus caerulescens caerulescens</i>	São Paulo		YES
0169	MZ_96755	<i>Thamnophilus caerulescens caerulescens</i>	São Paulo		YES
0170	MZ_96769	<i>Xiphocolaptes albicollis</i>	São Paulo	YES	YES
0176	MZ_98298	<i>Platyrrhynchus mystaceus</i>	Minas Gerais		YES
0177	MZ_98297	<i>Dysithamnus mentalis</i>	Minas Gerais		YES
0183	MZ_92715	<i>Xiphocolaptes promeropirhynchus paraensis</i>	Mato Grosso		YES
0184	MZ_94552	<i>Xiphocolaptes promeropirhynchus paraensis</i>	Pará		YES
0185	ML 1529	<i>Platyrrhynchus mystaceus</i>	São Paulo		YES
0186	SM 19	<i>Dysithamnus mentalis</i>	São Paulo		YES
0188	FRA_168	<i>Dysithamnus mentalis</i>	Paraná		YES
0189	FRA_178	<i>Lochmias nematura</i>	Paraná		YES
0190	FRA_230	<i>Philydor rufum</i>	Paraná		YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0191	FRA_233	<i>Philydor rufum</i>	Paraná		YES
0192	BOR-14-27	<i>Dysithamnus mentalis</i>	São Paulo		YES
0193	BOR-14-75	<i>Dysithamnus mentalis</i>	São Paulo		YES
0194	BOR-14-76	<i>Dysithamnus mentalis</i>	São Paulo		YES
0195	BOR-14-94	<i>Platyrinchus mystaceus</i>	São Paulo		YES
0196	BOR-14-95	<i>Platyrinchus mystaceus</i>	São Paulo		YES
0198	FRA_258	<i>Thamnophilus caerulescens</i>	São Paulo		YES
0199	PQP_16	<i>Philydor rufum</i>	Paraná	YES	YES
0200	PQP_21	<i>Dysithamnus mentalis</i>	São Paulo	YES	YES
0202	OBR-026	<i>Platyrinchus mystaceus</i>	Mato Grosso do Sul	YES	YES
0206	KU_40	<i>Platyrinchus mystaceus</i>	Concepcion	YES	YES
0207	KU_57	<i>Platyrinchus mystaceus</i>	Concepcion	YES	YES
0208	KU_160	<i>Xiphocolaptes major</i>	Concepcion	YES	YES
0209	KU_273	<i>Dysithamnus mentalis</i>	Caazapa	YES	YES
0210	KU_274	<i>Dysithamnus mentalis</i>	Caazapa	YES	YES
0211	KU_405	<i>Philydor rufus</i>	Concepcion	YES	YES
0212	KU_406	<i>Philydor rufus</i>	Concepcion		YES
0213	KU_3187	<i>Xiphocolaptes major</i>	Alto Paraguay		YES
0214	KU_3195	<i>Thamnophilus caerulescens</i>	Alto Paraguay	YES	YES
0215	KU_3215	<i>Xiphocolaptes major</i>	Alto Paraguay		YES
0216	KU_3700	<i>Thamnophilus caerulescens</i>	Itapua	YES	YES
0217	KU_3721	<i>Thamnophilus caerulescens</i>	Caazapa/Itapua	YES	YES
0218	KU_4023	<i>Platyrinchus mystaceus duidae</i>	Guyana	YES	YES
0219	KU_9040	<i>Xiphocolaptes promeropirhynchus</i>	El Salvador, Chalatenango	YES	YES
0220	KU_9772	<i>Xiphocolaptes major</i>	Jujuy	YES	YES
0221	KU_9864	<i>Thamnophilus ruficapillus cochabambae</i>	Jujuy	YES	YES
0222	KU_17412	<i>Thamnophilus palliatus</i>	Junin	YES	YES
0223	KU_18426	<i>Platyrinchus mystaceus</i>	Cusco	YES	YES
0224	KU_18521	<i>Platyrinchus mystaceus</i>	Cusco	YES	YES
0225	KU_18706	<i>Dysithamnus mentalis</i>	Cusco	YES	YES
0226	KU_18868	<i>Dysithamnus mentalis</i>	Cusco		YES
0227	KU_21588	<i>Thamnophilus ruficapillus</i>	Puno	YES	YES
0228	KU_21589	<i>Thamnophilus ruficapillus</i>	Puno	YES	YES
0229	KU_21634	<i>Thamnophilus caerulescens</i>	Puno		YES
0230	KU_21654	<i>Thamnophilus caerulescens</i>	Puno	YES	YES
0234	FMNH_334427	<i>Xiphocolaptes major castaneus</i>	Santa Cruz	YES	YES
0235	FMNH_334428	<i>Xiphocolaptes major castaneus</i>	El Beni	YES	YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0243	FMNH_397978	<i>Lochmias nematura obscurata</i>	Cusco	YES	YES
0244	FMNH_397980	<i>Lochmias nematura obscurata</i>	Cusco		YES
0245	FMNH_397982	<i>Lochmias nematura obscurata</i>	Cusco		YES
0246	FMNH_399228	<i>Dysithamnus mentalis emiliae</i>	Pernambuco		YES
0247	FMNH_399229	<i>Dysithamnus mentalis emiliae</i>	Pernambuco		YES
0248	FMNH_399230	<i>Dysithamnus mentalis emiliae</i>	Alagoas		YES
0249	FMNH_399231	<i>Dysithamnus mentalis emiliae</i>	Alagoas	YES	YES
0250	FMNH_399232	<i>Dysithamnus mentalis emiliae</i>	Alagoas		YES
0254	FMNH_429981	<i>Lochmias nematura obscurata</i>	Cusco	YES	YES
0255	FMNH_429983	<i>Lochmias nematura obscurata</i>	Cusco	YES	YES
0256	FMNH_429984	<i>Thamnophilus palliatus puncticeps</i>	Cusco	YES	YES
0257	FMNH_433368	<i>Lochmias nematura obscurata</i>	Cusco	YES	YES
0258	FMNH_433393	<i>Dysithamnus mentalis tavaresae</i>	Cusco		YES
0259	FMNH_433395	<i>Dysithamnus mentalis tavaresae</i>	Cusco	YES	YES
0260	FMNH_433397	<i>Dysithamnus mentalis tavaresae</i>	Cusco	YES	YES
0261	FMNH_474098	<i>Dysithamnus mentalis tambillanus</i>	Amazonas	YES	YES
0262	FMNH_474099	<i>Dysithamnus mentalis tambillanus</i>	Amazonas		YES
0263	FMNH_474100	<i>Dysithamnus mentalis tambillanus</i>	Amazonas	YES	YES
0264	FMNH_474102	<i>Dysithamnus mentalis tambillanus</i>	Amazonas		YES
0265	FMNH_474103	<i>Dysithamnus mentalis tambillanus</i>	Amazonas		YES
0266	FMNH_474104	<i>Dysithamnus mentalis tambillanus</i>	Amazonas		YES
0267	FMNH_481065	<i>Dysithamnus mentalis tambillanus</i>	Cajamarca	YES	YES
0268	ML 1862	<i>Lochmias nematura</i>	Minas Gerais	YES	YES
0269	ML 1863	<i>Lochmias nematura</i>	Minas Gerais	YES	YES
0270	ESS_196	<i>Lochmias nematura</i>	Santa Catarina	YES	YES
0271	ESS_198	<i>Lochmias nematura</i>	Santa Catarina		YES
0272	ML 2030	<i>Thamnophilus caeruleus</i>	Minas Gerais	YES	YES
0273	ML 2031	<i>Thamnophilus caeruleus</i>	Goiás	YES	YES
0274	BOR-14-23	<i>Dysithamnus mentalis</i>	São Paulo		YES
0275	BOR-14-32	<i>Thamnophilus caeruleus</i>	São Paulo		YES
0276	RM_06	<i>Lochmias nematura</i>	Minas Gerais	YES	YES
0277	MZ_85248	<i>Xiphocolaptes albicollis albicollis</i>	São Paulo	YES	YES
0278	MZ_95442	<i>Xiphocolaptes carajaensis</i>	Pará	YES	YES
0279	MZ_92713	<i>Xiphocolaptes promeropirhynchus paraensis</i>	Amazonas		YES
0280	MZ_92714	<i>Xiphocolaptes promeropirhynchus paraensis</i>	Amazonas		YES

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0281	MZ_99818	<i>Xiphocolaptes promeropirhynchus berlepschi</i>	Rondônia		YES
0282	BML_444	<i>Xiphocolaptes carajaensis</i>	Pará	YES	YES
0283	ML_2032	<i>Thamnophilus caerulescens</i>	Minas Gerais		YES
0284	MCP_2896	<i>Thamnophilus ruficapillus</i>	Rio Grande do Sul	YES	YES
0285	MCP_3110	<i>Thamnophilus ruficapillus</i>	Rio Grande do Sul	YES	YES
0286	MCP_3189	<i>Thamnophilus ruficapillus</i>	Rio Grande do Sul		YES
0287	MCP_3190	<i>Thamnophilus ruficapillus</i>	Rio Grande do Sul		YES
0288	MCP_3306	<i>Thamnophilus caerulescens</i>	Rio Grande do Sul	YES	YES
0290	MCP_3509	<i>Thamnophilus caerulescens</i>	Rio Grande do Sul		YES
0291	MCP_4038	<i>Thamnophilus ruficapillus</i>	Rio Grande do Sul		YES
0292	MCP_4051	<i>Lochmias nematura</i>	Rio Grande do Sul		YES
0293	MCP_4053	<i>Thamnophilus caerulescens</i>	Rio Grande do Sul		YES
0294	MCP_4058	<i>Thamnophilus ruficapillus</i>	Rio Grande do Sul		YES
0295	MCP_4085	<i>Dysithamnus mentalis</i>	Mato Grosso		YES
0296	MCP_4129	<i>Thamnophilus ruficapillus</i>	Rio Grande do Sul	YES	YES
0297	MCP_4389	<i>Philydor rufum</i>	Rio Grande do Sul	YES	YES
0298	MCP_4679	<i>Dysithamnus mentalis</i>	Santa Catarina		YES
0299	MCP_4843	<i>Thamnophilus caerulescens</i>	Santa Catarina	YES	YES
0300	MZ_70025	<i>Thamnophilus caerulescens ochraceiventer</i>	Goiás		
0306	ML_2030	<i>Thamnophilus caerulescens</i>	Minas Gerais		
0307	ML_2031	<i>Thamnophilus caerulescens</i>	Goiás		
0309	MPEG_T01670	<i>Thamnophilus palliatus</i>	Pará	YES	YES
0310	MPEG_T01987	<i>Philydor rufum</i>	Acre	YES	YES
0311	MPEG_T02234	<i>Dysithamnus mentalis</i>	Pará	YES	YES
0312	MPEG_T02538	<i>Xiphocolaptes promeropirhynchus</i>	Pará	YES	YES
0313	MPEG_T03450	<i>Dysithamnus mentalis</i>	Mato Grosso	YES	YES
0314	MPEG_T04522	<i>Xiphocolaptes promeropirhynchus</i>	Mato Grosso	YES	YES
0315	MPEG_T06852	<i>Thamnophilus torquatus</i>	Piauí		YES
0316	MPEG_T06873	<i>Thamnophilus torquatus</i>	Piauí	YES	YES
0317	MPEG_T06905	<i>Thamnophilus torquatus</i>	Piauí	YES	YES
0318	MPEG_T06924	<i>Thamnophilus torquatus</i>	Piauí	YES	YES
0319	MPEG_T08265	<i>Xiphocolaptes falcistrostris</i>	Maranhão	YES	YES
0323	MPEG_T09657	<i>Thamnophilus torquatus</i>	Piauí	YES	YES
0325	MPEG_T09706	<i>Dysithamnus mentalis</i>	Piauí		YES
0326	MPEG_T09855	<i>Dysithamnus mentalis</i>	Piauí		YES
0327	MPEG_T09867	<i>Dysithamnus mentalis</i>	Piauí		YES
0328	MPEG_T10072	<i>Thamnophilus torquatus</i>	Piauí		YES

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0329	MPEG_T10588	<i>Xiphocolaptes promeropirhynchus</i>	Mato Grosso	YES	YES
0332	MPEG_T11172	<i>Thamnophilus palliatus</i>	Mato Grosso	YES	YES
0333	MPEG_T11577	<i>Xiphocolaptes promeropirhynchus</i>	Mato Grosso		YES
0335	MPEG_T12338	<i>Xiphocolaptes promeropirhynchus</i>	Pará		YES
0336	MPEG_T12490	<i>Thamnophilus palliatus</i>	Pará	YES	YES
0337	MPEG_T12505	<i>Dysithamnus mentalis</i>	Pará		YES
0338	MPEG_T12705	<i>Thamnophilus palliatus</i>	Alagoas	YES	YES
0340	MPEG_T12861	<i>Dysithamnus mentalis</i>	Maranhão		
0341	MPEG_T12901	<i>Dysithamnus mentalis</i>	Maranhão		YES
0342	MPEG_T12907	<i>Dysithamnus mentalis</i>	Maranhão		YES
0343	MPEG_T12923	<i>Thamnophilus palliatus</i>	Maranhão	YES	YES
0344	MPEG_T12995	<i>Xiphocolaptes falcirostris</i>	Piauí	YES	YES
0347	MPEG_T13444	<i>Thamnophilus palliatus</i>	Bahia	YES	YES
0349	MPEG_T14940	<i>Thamnophilus caerulescens</i>	Santa Catarina	YES	YES
0351	MPEG_T14991	<i>Thamnophilus caerulescens</i>	Santa Catarina		YES
0352	MPEG_T15045	<i>Xiphocolaptes albicollis</i>	Santa Catarina	YES	YES
0353	MPEG_T15046	<i>Philydor rufum</i>	Santa Catarina		YES
0354	MPEG_T15047	<i>Philydor rufum</i>	Santa Catarina	YES	YES
0355	MPEG_T15048	<i>Philydor rufum</i>	Santa Catarina		YES
0356	MPEG_T15060	<i>Dysithamnus mentalis</i>	Santa Catarina		YES
0357	MPEG_T15076	<i>Lochmias nematura</i>	Santa Catarina	YES	YES
0358	MPEG_T15078	<i>Dysithamnus mentalis</i>	Santa Catarina		YES
0359	MPEG_T15098	<i>Dysithamnus mentalis</i>	Santa Catarina	YES	YES
0361	MPEG_T15175	<i>Dysithamnus mentalis</i>	Piauí	YES	YES
0362	MPEG_T15178	<i>Dysithamnus mentalis</i>	Piauí		
0363	MPEG_T15207	<i>Thamnophilus caerulescens</i>	Pernambuco		YES
0364	MPEG_T15223	<i>Dysithamnus mentalis</i>	Minas Gerais		YES
0365	MPEG_T15230	<i>Dysithamnus mentalis</i>	Minas Gerais		YES
0366	MPEG_T15231	<i>Dysithamnus mentalis</i>	Minas Gerais		YES
0367	MPEG_T15287	<i>Dysithamnus mentalis</i>	Mato Grosso	YES	YES
0368	MPEG_T15288	<i>Dysithamnus mentalis</i>	Mato Grosso	YES	YES
0369	MPEG_T15289	<i>Dysithamnus mentalis</i>	Mato Grosso	YES	YES
0370	MPEG_T15352	<i>Dysithamnus mentalis</i>	Goiás		YES
0371	MPEG_T15353	<i>Dysithamnus mentalis</i>	Goiás		YES
0372	MPEG_T15413	<i>Thamnophilus torquatus</i>	Minas Gerais		YES
0373	MPEG_T15414	<i>Thamnophilus torquatus</i>	Minas Gerais	YES	YES
0374	MPEG_T15415	<i>Thamnophilus torquatus</i>	Minas Gerais	YES	YES

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0375	MPEG_T15453	<i>Dysithamnus mentalis</i>	Mato Grosso		YES
0376	MPEG_T15454	<i>Dysithamnus mentalis</i>	Mato Grosso		YES
0377	MPEG_T15455	<i>Dysithamnus mentalis</i>	Mato Grosso		YES
0381	MPEG_T15530	<i>Dysithamnus mentalis</i>	Mato Grosso		YES
0386	MPEG_T15661	<i>Dysithamnus mentalis</i>	Tocantins	YES	YES
0387	MPEG_T15662	<i>Dysithamnus mentalis</i>	Tocantins		YES
0388	MPEG_T15683	<i>Philydor rufum</i>	Minas Gerais		
0389	MPEG_T15689	<i>Lochmias nematura</i>	Minas Gerais		YES
0390	MPEG_T15691	<i>Thamnophilus caerulescens</i>	Minas Gerais	YES	YES
0392	MPEG_T15720	<i>Thamnophilus caerulescens</i>	Minas Gerais		YES
0395	MPEG_T15741	<i>Thamnophilus torquatus</i>	Minas Gerais	YES	YES
0396	MPEG_T15750	<i>Dysithamnus mentalis</i>	Minas Gerais		YES
0397	MPEG_T15751	<i>Dysithamnus mentalis</i>	Minas Gerais		YES
0398	MPEG_T15752	<i>Dysithamnus mentalis</i>	Minas Gerais		YES
0399	MPEG_T15762	<i>Philydor rufum</i>	Minas Gerais		YES
0400	MPEG_T15783	<i>Thamnophilus caerulescens</i>	Minas Gerais		YES
0401	MPEG_T15786	<i>Philydor rufum</i>	Minas Gerais	YES	YES
0402	MPEG_T15792	<i>Dysithamnus mentalis</i>	Minas Gerais		
0403	MPEG_T16708	<i>Xiphocolaptes promeropirhynchus</i>	Pará		YES
0404	MPEG_T18772	<i>Xiphocolaptes promeropirhynchus</i>	Pará		YES
0405	MPEG_T18835	<i>Xiphocolaptes promeropirhynchus</i>	Pará		YES
0408	MPEG_T19396	<i>Xiphocolaptes promeropirhynchus</i>	Pará		YES
0409	MPEG_T19397	<i>Xiphocolaptes promeropirhynchus</i>	Pará		YES
0410	MPEG_T19427	<i>Xiphocolaptes promeropirhynchus</i>	Pará		YES
0411	MPEG_T19876	<i>Dysithamnus mentalis</i>	Maranhão		YES
0412	MPEG_T19877	<i>Dysithamnus mentalis</i>	Maranhão		YES
0413	MPEG_T19906	<i>Dysithamnus mentalis</i>	Maranhão		YES
0414	MPEG_T19916	<i>Thamnophilus palliatus</i>	Maranhão		YES
0415	MPEG_T20164	<i>Xiphocolaptes falcirostris</i>	Piauí		YES
0416	MPEG_T20167	<i>Xiphocolaptes falcirostris</i>	Piauí	YES	YES
0417	MPEG_T21092	<i>Dysithamnus mentalis</i>	Minas Gerais		YES
0418	MPEG_T21098	<i>Thamnophilus caerulescens</i>	Minas Gerais		
0419	MPEG_T21113	<i>Lochmias nematura</i>	Minas Gerais	YES	YES
0420	MPEG_T21152	<i>Dysithamnus mentalis</i>	Tocantins		YES
0421	MPEG_T21155	<i>Dysithamnus mentalis</i>	Tocantins	YES	YES
0422	MPEG_T21161	<i>Dysithamnus mentalis</i>	Tocantins		YES

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0423	MPEG_T21639	<i>Dysithamnus mentalis</i>	Tocantins		
0424	MPEG_T21651	<i>Dysithamnus mentalis</i>	Tocantins	YES	YES
0425	MPEG_T21688	<i>Dysithamnus mentalis</i>	Tocantins		YES
0426	MPEG_T21702	<i>Dysithamnus mentalis</i>	Tocantins		YES
0427	MPEG_T23067	<i>Thamnophilus palliatus</i>	Mato Grosso	YES	YES
0428	MPEG_T23096	<i>Dysithamnus mentalis</i>	Tocantins		YES
0429	MPEG_T23098	<i>Dysithamnus mentalis</i>	Tocantins		YES
0430	MPEG_T23718	<i>Thamnophilus palliatus</i>	Pará	YES	YES
0431	MPEG_T23982	<i>Dysithamnus mentalis</i>	Bahia		YES
0432	MPEG_T23983	<i>Dysithamnus mentalis</i>	Bahia		YES
0437	MPEG_T24942	<i>Xiphocolaptes promeropirhynchus</i>	Amazonas		YES
0438	MPEG_T24997	<i>Dysithamnus mentalis</i>	Pará		YES
0439	ML_5532	<i>Philydor rufum</i>	Santa Catarina		YES
0440	ML_5546	<i>Thamnophilus caerulescens</i>	Santa Catarina		YES
0442	ML_5590	<i>Philydor rufum</i>	Santa Catarina		YES
0443	UFG_4978	<i>Platyrrhinus mystaceus</i>	Maranhão		YES
0444	LSUB_12144	<i>Thamnophilus unicolor</i>	Ecuador	YES	YES
0445	BO475_EU295760	<i>Thamnophilus caerulescens</i>	Minas Gerais		YES
0446	BO513_EU295759	<i>Thamnophilus caerulescens</i>	Minas Gerais		YES
0447	FMNH_395426	<i>Thamnophilus caerulescens</i>	São Paulo		YES
0448	LSUB_1684	<i>Thamnophilus caerulescens</i>	Pasco		YES
0449	LSU_38284	<i>Thamnophilus caerulescens</i>	Santa Cruz		YES
0450	MPEG_CPEII037	<i>Thamnophilus caerulescens</i>	Pernambuco	YES	YES
0451	MZ_81155	<i>Thamnophilus caerulescens</i>	São Paulo		YES
0452	MZ_84352	<i>Thamnophilus caerulescens</i>	Santa Catarina		YES
0453	UWBM_77213	<i>Thamnophilus caerulescens</i>	Tarija	YES	YES
0454	UWBMRTB_407	<i>Thamnophilus caerulescens</i>	Cochabamba		YES
0455	YPM_10106_KJ_81 0434	<i>Thamnophilus caerulescens</i>	Artigas		YES
0456	MZ_90922	<i>Dysithamnus stictothorax</i>	Bahia		YES
0457	AMC_1266	<i>Dysithamnus mentalis</i>	Tachira		YES
0458	AMC_1310	<i>Dysithamnus mentalis</i>	Tachira		YES
0459	JM_1042	<i>Dysithamnus mentalis</i>	Tachira		YES
0460	JM_1102	<i>Dysithamnus mentalis</i>	Tachira		YES
0461	JPL_340	<i>Dysithamnus mentalis</i>	Tachira		YES
0462	JPL_341	<i>Dysithamnus mentalis</i>	Tachira		YES
0463	KCC_160	<i>Dysithamnus mentalis</i>	Tachira		YES
0464	KCC_178	<i>Dysithamnus mentalis</i>	Tachira		YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0465	KCC_246	<i>Dysithamnus mentalis</i>	Tachira		YES
0466	KCC_248	<i>Dysithamnus mentalis</i>	Tachira		YES
0467	KCC_255	<i>Dysithamnus mentalis</i>	Tachira		YES
0468	FMNH_293443	<i>Dysithamnus mentalis</i>	Pernambuco		YES
0469	IAvH_BT_112	<i>Dysithamnus mentalis</i>	Norte de Santander		YES
0470	IAvH_BT_114	<i>Dysithamnus mentalis</i>	Norte de Santander		YES
0471	LSU_72027	<i>Dysithamnus mentalis</i>	Costa Rica?		YES
0472	LSUB_25839	<i>Dysithamnus mentalis</i>	Caaguazu		YES
0473	LSUB_26463	<i>Dysithamnus mentalis</i>	Chiquiri	YES	YES
0474	LSUB_43612	<i>Dysithamnus mentalis</i>	San Martin		YES
0475	LSUB_48490	<i>Dysithamnus mentalis</i>	Guyana	YES	YES
0476	LSYUB_33085	<i>Dysithamnus mentalis</i>	Cajamarca	YES	YES
0477	ML_2720	<i>Platyrinchus mystaceus</i>	Alagoas		
0478	ML_2721	<i>Platyrinchus mystaceus</i>	Alagoas		
0479	ML_2731	<i>Platyrinchus mystaceus</i>	Alagoas		
0480	ML_2732	<i>Platyrinchus mystaceus</i>	Alagoas		
0481	ML_2716	<i>Dysithamnus mentalis</i>	Alagoas		YES
0482	ML_2733	<i>Dysithamnus mentalis</i>	Alagoas	YES	YES
0483	ML_2736	<i>Dysithamnus mentalis</i>	Alagoas		YES
0484	ML_2768	<i>Dysithamnus mentalis</i>	Alagoas		YES
0485	AMNH_12074_JF975324	<i>Lochmias nematura</i>	Misiones	YES	YES
0486	LSU_38510_KF705454	<i>Lochmias nematura</i>	SantaCruz	YES	YES
0487	GQ906717	<i>Xiphocolaptes major</i>	SantaCruz		YES
0488	UWBMMAB02	<i>Thamnophilus palliatus</i>	SantaCruz		YES
0489	UWBMRTB390	<i>Thamnophilus doliatus</i>	SantaCruz		YES
0490	LSUB38230	<i>Thamnophilus ruficapillus</i>	SantaCruz	YES	YES
0491	UWBMRTB347	<i>Thamnophilus ruficapillus</i>	SantaCruz		YES
0492	LSUB13900	<i>Thamnophilus torquatus</i>	SantaCruz	YES	YES
0493	LSUB14631	<i>Thamnophilus torquatus</i>	SantaCruz		YES
0494	MZ_85427	<i>Thamnophilus ruficapillus</i>	Minas Gerais		YES
0495	MPEG_55411_T1670	<i>Thamnophilus palliatus</i>	Pará		YES
0496	LSUMZ_B35610_KF705463	<i>Xiphocolaptes promeropirhynchus</i>	Pará	YES	YES
0497	LGEMA_P2333_JF975343	<i>Xiphocolaptes falcirostris</i>	Piauí	YES	YES
0498	IAvH2379	<i>Thamnophilus multistriatus</i>	Valle		YES
0499	IAvH8245	<i>Thamnophilus palliatus</i>	Vichada	YES	YES
0500	ANSP1686	<i>Thamnophilus tenuipunctatus</i>	Ecuador	YES	YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0501	KF705462	<i>Xiphocolaptes promeropirhynchus</i>	Honduras		YES
0502	SI_607841_EF501889	<i>Platyrrhinus mystaceus</i>	Panamá		YES
0503	AY089872	<i>Xiphocolaptes promeropirhynchus</i>	Cajamarca		YES
0504	JF975342	<i>Xiphocolaptes promeropirhynchus</i>	Cajamarca		YES
0505	LSUB32657	<i>Thamnophilus ruficapillus</i>	Cajamarca	YES	YES
0506	LSU_40199_JF975306	<i>Philydor rufum</i>	Loreto	YES	YES
0507	LSUB58400	<i>Thamnophilus palliatus</i>	Puno	YES	YES
0508	LSUB58333	<i>Thamnophilus ruficapillus</i>	Puno	YES	YES
0509	LSUB44648	<i>Thamnophilus tenuipunctatus</i>	San Martin	YES	YES
0510	JF975349	<i>Dendrocolaptes platyrostris</i>	Paraguay		YES
0511	LSUMZ_25944_JF975344	<i>Xiphocolaptes albicollis</i>	Paraguay	YES	YES
0512	NRM_976724_KF228509	<i>Platyrrhinus mystaceus</i>	Concepcion		YES
0515	YPM_1141_KJ810387	<i>Lochmias nematura</i>	Uruguay		YES
0516	LSU_7481_HM125593	<i>Lochmias nematura</i>	Amazonas		YES
0518	Pla_mys_28375	<i>Platyrrhinus mystaceus</i>	Panama		YES
0519	LSUMZ_25794	<i>Xiphocolaptes major</i>	Paraguay	YES	YES
0520	Xip_pro_4526	<i>Xiphocolaptes promeropirhynchus</i>	Loreto		YES
0521	Xip_pro_7998	<i>Xiphocolaptes promeropirhynchus</i>	Pasco		YES
0522	Xip_pro_41765	<i>Xiphocolaptes promeropirhynchus</i>	Cochabamba		YES
0523	MZ_92166	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		
0524	MZ_92167	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		
0525	MZ_92484	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		
0526	MZ_92485	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		
0527	MZ_92486	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		
0528	MZ_93536	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		
0529	MZ_93537	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		
0530	MZ_93538	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		
0531	BOR 14-46	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		YES
0532	BOR 14-78	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		YES
0533	SM_04	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		YES
0534	BOR 14-05	<i>Platyrrhinus mystaceus mystaceus</i>	São Paulo		YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0535	MZ_94442	<i>Platyrrhinus mystaceus cancrum</i>	Minas Gerais		
0536	UFG_4483	<i>Platyrrhinus mystaceus cancrum</i>	Maranhão	YES	
0537	MCP_5493	<i>Platyrrhinus mystaceus cancrum</i>	Santa Catarina		YES
0538	MCP_5495	<i>Platyrrhinus mystaceus cancrum</i>	Santa Catarina		YES
0539	MCP_5514	<i>Platyrrhinus mystaceus cancrum</i>	Santa Catarina	YES	YES
0540	MCP_5527	<i>Platyrrhinus mystaceus cancrum</i>	Santa Catarina	YES	YES
0541	ALG-159	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0542	ALG-158	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0543	ALG-39	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0544	ALG-48	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0545	FMNH_427096	<i>Platyrrhinus mystaceus niveigularis</i>	Pernambuco		YES
0546	FMNH_427097	<i>Platyrrhinus mystaceus niveigularis</i>	Pernambuco		YES
0547	FMNH_427098	<i>Platyrrhinus mystaceus niveigularis</i>	Pernambuco		YES
0548	FMNH_427099	<i>Platyrrhinus mystaceus niveigularis</i>	Pernambuco		YES
0549	FMNH_427100	<i>Platyrrhinus mystaceus niveigularis</i>	Pernambuco	YES	YES
0550	FMNH_427101	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0551	FMNH_427102	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0552	FMNH_427103	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0553	FMNH_427104	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0554	FMNH_427105	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0555	FMNH_427106	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0556	MCP_3089	<i>Platyrrhinus mystaceus mystaceus</i>	Rio Grande do Sul	YES	YES
0557	MCP_4699	<i>Platyrrhinus mystaceus cancrum</i>	Santa Catarina		YES
0558	MPEG_68442	<i>Platyrrhinus mystaceus cancrum</i>	Maranhão		
0559	MPEG_68441	<i>Platyrrhinus mystaceus cancrum</i>	Maranhão		
0560	LZUFPI_0174	<i>Platyrrhinus mystaceus cancrum</i>	Piauí	YES	YES
0561	LZUFPI_0176	<i>Platyrrhinus mystaceus cancrum</i>	Piauí		
0562	LZUFPI_0322	<i>Platyrrhinus mystaceus cancrum</i>	Piauí		
0563	COUFT_0515	<i>Platyrrhinus mystaceus cancrum</i>	Tocantins	YES	YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0564	MPEG_T23638	<i>Platyrrhinus mystaceus cancrum</i>	Piauí	YES	YES
0565	MPEG_70184	<i>Platyrrhinus mystaceus cancrum</i>	Maranhão	YES	YES
0566	MPEG_DZ_4934	<i>Platyrrhinus mystaceus cancrum</i>	Minas Gerais	YES	YES
0567	MPEG_DZ_6768	<i>Platyrrhinus mystaceus cancrum</i>	Minas Gerais		
0568	DZ_4935	<i>Platyrrhinus mystaceus cancrum</i>	Minas Gerais		YES
0569	DZ_5020	<i>Platyrrhinus mystaceus cancrum</i>	Minas Gerais	YES	YES
0570	DZ_6769	<i>Platyrrhinus mystaceus cancrum</i>	Minas Gerais		
0571	DZ_6772	<i>Platyrrhinus mystaceus cancrum</i>	Minas Gerais	YES	YES
0572	DZ_6770	<i>Platyrrhinus mystaceus cancrum</i>	Minas Gerais		YES
0573	MPEG_74929	<i>Platyrrhinus mystaceus cancrum</i>	Pará	YES	YES
0574	CFL-CO_122	<i>Platyrrhinus mystaceus cancrum</i>	Minas Gerais		YES
0575	MPEG_74360	<i>Platyrrhinus mystaceus cancrum</i>	Piauí		
0576	MPEG_79462	<i>Platyrrhinus mystaceus cancrum</i>	Tocantins		YES
0577	MPEG_79465	<i>Platyrrhinus mystaceus cancrum</i>	Tocantins		YES
0578	MPEG_79466	<i>Platyrrhinus mystaceus cancrum</i>	Tocantins	YES	YES
0579	MPEG_79463	<i>Platyrrhinus mystaceus cancrum</i>	Tocantins		YES
0580	MPEG_72017	<i>Platyrrhinus mystaceus cancrum</i>	Santa Catarina		YES
0581	MPEG_71977	<i>Platyrrhinus mystaceus cancrum</i>	Santa Catarina		YES
0582	MPEG_71978	<i>Platyrrhinus mystaceus cancrum</i>	Santa Catarina		YES
0583	DZ_6771	<i>Platyrrhinus mystaceus cancrum</i>	Minas Gerais		YES
0584	COUFT_0531	<i>Platyrrhinus mystaceus cancrum</i>	Tocantins		YES
0585	COUFT_0434	<i>Platyrrhinus mystaceus cancrum</i>	Tocantins		YES
0586	MPEG_74361	<i>Platyrrhinus mystaceus cancrum</i>	Piauí		YES
0587	MPEG_79461	<i>Platyrrhinus mystaceus cancrum</i>	Tocantins	YES	YES
0588	MPEG_70476	<i>Platyrrhinus mystaceus niveigularis</i>	Alagoas		YES
0589	MPEG_71880	<i>Platyrrhinus mystaceus mystaceus</i>	Bahia		YES
0590	MPEG_71881	<i>Platyrrhinus mystaceus mystaceus</i>	Bahia		YES
0591	MPEG_76409	<i>Platyrrhinus m.c. (platyrinchos)</i>	Pará		YES
0592	MPEG_76444	<i>Platyrrhinus mystaceus cancrum</i>	Pará	YES	YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0593	FMNH_394013	<i>Xiphocolaptes promeropirhynchus</i>	Hidalgo	YES	YES
0594	IAvH_14827_H11442	<i>Xiphocolaptes promeropirhynchus</i>	Norte de Santander	YES	YES
0595	LSUMZ_105996	<i>Dysithamnus mentalis olivaceus</i>	Pasco	YES	YES
0596	IAvH-BT_4241	<i>Dysithamnus mentalis extremus</i>	Valle del Cauca	YES	YES
0597	IAvH-BT_34527	<i>Dysithamnus mentalis semicinctus</i>	Antioquia	YES	YES
0598	ANSP_185449	<i>Dysithamnus mentalis napensis</i>	Napo	YES	YES
0599	LSUMZ_162665	<i>Dysithamnus mentalis tavarai</i>	La Paz	YES	YES
0600	LSUMZ_183140	<i>Dysithamnus mentalis aequatorialis</i>	Tumbes	YES	YES
0601	LSUMZ_45867	<i>Dysithamnus mentalis andrei</i>	Trinidad	YES	YES
0602	LSUMZ_46017	<i>Dysithamnus mentalis oberi</i>	Tobago	YES	YES
0603	LSUMZ_105988	<i>Thamnophilus caeruleus melanocephalus</i>	Pasco	YES	YES
0604	LSUMZ_171295	<i>Thamnophilus caeruleus paraguayensis</i>	Santa Cruz	YES	YES
0605	LSUMZ_168944	<i>Thamnophilus caeruleus connectens</i>	Santa Cruz	YES	YES
0606	LSUMZ_170871	<i>Thamnophilus caeruleus subandinus</i>	Loreto	YES	YES
0607	LSUMZ_179678	<i>Thamnophilus caeruleus aspersiventer</i>	Puno	YES	YES
0608	MZUSP_81155	<i>Thamnophilus caeruleus caeruleus</i>	São Paulo	YES	YES
0609	LSUMZ_B1134	<i>Dysithamnus mentalis</i>	La Paz	YES	YES
0610	LSUMZ_B6155	<i>Dysithamnus mentalis</i>	Morona-Santiago	YES	YES
0611	LSUMZ_B13848	<i>Dysithamnus mentalis</i>	Santa Cruz	YES	YES
0612	LSUMZ_B38408	<i>Dysithamnus mentalis</i>	Santa Cruz	YES	YES
0613	LSUMZ_B38935	<i>Dysithamnus mentalis</i>	Cochabamba	YES	YES
0614	LSUMZ_B40022	<i>Dysithamnus mentalis</i>	Loreto	YES	YES
0615	LSUMZ_B68224	<i>Dysithamnus mentalis</i>	Beni	YES	YES
0616	LSUMZ_B72029	<i>Dysithamnus mentalis</i>	Cartago	YES	YES
0617	LSUMZ_B76452	<i>Dysithamnus mentalis</i>	Ucayali	YES	YES
0618	LSUMZ_B89140	<i>Dysithamnus mentalis</i>	Ucayali	YES	YES
0619	LSUMZ_B2033	<i>Lochmias nematura</i>	Pasco	YES	YES
0620	LSUMZ_B7488	<i>Lochmias nematura</i>	Amazonas	YES	YES
0621	LSUMZ_B22682	<i>Lochmias nematura</i>	La Paz	YES	YES
0622	LSUMZ_B25963	<i>Lochmias nematura</i>	Caazapa	YES	YES
0623	LSUMZ_B33710	<i>Lochmias nematura</i>	Cajamarca	YES	YES
0624	LSUMZ_B43594	<i>Lochmias nematura</i>	San Martin	YES	YES
0625	LSUMZ_B48459	<i>Lochmias nematura</i>	Potaro-Siparuni	YES	YES
0626	LSUMZ_B38369	<i>Philydor rufum</i>	Santa Cruz	YES	YES
0627	LSUMZ_B81957	<i>Philydor rufum</i>	San Jose	YES	YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0628	LSUMZ_B11885	<i>Philydor rufum</i>	Esmeraldas	YES	YES
0629	LSUMZ_B12127	<i>Philydor rufum</i>	Pichincha	YES	YES
0630	LSUMZ_B29942	<i>Philydor rufum</i>	Imbabura	YES	YES
0631	LSUMZ_B25966	<i>Philydor rufum</i>	Caazapa	YES	YES
0632	LSUMZ_B40199	<i>Philydor rufum</i>	Loreto	YES	YES
0633	LSUMZ_B89099	<i>Philydor rufum</i>	Ucayali	YES	YES
0637	LSUMZ_B22863	<i>Thamnophilus palliatus</i>	La Paz	YES	YES
0638	LSUMZ_B38417	<i>Thamnophilus palliatus</i>	Santa Cruz	YES	YES
0639	LSUMZ_B46060	<i>Thamnophilus palliatus</i>	San Martin	YES	YES
0640	LSUMZ_B68260	<i>Thamnophilus palliatus</i>	Beni	YES	YES
0641	LSUMZ_B89121	<i>Thamnophilus palliatus</i>	Ucayali	YES	YES
0642	LSUMZ_B87886	<i>Thamnophilus ruficapillus</i>	La Paz	YES	YES
0643	LSUMZ_B25944	<i>Xiphocolaptes albicollis</i>	Caaguazu	YES	YES
0644	LSUMZ_B25756	<i>Xiphocolaptes major</i>	Alto Paraguay	YES	YES
0645	LSUMZ_B38885	<i>Xiphocolaptes major</i>	Santa Cruz	YES	YES
0646	LSUMZ_B1874	<i>Xiphocolaptes promeropirhynchus</i>	Pasco	YES	YES
0647	LSUMZ_B4526	<i>Xiphocolaptes promeropirhynchus</i>	Loreto	YES	YES
0648	LSUMZ_B7774	<i>Xiphocolaptes promeropirhynchus</i>	Pichincha	YES	YES
0649	LSUMZ_B8795	<i>Xiphocolaptes promeropirhynchus</i>	Toledo	YES	YES
0650	LSUMZ_B32421	<i>Xiphocolaptes promeropirhynchus</i>	Cajamarca	YES	YES
0651	LSUMZ_B41765	<i>Xiphocolaptes promeropirhynchus</i>	Cochabamba	YES	YES
0652	LSUMZ_B44821	<i>Xiphocolaptes promeropirhynchus</i>	Loreto	YES	YES
0653	LSUMZ_B60983	<i>Xiphocolaptes promeropirhynchus</i>	Francisco Morazan	YES	YES
0654	LSUMZ_B66570	<i>Xiphocolaptes promeropirhynchus</i>	Tumbes	YES	YES
0655	LSUMZ_B87638	<i>Xiphocolaptes promeropirhynchus</i>	Cochabamba	YES	YES
0656	LSUMZ_B89012	<i>Xiphocolaptes promeropirhynchus</i>	Ucayali	YES	YES
0657	LSUMZ_B103529	<i>Xiphocolaptes promeropirhynchus</i>	Loreto	YES	YES
0659	MZ_81269	<i>Thamnophilus aethiops incertus</i>	Maranhão	YES	YES
0660	MZ_93741	<i>Thamnophilus aethiops polionotus</i>	Roraima	YES	YES
0661	J_1799	<i>Thamnophilus aethiops injunctus</i>	Rondônia	YES	YES
0662	LSU_58402	<i>Thamnophilus aroyae</i>	Puno	YES	YES
0663	H_2314	<i>Thamnophilus unicolor</i>	Huila	YES	YES
0664	USNM_625181_C MM 981	<i>Dysithamnus mentalis</i>	Upper Takutu-Upper Essequibo	YES	YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0665	USNM_635781_C MM_3056	<i>Lochmias nematura</i>	Maldonado	YES	YES
0668	USNM_630526_CA G_773	<i>Thamnophilus ruficapillus</i>	Colonia	YES	YES
0669	USNM_637091_C MM_3391	<i>Xiphocolaptes promeropirhynchus</i>	Upper Takutu-Upper Essequibo	YES	YES
0670	USNM_586354	<i>Xiphocolaptes promeropirhynchus</i>	Barima-Waini	YES	YES
0671	LSU_58381	<i>Thamnophilus palliatus</i>	Puno	YES	YES
0672	LSU_58414	<i>Thamnophilus palliatus</i>	Puno	YES	YES
0673	LSU_31651	<i>Thamnophilus ruficapillus</i>	SantaCruz	YES	YES
0674	LSU_14842	<i>Thamnophilus torquatus</i>	SantaCruz	YES	YES
0675	YPM_148411	<i>Thamnophilus ruficapillus</i> <i>ruficapillus</i>	Cerro Largo	YES	YES
0685	LSU_6111	<i>Dysithamnus leucostictus</i>	Morona-Santiago	YES	YES
0686	LSU_10637	<i>Ancistrops strigilatus</i>	Ucayali	YES	YES
0687	AMNH_12102	<i>Phleocryptes melanops</i>	Buenos Aires	YES	YES
0688	LSUMZ_39987	<i>Platyrrhinus mystaceus</i>	Loreto	YES	YES
0691	LSUMZ_35598	<i>Xiphorhynchus ocellatus</i>	Pará	YES	YES
0692	LSU_25854	<i>Philydor atricapillus</i>	Caazapa	YES	YES
0693	LSU_6965	<i>Philydor erythrocerum</i>	Loreto	YES	YES
0694	LSU_2250	<i>Philydor fuscipenne</i>	Darien	YES	YES
0695	LSU_10571	<i>Philydor erythropterum</i>	Ucayali	YES	YES
0696	LSU_10585	<i>Philydor pyrrhodes</i>	Ucayali	YES	YES
0697	LSUMZ_178807	<i>Thamnophilus doliatus</i>	Veraguas	YES	YES
0698	IAvH_12330	<i>Thamnophilus multistriatus</i>	Valle	YES	YES
0699	LSUMZ_183135	<i>Thamnophilus zarumae</i>	Tumbes	YES	YES
0700	MZ_94442	<i>Platyrrhinus mystaceus</i> <i>cancromus</i>	Minas Gerais	YES	YES
0701	MZ_92167	<i>Platyrrhinus mystaceus</i>	São Paulo	YES	YES
0702	MZ_92484	<i>Platyrrhinus mystaceus</i>	São Paulo	YES	YES
0703	MZ_92485	<i>Platyrrhinus mystaceus</i>	São Paulo	YES	YES
0704	MZ_93536	<i>Platyrrhinus mystaceus</i>	São Paulo	YES	YES
0705	MZ_99454	<i>Platyrrhinus mystaceus</i>	Alagoas	YES	YES
0706	MZ_99412	<i>Platyrrhinus mystaceus</i>	Alagoas	YES	YES
0707	LSUMZ_B5542	<i>Platyrrhinus mystaceus</i> <i>zamorae</i>	San Martin	YES	YES
0708	LSUMZ_B5970	<i>Platyrrhinus mystaceus</i> <i>zamorae</i>	Morona-Santiago	YES	YES
0709	LSUMZ_B7434	<i>Platyrrhinus mystaceus duidae</i>	Amazonas	YES	YES
0710	LSUMZ_B7616	<i>Platyrrhinus mystaceus</i> <i>bifasciatus</i>	Beni	YES	YES
0711	LSUMZ_B11966	<i>Platyrrhinus mystaceus</i> <i>albugularis</i>	Esmeraldas	YES	YES
0712	LSUMZ_B16047	<i>Platyrrhinus mystaceus</i> <i>neglectus</i>	Heredia	YES	YES

Internal number	number/field number	Taxon	State	UCEs Sequences	ND2 Sequences
0713	LSUMZ_B22637	<i>Platyrrhinus mystaceus partridgei</i>	La Paz	YES	YES
0714	LSUMZ_B26448	<i>Platyrrhinus mystaceus neglectus</i>	Chiriqui	YES	YES
0715	LSUMZ_B27767	<i>Platyrrhinus mystaceus zamorae</i>	Loreto	YES	YES
0716	LSUMZ_B32985	<i>Platyrrhinus mystaceus</i>	Cajamarca	YES	YES
0717	LSUMZ_B35967	<i>Platyrrhinus mystaceus insularis</i>	Caroni	YES	YES
0718	LSUMZ_B39987	<i>Platyrrhinus mystaceus</i>	Loreto		YES
0719	L_28375	<i>Platyrrhinus mystaceus</i>	Panama District	YES	YES
0720	USNM_607842	<i>Platyrrhinus cancrivorus</i>	Bocas del Toro	YES	YES
0721	L_55356	<i>Platyrrhinus saturatus</i>	Sipaliwini	YES	YES
0722	USNM_625250	<i>Platyrrhinus platyrhynchos</i>	Upper Takutu-Upper Essequibo	YES	YES
0723	LSUMZ_33080	<i>Platyrrhinus flavigularis</i>	Cajamarca	YES	YES
0724	KU_88454	<i>Platyrrhinus leucorhynchus</i>	Caazapa	YES	YES
0725	L_11136	<i>Platyrrhinus coronatus</i>	Ucayali	YES	YES
0726	MPEG_79461	<i>Platyrrhinus mystaceus cancrivorus</i>	Tocantins	YES	YES
0727	FMNH_399223	<i>Thamnomphylus aethiops</i>	Alagoas		YES
0728	MPEG_62216	<i>Thamnomphylus aethiops</i>	Amazonas		YES

Table S2. Samples of ND2 gene for all species analyzed.

Species	Number ND2 samples	Outgroup
<i>Dysithamnus mentalis</i>	135	<i>D. leucostictus</i>
<i>Lochmias nematura</i>	26	<i>Phleocryptes melanops</i>
<i>Philydor rufum</i>	23	<i>P. erythropterus/P. atricapillus</i>
<i>Platyrrhinus mystaceus</i>	136	<i>P. flavigularis/P. leucorhynchus</i>
<i>Thamnomphylus caeruleus</i>	53	<i>Thamnomphylus aethiops</i>
<i>T. palliatus/tenuipunctatus</i> complex	26/2	<i>Thamnomphylus zarumae</i>
<i>T. ruficapillus/torquatus</i> complex	13/12	<i>Thamnomphylus doliatus</i>
<i>Xiphocolaptes</i> complex	68	<i>Xiphorhynchus ocellatus</i>

Table S3. Nucleotide diversity all species.

Species	Nucleotide Diversity	Variance
<i>Dysithamnus mentalis</i>	0.00869463	1.99E-05
<i>Lochmias nematura</i>	0.031939979	0.000256931
<i>Platyrinchus mystaceus</i>	0.023392946	0.000131059
<i>Philydor rufum</i>	0.012618761	4.32E-05
<i>Thamnophilus caerulescens</i>	0.012732651	4.17E-05
<i>Thamnophilus palliatus/tenuipunctatus</i> complex	0.006864306	1.36E-05
<i>Thamnophilus ruficapillus/torquatus</i> complex	0.023857934	0.000145938
<i>Xiphocolaptes</i> complex	0.020094585	9.91E-05

Table S4. D' Tajima test for all species.

Species	D' Tajima	Pval_normal	Pval_beta
<i>Dysithamnus mentalis</i>	-2.251003653	0.024385306	0.005592793
<i>Lochmias nematura</i>	-0.620660997	0.534822697	0.575138869
<i>Platyrinchus mystaceus</i>	-3.045099416	0.002326034	2.93E-12
<i>Philydor rufum</i>	-3.383077795	0.000716783	0
<i>Thamnophilus caerulescens</i>	-2.9958257	0.002737028	9.17E-11
<i>Thamnophilus palliatus/tenuipunctatus</i> complex	-2.413419957	0.015803599	0.001768009
<i>Thamnophilus ruficapillus/torquatus</i> complex	-0.157467034	0.874876787	0.910419562
<i>Xiphocolaptes</i> complex	-2.268353921	0.023307644	0.005799934

Table S5. AMOVA values for all species.

Species	Variations between groups	Variations between samples within groups	Variations within samples	Total variations
<i>Dysithamnus mentalis</i>	34.76625693	43.54157179	21.69217128	100
<i>Lochmias nematura</i>	51.70021181	20.68458654	27.61520165	100
<i>Platyrinchus mystaceus</i>	67.69385985	27.05626627	5.249873881	100
<i>Philydor rufum</i>	62.52351139	31.9792931	5.497195517	100
<i>Thamnophilus caeruleus</i>	43.20605233	34.08672707	22.70722059	100
<i>T. palliatus/tenuipunctatus</i> complex	33.82054327	38.80766396	27.37179277	100
<i>T. ruficapillus/torquatus</i> complex	14.67363551	21.94052388	63.38584061	100
<i>Xiphocolaptes</i> complex	53.34949299	23.51860245	23.13190457	100

Table S6. Watterson test for all species.

Species	Theta	Variance
<i>Dysithamnus mentalis</i>	27.0873717	42.85078595
<i>Lochmias nematura</i>	35.37774622	132.6569364
<i>Platyrinchus mystaceus</i>	123.370606	810.7423874
<i>Philydor rufum</i>	38.20296245	162.7101482
<i>Thamnophilus caeruleus</i>	61.74187531	293.7406216
<i>Thamnophilus palliatus/tenuipunctatus</i> complex	13.61957831	20.97534304
<i>Thamnophilus ruficapillus/torquatus</i> complex	25.4240104	71.42068774
<i>Xiphocolaptes</i> complex	52.19912396	190.966409

Table S7. Nucleotide diversity of populations of *D. mentalis*.

Groups/ <i>D. mentalis</i>	Nucleotide diversity	Variance
<i>affinis</i>	0.003418803	4.3574E-06
<i>mentalis</i>	0.007060315	0.000014104
Andes	0.006964809	1.36037E-05
Northern Brazil	0.004392126	6.0192E-06

Table S8. Fst values for the populations of *D. mentalis*.

fst - Groups/<i>D. mentalis</i>	Northern Brazil	<i>mentalis</i>	<i>affinis</i>	Andes
Northern Brazil	0	0.28071366	0.208782539	0.186198921
<i>mentalis</i>	0.28071366	0	0.259570255	0.262508232
<i>affinis</i>	0.208782539	0.259570255	0	0.109405627
Andes	0.186198921	0.262508232	0.109405627	0

Table S9. Nucleotide diversity of populations of *L. nematura*.

Groups/<i>L. nematura</i>	Nucleotide diversity	Variance
Atlantic Forest	0.005226719	0.00000915
Central Andes	0.032928693	0.000308371
Tepuis	0.000970874	0.00000188

Table S10. Fst values for the populations of *L. nematura*.

fst – Groups/<i>L. nematura</i>	Atlantic Forest	Central Andes	Tepuis
Atlantic Forest	0	0.47698182	0.276255343
Central Andes	0.47698182	0	0.255304392
Tepuis	0.276255343	0.255304392	0

Table S11. Nucleotide diversity of populations of *P. mystaceus*.

Groups/<i>P. mystaceus</i>	Nucleotide diversity	Variance
Andes	0.032865845	0.000296936
Atlantic Forest	0.01040153	0.000028
<i>niveigularis</i>	0.003384841	0.0000039

Table S12. Fst values for the populations of *P. mystaceus*.

fst – Groups/<i>P. mystaceus</i>	<i>niveigularis</i>	Atlantic Forest	Andes
<i>niveigularis</i>	0	0.577715915	0.510731188
Atlantic Forest	0.577715915	0	0.253501627
Andes	0.510731188	0.253501627	0

Table S13. Nucleotide diversity of populations of *P. rufum*.

Groups/<i>P. rufum</i>	Nucleotide diversity	Variance
Atlantic Forest	0.001905654	1.69E-06
Andes	0.012045925	4.42E-05

Table S14. Fst values for the populations of *P. rufum*.

fst – Groups/<i>P. rufum</i>	Atlantic Forest	Andes
Atlantic Forest	0	0.510964386
Andes	0.510964386	0

Table S15. Nucleotide diversity of populations of *T. caerulescens*.

Groups/<i>T. caerulescens</i>	Nucleotide diversity	Variance
Andean	0.013748868	0.0000558
<i>caerulescens</i>	0.005067237	0.00000782
<i>cearensis</i>	0.001976422	0.00000198

Table S16. Fst values for the populations of *T. caerulescens*.

fst – Groups/<i>T. caerulescens</i>	<i>cearensis</i>	<i>caerulescens</i>	Andean
<i>cearensis</i>	0	0.538138706	0.423313568
<i>caerulescens</i>	0.538138706	0	0.229798545
Andean	0.423313568	0.229798545	0

Table S17. Nucleotide diversity of populations of *T. palliatus-tenuepunctatus* complex.

Groups/ <i>T. palliatus-tenuepunctatus</i>	Nucleotide diversity	Variance
Atlantic Forest (<i>T. p. vestitus</i>)	0.000455996	0.000000274
Central Andes (<i>T. p. puncticeps</i>)	0.005723577	0.0000135
Northern Andes	0.007284553	0.000021
<i>palliatus</i>	0.004054054	0.00000617

Table S18. Fst values for the populations of *T. palliatus-tenuepunctatus* complex.

fst – Groups/ <i>T. palliatus-tenuepunctatus</i>	Northern Andes	Atlantic Forest (<i>T. p. vestitus</i>)	<i>palliatus</i>	Central Andes (<i>T. p. vestitus</i>)
Northern Andes	0	0.333535855	0.17584282	0.374625835
Atlantic Forest (<i>T. p. vestitus</i>)	0.333535855	0	0.117723638	0.584490405
<i>palliatus</i>	0.17584282	0.117723638	0	0.425881627
Central Andes (<i>T. p. puncticeps</i>)	0.374625835	0.584490405	0.425881627	0

Table S19. Nucleotide diversity of populations of *T. ruficapillus-torquatus* complex.

Groups/ <i>T. ruficapillus-torquatus</i>	Nucleotide diversity	Variance
Northern Atlantic Forest	0.027636364	0.00021892
Southern Atlantic Forest	0.005774783	0.0000137
Central Andes	0.021707317	0.000149177

Table S20. Fst values for the populations of *T. ruficapillus-torquatus* complex.

fst – Groups/<i>T. ruficapillus-torquatus</i>	Central Andes	Southern Atlantic Forest	Northern Atlantic Forest
Central Andes	0	0.221523446	0.08710577
Southern Atlantic Forest	0.221523446	0	0.258282196
Northern Atlantic Forest	0.08710577	0.258282196	0

Table S21. Nucleotide diversity of populations of *Xiphocolaptes* complex.

Groups/<i>Xiphocolaptes</i> complex	Nucleotide diversity	Variance
Amazonian (<i>X. p. orenocensis</i>)	0.007103464	0.0000148
Andes (highlands)	0.010997632	0.0000335
Atlantic Forest (<i>X. albicollis</i>)	0.002405396	0.00000242
Caatinga (<i>X. falcistrotris</i>)	0.000768492	0.000000586
Tepuis + Central America	0.009450338	0.000034

Table S22. Fst values for the populations of *Xiphocolaptes* complex.

fst – Groups/<i>Xiphocolaptes</i> complex	Atlantic Forest (<i>X. albicollis</i>)	Amazonian (<i>X. p. orenocensis</i>)	Andes (highlands)	Tepuis + Central America	Caatinga (<i>X. falcistrotris</i>)
Atlantic Forest (<i>X. albicollis</i>)	0	0.672407001	0.488897976	0.667094017	0.864127982
Amazonian (<i>X. p. orenocensis</i>)	0.672407001	0	0.480218347	0.380000248	0.580884235
Andes (highlands)	0.488897976	0.480218347	0	0.255366951	0.4195593
Tepuis + Central America	0.667094017	0.380000248	0.255366951	0	0.703045975
Caatinga (<i>X. falcistrotris</i>)	0.864127982	0.580884235	0.4195593	0.703045975	0

Table S23. Cross-entropy values for *D. mentalis* ($\alpha=1, 10, 50, 100, 500, 1000$).

Alpha=1	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.32819	0.30028	0.29311	0.28945	0.29359	0.30219	0.30352	0.31382	0.31463	0.33262	0.28945	0.29311	0.00365
mean	0.35265	0.32493	0.31938	0.31803	0.32229	0.32807	0.33356	0.34061	0.34734	0.35557	0.31803	0.31938	0.00135
max	0.38116	0.34961	0.34756	0.34027	0.34762	0.35868	0.36573	0.37150	0.38269	0.39560	0.34027	0.34756	0.00729
Alpha=10	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.32956	0.30167	0.29540	0.29131	0.29841	0.30421	0.30558	0.31345	0.32293	0.32694	0.29131	0.29540	0.00410
mean	0.35537	0.32758	0.32189	0.32119	0.32558	0.33108	0.33663	0.34414	0.35163	0.35897	0.32119	0.32189	0.00071
max	0.37523	0.34639	0.34331	0.34755	0.35264	0.35410	0.37069	0.37017	0.37785	0.38424	0.34331	0.34639	0.00308
Alpha=50	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.32465	0.29819	0.29250	0.28969	0.29700	0.29708	0.30786	0.31099	0.32365	0.32405	0.28969	0.29250	0.00281
mean	0.35385	0.32599	0.32034	0.31986	0.32394	0.32970	0.33658	0.34437	0.35298	0.36065	0.31986	0.32034	0.00048
max	0.38727	0.36026	0.36137	0.35683	0.35866	0.36559	0.36770	0.38910	0.39455	0.39349	0.35683	0.35866	0.00183
Alpha=100	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.32414	0.29326	0.28900	0.28704	0.28995	0.29752	0.30972	0.31400	0.32447	0.32914	0.28704	0.28900	0.00196
mean	0.35298	0.32518	0.31965	0.31890	0.32444	0.33036	0.33944	0.34641	0.35376	0.36420	0.31890	0.31965	0.00074
max	0.37519	0.34766	0.34597	0.34249	0.34764	0.36089	0.36607	0.37134	0.38263	0.39334	0.34249	0.34597	0.00348
Alpha=500	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.31913	0.29234	0.29297	0.28644	0.28949	0.30357	0.30913	0.31466	0.33568	0.33667	0.28644	0.28949	0.00305
mean	0.35284	0.32592	0.32475	0.32428	0.33154	0.34014	0.35030	0.36028	0.37206	0.38411	0.32428	0.32475	0.00047
max	0.39593	0.36736	0.36236	0.37350	0.37060	0.38341	0.39135	0.40364	0.42117	0.43984	0.36236	0.36736	0.00500
Alpha=1000	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.32370	0.29830	0.29160	0.29250	0.30225	0.30658	0.31613	0.33990	0.34588	0.35339	0.29160	0.29250	0.00090
mean	0.35325	0.32749	0.32929	0.32995	0.33873	0.34953	0.36085	0.37407	0.38759	0.40072	0.32749	0.32929	0.00180
max	0.38054	0.35459	0.35662	0.36867	0.37101	0.38151	0.40102	0.40207	0.42617	0.44522	0.35459	0.35662	0.00202

Table S24. Cross-entropy values for *T. caeruleus* ($\alpha=1, 10, 50, 100, 500, 1000$).

Alpha=1	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.41463	0.37810	0.37439	0.38679	0.40498	0.40998	0.42651	0.43924	0.46538	0.46480	0.488458	0.5041613	0.37439	0.37810	0.00370
mean	0.46818	0.43040	0.42527	0.43747	0.45027	0.46680	0.48686	0.50796	0.52824	0.54831	0.5722283	0.5980912	0.42527	0.43040	0.00513
max	0.51230	0.47448	0.47385	0.49359	0.50404	0.52809	0.56818	0.57198	0.62220	0.63828	0.660845	0.6886311	0.47385	0.47448	0.00063
Alpha=10	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.42668	0.38206	0.37474	0.39066	0.38981	0.41915	0.41590	0.43532	0.45610	0.49724	0.5225096	0.5146925	0.37474	0.38206	0.00732
mean	0.46730	0.42947	0.42333	0.43588	0.44978	0.46952	0.48733	0.50797	0.53013	0.54987	0.5744045	0.5983819	0.42333	0.42947	0.00614
max	0.51302	0.47696	0.50495	0.50696	0.51499	0.53598	0.53778	0.57670	0.62257	0.63576	0.7052284	0.6887136	0.47696	0.50495	0.02799
Alpha=50	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.42023	0.38590	0.37785	0.38267	0.38716	0.42027	0.41344	0.45151	0.46307	0.49679	0.4992932	0.5330865	0.37785	0.38267	0.00482
mean	0.46999	0.43371	0.42788	0.44203	0.45580	0.47623	0.49685	0.51848	0.53777	0.56201	0.5846736	0.6082007	0.42788	0.43371	0.00583
max	0.51047	0.46892	0.49179	0.49246	0.52463	0.53898	0.54475	0.59322	0.59113	0.65335	0.6883291	0.7150304	0.46892	0.49179	0.02287
Alpha=100	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.41976	0.38379	0.37935	0.38487	0.39180	0.40879	0.43221	0.46163	0.48039	0.49214	0.5288857	0.5362145	0.37935	0.38379	0.00443
mean	0.46993	0.43360	0.42808	0.44140	0.45668	0.47602	0.49718	0.52316	0.53976	0.56591	0.5922528	0.6147111	0.42808	0.43360	0.00552
max	0.51528	0.48304	0.48267	0.50933	0.50896	0.54028	0.55194	0.59271	0.62097	0.65933	0.7248343	0.6998336	0.48267	0.48304	0.00037
Alpha=500	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.41880	0.38092	0.38137	0.39765	0.40557	0.44746	0.44972	0.50243	0.50964	0.53512	0.5661571	0.5901958	0.38092	0.38137	0.00045
mean	0.46720	0.43245	0.43261	0.44980	0.47214	0.49230	0.52136	0.54960	0.57662	0.60627	0.6349305	0.6638951	0.43245	0.43261	0.00016
max	0.53756	0.50182	0.50858	0.52420	0.54205	0.57109	0.62757	0.60047	0.65621	0.68353	0.7254975	0.7601563	0.50182	0.50858	0.00675
Alpha=1000	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	K=11	K=12	lowest	2d. lowest	Difference
min	0.43014	0.39367	0.39913	0.40786	0.43649	0.45183	0.48806	0.50107	0.50813	0.55429	0.5805905	0.596142	0.39367	0.39913	0.00546
mean	0.46897	0.43501	0.43493	0.45501	0.47874	0.51062	0.53522	0.56459	0.59446	0.62411	0.6530534	0.6837274	0.43493	0.43501	0.00008
max	0.52614	0.48990	0.48405	0.52469	0.54719	0.60167	0.60715	0.64636	0.66495	0.73103	0.7408487	0.7669721	0.48405	0.48990	0.00586

Table S25. Cross-entropy values for *T. palliatus/tenuipunctatus* complex ($\alpha=1, 10, 50, 100, 500, 1000$).

Alpha=1	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.34895	0.33344	0.33610	0.33175	0.34725	0.34923	0.36967	0.39404	0.40350	0.42788	0.33175	0.33344	0.00169
mean	0.39979	0.38348	0.38244	0.38363	0.39358	0.41104	0.42897	0.44658	0.46690	0.48372	0.38244	0.38348	0.00105
max	0.46923	0.44864	0.44268	0.45043	0.46121	0.48465	0.48939	0.51920	0.55222	0.56433	0.44268	0.44864	0.00597
Alpha=10	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.34911	0.33645	0.33948	0.33458	0.34774	0.36080	0.38066	0.39031	0.41705	0.43733	0.33458	0.33645	0.00186
mean	0.40088	0.38381	0.38356	0.38616	0.39666	0.41333	0.43294	0.45061	0.46812	0.48892	0.38356	0.38381	0.00025
max	0.45002	0.42801	0.43283	0.43207	0.44712	0.47304	0.51356	0.51810	0.52441	0.55911	0.42801	0.43207	0.00406
Alpha=50	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.35037	0.33511	0.33255	0.33746	0.34944	0.35679	0.39422	0.39104	0.40386	0.44513	0.33255	0.33511	0.00256
mean	0.40163	0.38466	0.38509	0.38744	0.40167	0.41723	0.43627	0.45454	0.47645	0.49463	0.38466	0.38509	0.00042
max	0.45600	0.44169	0.44560	0.44520	0.47858	0.47270	0.50525	0.53611	0.54382	0.55767	0.44169	0.44520	0.00351
Alpha=100	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.34138	0.32672	0.32561	0.33214	0.34836	0.35298	0.38003	0.38453	0.40861	0.43222	0.32561	0.32672	0.00111
mean	0.39995	0.38330	0.38415	0.38862	0.40233	0.42361	0.43781	0.46068	0.48396	0.50154	0.38330	0.38415	0.00085
max	0.44814	0.43570	0.45058	0.46120	0.47361	0.49105	0.50345	0.54608	0.54568	0.57023	0.43570	0.44814	0.01244
Alpha=500	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.35293	0.34328	0.34314	0.33252	0.36548	0.37437	0.40765	0.42799	0.46215	0.47329	0.33252	0.34314	0.01062
mean	0.40472	0.39165	0.39462	0.40667	0.42093	0.44532	0.47135	0.49721	0.52539	0.55383	0.39165	0.39462	0.00297
max	0.44992	0.43264	0.44195	0.45572	0.47572	0.52132	0.54690	0.58767	0.58607	0.61253	0.43264	0.44195	0.00931
Alpha=1000	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.34914	0.33894	0.33566	0.36650	0.38738	0.39328	0.42309	0.43808	0.48324	0.49422	0.33566	0.33894	0.00328
mean	0.39999	0.39048	0.40488	0.42179	0.44114	0.46430	0.48548	0.51226	0.54096	0.56743	0.39048	0.39999	0.00951
max	0.45629	0.44835	0.47233	0.49399	0.52017	0.54224	0.57160	0.58032	0.62198	0.65834	0.44835	0.45629	0.00795

Table S26. Cross-entropy values for *T. ruficapillus/torquatus* complex ($\alpha=1, 10, 50, 100, 500, 1000$).

Alpha=1	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.49267	0.45822	0.44005	0.43519	0.45563	0.47468	0.48782	0.53188	0.54545	0.59507	0.43519	0.44005	0.00486
mean	0.53785	0.50804	0.49211	0.49673	0.51557	0.53964	0.56732	0.59732	0.63337	0.66947	0.49211	0.49673	0.00462
max	0.58564	0.56009	0.54069	0.56506	0.56672	0.59606	0.63945	0.67310	0.72644	0.77273	0.54069	0.56009	0.01940
Alpha=10	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.46682	0.43610	0.42425	0.41637	0.44501	0.45089	0.48852	0.51167	0.52053	0.59207	0.41637	0.42425	0.00787
mean	0.53148	0.50230	0.48742	0.49250	0.51089	0.53285	0.56017	0.59181	0.62984	0.66798	0.48742	0.49250	0.00507
Max	0.58154	0.55338	0.54329	0.55808	0.58843	0.59285	0.62205	0.68291	0.73418	0.74853	0.54329	0.55338	0.01009
Alpha=50	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
Min	0.47516	0.44728	0.42825	0.42897	0.44527	0.46398	0.48714	0.51459	0.54588	0.57311	0.42825	0.42897	0.00072
Mean	0.53615	0.50717	0.49143	0.49911	0.51397	0.53731	0.56801	0.60317	0.64069	0.67418	0.49143	0.49911	0.00768
Max	0.61079	0.58361	0.57282	0.56192	0.58625	0.61433	0.65623	0.68508	0.75240	0.75916	0.56192	0.57282	0.01091
Alpha=100	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
Min	0.46698	0.44859	0.42876	0.44289	0.43808	0.46306	0.49952	0.51819	0.54936	0.61190	0.42876	0.43808	0.00932
Mean	0.53595	0.50805	0.49237	0.49764	0.51958	0.54381	0.57597	0.60946	0.65168	0.69041	0.49237	0.49764	0.00527
Max	0.59661	0.56510	0.55050	0.58079	0.60414	0.62367	0.64650	0.70146	0.73459	0.77481	0.55050	0.56510	0.01460
Alpha=500	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
Min	0.47058	0.43982	0.42161	0.43688	0.44823	0.49136	0.50839	0.55517	0.61079	0.66015	0.42161	0.43688	0.01527
Mean	0.53154	0.50704	0.49501	0.50784	0.53177	0.56256	0.60173	0.64527	0.68518	0.72822	0.49501	0.50704	0.01203
Max	0.57850	0.55387	0.54696	0.59900	0.61060	0.67794	0.67169	0.71967	0.76535	0.84939	0.54696	0.55387	0.00691
Alpha=1000	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
Min	0.45984	0.42380	0.40959	0.41128	0.45259	0.50030	0.51632	0.54784	0.59120	0.64796	0.40959	0.41128	0.00169
Mean	0.53262	0.51052	0.49733	0.51221	0.53596	0.57540	0.61159	0.65855	0.69569	0.74571	0.49733	0.51052	0.01318
Max	0.60933	0.59433	0.58038	0.58370	0.63600	0.70071	0.72283	0.75752	0.76529	0.85972	0.58038	0.58370	0.00332

Table S27. Cross-entropy values for *L.nematura* ($\alpha=1, 10, 50, 100, 500, 1000$).

Alpha=1	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.60990	0.50516	0.49789	0.50455	0.54089	0.59930	0.63869	0.67622	0.72909	0.79960	0.49789	0.50455	0.00666
mean	0.67894	0.57528	0.57236	0.59124	0.63297	0.68865	0.75285	0.81761	0.88684	0.95141	0.57236	0.57528	0.00291
max	0.76157	0.66113	0.65799	0.72633	0.80373	0.85768	0.88816	1.00061	1.08490	1.07347	0.65799	0.66113	0.00314
Alpha=10	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.60583	0.50068	0.49812	0.48955	0.52676	0.58458	0.60548	0.71512	0.73705	0.79033	0.48955	0.49812	0.00857
mean	0.68653	0.58135	0.57854	0.59676	0.64035	0.69457	0.75948	0.82949	0.89897	0.96412	0.57854	0.58135	0.00281
max	0.75950	0.65388	0.66649	0.69955	0.79747	0.87338	0.89724	0.98309	1.03404	1.15642	0.65388	0.66649	0.01261
Alpha=50	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.58726	0.48435	0.47930	0.47105	0.54175	0.58140	0.61452	0.67960	0.72863	0.77279	0.47105	0.47930	0.00825
mean	0.67698	0.57311	0.57030	0.58382	0.63684	0.70106	0.76477	0.83526	0.89544	0.96835	0.57030	0.57311	0.00281
max	0.74773	0.65196	0.64423	0.69917	0.83364	0.89204	0.94157	1.00155	1.08856	1.11811	0.64423	0.65196	0.00773
Alpha=100	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.61372	0.52019	0.50996	0.50916	0.53555	0.57746	0.64699	0.69644	0.76304	0.80170	0.50916	0.50996	0.00080
mean	0.68213	0.57974	0.57757	0.59005	0.64189	0.70745	0.78626	0.84383	0.91216	0.98891	0.57757	0.57974	0.00217
max	0.76549	0.66742	0.66446	0.75013	0.82982	0.84172	0.99709	0.99283	1.07436	1.13987	0.66446	0.66742	0.00296
Alpha=500	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.59193	0.49169	0.48529	0.50993	0.54894	0.61209	0.66448	0.74065	0.76002	0.86159	0.48529	0.49169	0.00640
mean	0.68041	0.57942	0.58073	0.60745	0.65791	0.73229	0.81180	0.88615	0.95348	1.02939	0.57942	0.58073	0.00131
max	0.74564	0.65041	0.66054	0.76708	0.84825	0.95444	0.98711	1.02362	1.15037	1.17684	0.65041	0.66054	0.01014
Alpha=1000	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.57567	0.47543	0.47271	0.49585	0.55774	0.59862	0.66333	0.74396	0.83439	0.86933	0.47271	0.47543	0.00272
mean	0.68131	0.58246	0.58827	0.61537	0.66507	0.73841	0.81357	0.88680	0.96906	1.05242	0.58246	0.58827	0.00581
max	0.76504	0.67127	0.66495	0.75899	0.76899	0.92900	1.01810	1.02045	1.13161	1.19925	0.66495	0.67127	0.00633

Table S28. Cross-entropy values for *P. rufum* ($\alpha=1, 10, 50, 100, 500, 1000$).

Alpha=1	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.31044	0.27201	0.28697	0.31353	0.33774	0.35125	0.37481	0.41477	0.44228	0.45762	0.27201	0.28697	0.01496
mean	0.36205	0.32661	0.34514	0.36504	0.38786	0.41427	0.44186	0.47992	0.51629	0.55625	0.32661	0.34514	0.01853
max	0.42185	0.38370	0.41824	0.42217	0.46327	0.49052	0.51465	0.59850	0.59157	0.67275	0.38370	0.41824	0.03454
Alpha=10	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.30334	0.26469	0.28441	0.29492	0.31050	0.33977	0.35876	0.36902	0.41875	0.45656	0.26469	0.28441	0.01972
mean	0.36051	0.32529	0.34337	0.36134	0.38384	0.41670	0.44491	0.47955	0.51770	0.56055	0.32529	0.34337	0.01807
max	0.42982	0.39010	0.42236	0.43071	0.48111	0.51442	0.53007	0.58329	0.64714	0.67959	0.39010	0.42236	0.03226
Alpha=50	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.29159	0.25728	0.25877	0.28289	0.30713	0.32088	0.38363	0.39929	0.41533	0.44315	0.25728	0.25877	0.00149
mean	0.35749	0.32280	0.34230	0.36297	0.38523	0.41561	0.44910	0.48102	0.51776	0.55742	0.32280	0.34230	0.01950
max	0.43079	0.41189	0.45423	0.44276	0.47825	0.49644	0.53566	0.56467	0.62612	0.65629	0.41189	0.43079	0.01890
Alpha=100	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.29832	0.26831	0.27690	0.29277	0.30278	0.31990	0.34859	0.36864	0.42728	0.47106	0.26831	0.27690	0.00859
mean	0.35655	0.32185	0.34327	0.36266	0.38670	0.41870	0.45477	0.48473	0.52319	0.56132	0.32185	0.34327	0.02143
max	0.41137	0.37335	0.39114	0.42963	0.48056	0.51216	0.54805	0.57355	0.62134	0.65445	0.37335	0.39114	0.01779
Alpha=500	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.31543	0.28907	0.29545	0.32749	0.33800	0.37552	0.40172	0.44676	0.46345	0.52845	0.28907	0.29545	0.00638
mean	0.36166	0.32923	0.35565	0.38201	0.41578	0.45352	0.48747	0.52850	0.56820	0.61253	0.32923	0.35565	0.02641
max	0.40986	0.37512	0.41986	0.45842	0.50136	0.51847	0.56323	0.60460	0.64806	0.69836	0.37512	0.40986	0.03474
Alpha=1000	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.28654	0.24859	0.29454	0.31303	0.32210	0.37667	0.42101	0.43086	0.48324	0.52566	0.24859	0.28654	0.03795
mean	0.35563	0.32400	0.35669	0.38764	0.41807	0.45284	0.49172	0.53007	0.57011	0.61268	0.32400	0.35563	0.03163
max	0.41902	0.38822	0.42991	0.48016	0.49164	0.55102	0.55387	0.63554	0.70410	0.69169	0.38822	0.41902	0.03080

Table S29. Cross-entropy values for *P. mystaceus* ($\alpha=1, 10, 50, 100, 500, 1000$).

Alpha=1	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.17063	0.16457	0.15936	0.16100	0.16135	0.16188	0.16830	0.17090	0.17686	0.17724	0.15936	0.16100	0.00164
mean	0.19440	0.18902	0.18582	0.18642	0.18768	0.18937	0.19259	0.19670	0.20032	0.20440	0.18582	0.18642	0.00060
max	0.21482	0.21139	0.20753	0.20862	0.20738	0.21028	0.21794	0.21977	0.22350	0.22530	0.20738	0.20753	0.00015
Alpha=10	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.17180	0.16532	0.16100	0.16498	0.15977	0.16680	0.16764	0.17238	0.17262	0.17428	0.15977	0.16100	0.00123
mean	0.19452	0.18931	0.18584	0.18706	0.18791	0.19032	0.19397	0.19730	0.20167	0.20539	0.18584	0.18706	0.00121
max	0.22272	0.21375	0.21058	0.21656	0.21626	0.21627	0.22619	0.22747	0.23292	0.23403	0.21058	0.21375	0.00317
Alpha=50	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.16758	0.16065	0.15754	0.15630	0.16153	0.15866	0.16290	0.16672	0.17011	0.17264	0.15630	0.15754	0.00124
mean	0.19227	0.18732	0.18421	0.18488	0.18648	0.18921	0.19187	0.19561	0.20009	0.20426	0.18421	0.18488	0.00068
max	0.21440	0.20820	0.20909	0.20905	0.20802	0.21692	0.21694	0.21847	0.23055	0.22869	0.20802	0.20820	0.00018
Alpha=100	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.16700	0.16232	0.15982	0.15815	0.15538	0.15698	0.16088	0.17101	0.16957	0.17281	0.15538	0.15698	0.00159
mean	0.19370	0.18872	0.18583	0.18668	0.18865	0.19112	0.19468	0.19937	0.20279	0.20727	0.18583	0.18668	0.00086
max	0.22094	0.21474	0.21060	0.21205	0.21403	0.21905	0.21791	0.22889	0.23068	0.23783	0.21060	0.21205	0.00145
Alpha=500	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.17171	0.16776	0.16440	0.16213	0.16387	0.17265	0.17346	0.17347	0.18600	0.18632	0.16213	0.16387	0.00175
mean	0.19309	0.18812	0.18573	0.18810	0.19052	0.19435	0.19909	0.20377	0.20955	0.21424	0.18573	0.18810	0.00238
max	0.22274	0.21628	0.21059	0.21801	0.21803	0.23174	0.22885	0.23824	0.24377	0.24171	0.21059	0.21628	0.00569
Alpha=1000	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.17638	0.17234	0.17039	0.17066	0.17580	0.17876	0.18613	0.19017	0.19645	0.20003	0.17039	0.17066	0.00027
mean	0.19364	0.18927	0.18836	0.19100	0.19435	0.19998	0.20595	0.21244	0.21762	0.22477	0.18836	0.18927	0.00091
max	0.21227	0.20941	0.20802	0.22116	0.21540	0.22620	0.23964	0.23640	0.25325	0.25085	0.20802	0.20941	0.00138

Table S30. Cross-entropy values for *Xiphocolaptes* complex ($\alpha=1, 10, 50, 100, 500, 1000$).

Alpha=1	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.27354	0.26023	0.24399	0.24131	0.23824	0.23665	0.23950	0.24753	0.26189	0.26460	0.23665	0.23824	0.00159
mean	0.30609	0.29141	0.27811	0.27427	0.27312	0.27428	0.27765	0.28696	0.29530	0.30216	0.27312	0.27427	0.00115
max	0.33309	0.32076	0.31275	0.31368	0.31105	0.31851	0.32231	0.32889	0.33255	0.33964	0.31105	0.31275	0.00170
Alpha=10	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.26958	0.25436	0.24392	0.23730	0.23501	0.23088	0.23932	0.24116	0.25107	0.25905	0.23088	0.23501	0.00414
mean	0.30466	0.29012	0.27690	0.27345	0.27207	0.27519	0.27792	0.28396	0.29261	0.30192	0.27207	0.27345	0.00138
max	0.33972	0.32788	0.31496	0.31114	0.30871	0.31987	0.32370	0.32972	0.34480	0.34448	0.30871	0.31114	0.00243
Alpha=50	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.26547	0.25174	0.23822	0.23541	0.23209	0.23363	0.22994	0.24003	0.23853	0.24587	0.22994	0.23209	0.00215
mean	0.30547	0.29153	0.27839	0.27522	0.27506	0.27478	0.28039	0.28679	0.29662	0.30409	0.27478	0.27506	0.00028
max	0.34057	0.32617	0.30782	0.30944	0.30991	0.30547	0.32172	0.31462	0.33297	0.34702	0.30547	0.30782	0.00235
Alpha=100	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.27471	0.25807	0.24397	0.24006	0.23523	0.23593	0.24656	0.25281	0.25774	0.26924	0.23523	0.23593	0.00070
mean	0.30491	0.29078	0.27854	0.27500	0.27451	0.27683	0.28062	0.28561	0.29675	0.30679	0.27451	0.27500	0.00050
max	0.34388	0.33194	0.31695	0.31229	0.31345	0.31807	0.32608	0.32344	0.34684	0.35690	0.31229	0.31345	0.00116
Alpha=500	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.25738	0.24768	0.23483	0.22961	0.23350	0.23887	0.23803	0.24626	0.26431	0.26446	0.22961	0.23350	0.00390
mean	0.30361	0.29056	0.27834	0.27715	0.27854	0.27993	0.28740	0.29643	0.30581	0.32117	0.27715	0.27834	0.00119
max	0.33605	0.32535	0.31317	0.31300	0.34625	0.31976	0.33051	0.35014	0.35485	0.37093	0.31300	0.31317	0.00016
Alpha=1000	K=1	K=2	K=3	K=4	K=5	K=6	K=7	K=8	K=9	K=10	lowest	2d. lowest	Difference
min	0.26983	0.25686	0.24715	0.24260	0.24513	0.23913	0.25871	0.26255	0.26954	0.29460	0.23913	0.24260	0.00347
mean	0.30520	0.29312	0.28227	0.28120	0.28487	0.28976	0.29473	0.30535	0.31685	0.32941	0.28120	0.28227	0.00107
max	0.34083	0.32566	0.31874	0.31764	0.33631	0.33389	0.33714	0.35137	0.37321	0.37445	0.31764	0.31874	0.00110

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