Geographic dispersion of Phyllostomidae family (Chiroptera) based on *Cytochrome b* sequences

Dispersão geográfica da família Phyllostomidae (Chiroptera) baseado nas sequências do *citocromo b*

Dispersión geográfica de la familia Phyllostomidae (Chiroptera) basada en las secuencias del *citocromo b*

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ABSTRACT

The Chiroptera order is one of the most successful species of mammals with a wide geographical distribution. This order has been traditionally divided into two suborders, Microchiroptera and Megachiroptera, and the family Phyllostomidae is included in the suborder Microchiroptera. However, studies with molecular analysis show a different classification in two different suborders: Yangochiroptera and Yinpterochiroptera. Studies with various species describe a wide dispersal of these animals from Central America to South America and specimens of different places, creating new karyotypes and different nucleotide sequences, especially in the widely known *Cytochrome b* gene. In this study, we analyzed a phylogeographic dispersion of the Pyllostomidae family using the mitochondrial *Cytochrome b* gene, a possible dispersion pattern for family and new evolutionary proposals. All the sequences were obtained from the online database (GenBank) and the analysis and formation of phylogenetic trees were performed by maximum parsimony and maximum likelihood methods. Some dispersion patterns were observed for species of genus *Carollia* and *Glossophaga* in individual analysis and other species pattern of dispersion from South to West. But in general analysis, a pattern of dispersal to the North of the American Continent was evidenced for the family, following South America to Central America, despite many landforms that could cause speciation of some genera such as isolation by the Andes mountains. Further analysis, with a greater number of specimens from different locations, must be done to confirm this theory.

Keywords: Phylogeography; Chiroptera; Genes; *Cytochromes b*.

INTRODUCTION

Bats, classified in the order Chiroptera (*cheir* = hand; *pteron* = wing), are the only mammals that exhibit morphological and physiological adaptations for true powered flight. Their membranous wings extend between fingers, constituting dactilopatagium, which allow them flap the wings and fly. Other features that distinguish bats are the presence of membranes in the lower limbs called uropatagium and above the lower limbs, called protopatagium[1,2].

The order has a wide geographical distribution, found on all continents, except in the Polar Regions. Among all continents, the South and Central America have the high diversity of species, in contrast to North America and northern Eurasia, which have a low diversity, due to increasing latitude and consequently reducing the temperature[3,4,5,6,7,8].

Over the decades, the classification of Chiroptera changed several times. The traditional classification recognized two suborders: Megachiroptera and Microchiroptera. Simmons[9] has described a total of 18 families, 202 genera and 1,120 species.

The Megachiroptera is composed of a single family Pteropodidae, which has 190 species divide into four subfamilies: Pteropodinae, Harpyonycterinae, Nyctimeninae and Macroglossinae. Microchiroptera has 930 species divide into 17 families: Rhinolophidae, Hipposideridae, Megadermatidae, Rhinopomatidae,

Phyllostomidae, Craseonycterinae, Emballonuridae, Nycteridae, Myzopodidae, Mystacinidae, Molossidae, Vespertilionidae, Mormoopidae, Noctilionidae, Furipteridae, Thyropteridae and Natalidae[9].

In contrast to the traditional morphological classification, recent cytogenetic and molecular studies have proposed a different classification for bats. Some authors have divided the order into two new suborders Yangochiroptera (consisting of Microchiroptera, except Rhinopomatidae, Rhinolophidae and Megadermatidae) and Yinpterochiroptera (consisting of Megachiroptera and families Rhinopomatidae, Rhinolophidae and Megadermatidae)[10,11,12].

Among the several bat families that have been found in Brazil, the most common is the Phyllostomidae (from greek: *phyllo* = leaf + *stoma* = mouth), which is composed by a variety of bats that have different eating habits, such as insectivorous, frugivorous, carnivorous, herbivorous, nectarivorous, omnivorous and hematophagous[2,13].

The Phyllostomidae family is divided into seven subfamilies: Desmodontinae, Glossophaginae, Phyllostominae, Carolliinae, Stenodermatinae, Phyllonycterinae and Brachyphyllinae and more than 160 species are grouped in 48 genera[9]. The family was classified in Microchiroptera or Yangochiroptera[10,11,12].

The main morphological feature is an appendix in the format of a shaped spearhead, also called "leaf nose", except for Desmodontinae subfamily, and the species *Centurio senex* (the structure is reduced or absent). Its species are mostly adapted to low altitudes in the tropical and subtropical regions of the New World[9]. They can be found from the Southeastern United States to northern of Argentina[13].

At the beginning of this century, there was a large number of taxonomic and systematic revisions in several groups of bats present in Brazil, proposing new classifications between families and genera of Chiroptera[9,14,15,16,17].

According to Baker[18] there are 49 genera in three subfamilies, Koopman[19] recognized 49 genera in eight subfamilies, McKenna and Bell[20] recognized 48 genera in four subfamilies, Nowak[13] recognized 52 genera in five subfamilies and Wetterer et al[16] recognized 53 genera in seven subfamilies. Again Baker et al[21] proposed another classification with 11 subfamilies, 57 genera, ten tribes and seven unrated taxa.

Since the 1970s, several molecular techniques, such as electrophoresis, polymerase chain reaction (PCR), DNA sequencing, proteomics and others were used in several studies, mainly in phylogenetic[14,21,22]. These techniques can be used to analyze nuclear DNA and DNA from organelles, allowing the measurement of phylogeographic parameters, gene flow and it's inter and intraspecific historical relationships[14,17,21].

Currently, one of the most widely used markers for studying phylogeny and phylogeography is the mitochondrial DNA (mtDNA), which is circular, haploid and matrilineal (maternal inheritance pattern). It is found in the mitochondrial lumen with thousands of copies per cell, almost all of the genome is involved in coding functions and the existence of pseudogenes, introns and repetitive DNA is rare[23,24]. One of the suitable features for the genetic analysis is the ability to accumulate base substitutions, insertions and deletions at a rate of five to ten times faster than nuclear DNA, due to low replication fidelity, no repair mechanisms, corrosive oxygen-rich environment and no DNA compaction[23]. The phylogeny based on mtDNA allows a good description of the geographical distribution, genetic distances and divergence times between lineages[1].

The most widely used marker is the *Cytochrome b* gene that has one of the best resolutions for phylogenetic studies in mammals with divergence times from four to 44 million years[1,25]. The gene contains codons with fast and slow evolution, conserved regions and variable regions[26]. It has been widely used in analyzes that involves geographic distribution of genetic lineages, evolution, reproductive isolation, origin, distribution, biodiversity maintenance and the emergence of new species[27]. Based on its variability, *Cytochrome b* gene is considered appropriate to elucidate relationships to a genus level, the saturation may complicate at higher taxonomic levels[14].

Phylogeography studies using molecular data (usually mtDNA and microsatellite) can propose a geographic evolution (based on vicariance, diversification of species and patterns of migration) and demographic history (fixation of species, population growth and decline)[3].

Among several works about the phylogeography of the Phyllostomidae family, little is known of its evolution, dispersal and establishment of the species, in general perspective. Most studies use only a few genera, species or small groups, never with a general group, using various genera[3,4,5,6,7,8].

In Phyllostomidae, only *Leptonycteris curasoae*, *Leptonycteris nivalis*, *Choernycteris mexicana* and *Platalina genovensium* needs a migratory behavior. In other families, few species have this behavior and most are classified in the Vespertillionidae family[28]. This migration, in some species, may be greater in females than in males and changes may occur especially in Neotropics wet and dry seasons[29]. What differentiates bats from birds, in the migratory aspect, is that bats hibernate in caves and mines during the winter and birds migrate to different locations to get out of the food shortages and climate change[30,31].

Bats from North America and South America have been exchanging genetic information and fauna over a millions years, compounding the tropical fauna of mammals in the Americas[5]. The dispersion has occurred in regions that had a higher amount of food, especially in autumn season[32].

Thus, the aim of this study was to analyze the evolutionary and phylogeographic dispersal involving species of bats of the Phyllostomidae using the mitochondrial gene, *Cytochrome b*, and suggesting a possible dispersion pattern for the family.

MATERIALS AND METHODS

All procedures were performed at Instituto Evandro Chagas in the Centro de Inovações Tecnológicas. The DNA sequences of *Cytochrome b* gene were obtained directly from GenBank (NCBI)

(http://www.ncbi.nlm.nih.gov/genbank). It was retrieved 50 complete *Cytochrome b* sequences of 1,140 bp for a variety of localities throughout the American Continent (Table 1). It was only used sequences with the locality referred in the original articles.

Table 1 – List of *Cytochrome b* sequences retrieved from online database GenBank (NCBI)

Taxon	Author	Locality	GenBank No.
Artibeus jamaicensis	Van Den Bussche et al[33]	Suriname	TK 17303
Artibeus jamaicensis	Hoffer et al[34]	Ecuador	TK 135290
Artibeus jamaicensis	Larsen et al[35]	Ecuador	FJ179185
Artibeus lituratus	Hoffer et al[34]	St. Vicent and Grenadines, Union Islands	TK 128642
Artibeus lituratus	Larsen et al[6]	Ecuador	TK104525
Artibeus lituratus	Larsen et al[6]	Ecuador	FJ179233
Carollia brevicauda	Baker et al[36]	Venezuela	TK19273
Carollia brevicauda	Baker et al[36]	Panama	FMNH 38117
Carollia brevicauda	Baker et al[36]	Venezuela	TK19316
Carollia brevicauda	Baker et al[36]	Peru	TK70412
Carollia castanea	Hoffmann and Baker[5]	Bolivia	NK30150
Carollia castanea	Hoffmann and Baker[5]	Ecuador	F37061
Carollia castanea	Hoffmann and Baker[5]	Panama	F38156
Carollia castanea	Hoffmann and Baker[5]	Panama	F38195
Carollia castanea	Wright et al[37]	Peru	TK70672
Carollia perspicillata	Pavan et al[38]	Brazil, Amazon Forest	AD913
Carollia perspicillata	Pavan et al[38]	Brazil, Amazon Forest	AD843
Carollia perspicillata	Hoffmann and Baker[5]	Brazil, Minas Gerais	MVZ185533
Carollia perspicillata	Hoffmann and Baker[5]	Ecuador	F37084
Carollia perspicillata	Hoffmann and Baker[5]	Mexico	F33206
Carollia perspicillata	Hoffmann and Baker[5]	Suriname	TK17466
Ectophylla alba	Hoffer and Baker[39]	Costa Rica	TK125309
Ectophylla alba	Porter and Baker[40]	Costa Rica	TK16395
Ectophylla alba	Hoffer and Baker[39]	Panama	TK125308
Glossophaga comissarisi	Hoffmann and Baker[4]	Mexico	TK20562
Glossophaga comissarisi	Hoffmann and Baker[4]	Mexico	TK20586
Glossophaga comissarisi	Hoffmann and Baker[4]	Panama	NMNH 578998
Glossophaga soricina	Hoffmann and Baker[4]	El Salvador	TK 34707
Glossophaga soricina	Hoffmann and Baker[4]	Jamaica	TK 9251
Glossophaga soricina	Hoffmann and Baker[4]	Mexico	TK 43208
Glossophaga soricina	Hoffmann and Baker[4]	Panama	NMNH 578997
Glossophaga soricina	Hoffmann and Baker[4]	Paraguay	TK 57056
Glossophaga soricina	Hoffmann and Baker[4]	Venezuela	TK 15194
Mesophylla maconelli	Porter and Baker[40]	Bolivia	TK14583
Mesophylla maconelli	Porter and Baker[40]	Colombia	TK16042
Mesophylla maconelli	Porter and Baker[40]	Ecuador	TK104077
Mesophylla maconelli	Porter and Baker[40]	Ecuador	TTU84849
Mesophylla maconelli	Porter and Baker[40]	French Guiana	TK18786
Platyrrhinus dorsalis	Hoffer and Baker[39]	Bolivia	NK30133
Platyrrhinus dorsalis	Hoffer and Baker[39]	Ecuador	TK135914
Platyrrhinus dorsalis	Hoffer and Baker[39]	Ecuador	TK135942
Uroderma bilobatum	Hoffmann et al[41]	Ecuador	TK104603
Uroderma bilobatum	Hoffmann et al[41]	Honduras	TK40314
Uroderma bilobatum	Hoffmann et al[41]	Panama	ROM104368
Vampyressa thyone	Hoffer and Baker[39]	Costa Rica	TTU34398
Vampyressa thyone	Hoffer and Baker[39]	Costa Rica	TK9020
Vampyressa thyone	Hoffer and Baker[39]	Panama	TK22534
Vampyrodes caraccioli	Hoffer and Baker[39]	Peru	TK70540
Vampyrodes caraccioli	Hoffer and Baker[39]	Trinidad and Tobago, Trinidad	CM94707
Vampyrodes caraccioli	Velazco and Simmons[42]	Brazil	MZUSP34655

The numbers of retrieved sequences were low because many sequences were not in the referenced article, others have not been published in articles and others did not mention the sites that the specimens were captured.

PHYLOGENETIC ANALYZES

In order to observe genetic variations, the nucleotide sequences were aligned and compared using BioEdit 7.0 software. For phylogenetic tree formation, it was used the maximum parsimony and maximum likelihood methods. Analysis were performed considering all nucleotides and codons substitutions with heuristic search in PAUP 4.0b10 software using the tree bisection-reconnection (TBR). The bootstrap value was expected in one thousand replications using the heuristic test. In the maximum likelihood analysis were used GTR nucleotide substitution models and TBR with gamma frequencies chosen by software J Model Test 2.1.3. Both analysis were based on the parameters described in Baker[21].

It was used the genus *Mormoops* from the Mormoopidae as outgroup because it is considered one of the closest to the Phyllostomidae according to Baker et al[21] and Jones et al[17]. Intraspecific analysis were performed for each species and interspecific with all genera retrieved from GenBank (Table 1).

RESULTS

In the maximum parsimony analysis, from 1,140 characters, 651 were invariant, 455 were informative and 34 uninformative.

It could be observed seven distinct groups without evolutionary information between them, but internally for the genus *Artibeus*, it was observed that *Artibeus jamaicensis* had basal status in relation to *Artibeus lituratus*. The specimen of *Carollia brevicauda* had basal status in relation to specimens of the same species and to *Carollia pespecillata*. Regarding the species *Ectophylla alba*, the specimen that was obtained from Panama had a basal status compared the ones in Costa Rica. The species *Glossophaga commissarisi*, from Panama also has basal status relative to all other species from *Glossophaga* genus (Figure 1).

In groups 5, 6, 7 and 8 the specimens with basal status are: *Uroderma bilobatum* from Honduras, *Vampyrodes caraccioli* from Peru, *Vampyressa thyone* from Panama and *Micronycteris megalotis* from Ecuador (specifically in El Oro, Puyango, Petrified Forest), respectively (Figure 2).

Regarding the analysis by maximum likelihood, three groups were formed, one with basal status in the family, having the specimens of *Micronycteris megalotis*, following two distinct groups composed of group 1 (with *Tonatia*, *Glossophaga* and *Carollia*) and group 2 by the remaining genus, with the most basal status for *Ectophylla alba*.

Artibeus jamaicensis – It was analyzed specimens from two different localities (Suriname and Ecuador).

In maximum parsimony and maximum likelihood, the species was dispersed from East to West of South America, in which the specimens from Ecuador are more derived in the phylogenetic analysis than from Suriname.

Artibeus lituratus – It was analyzed specimens from two different localities (St. Vincent and the Grenadines and Ecuador). In maximum parsimony and maximum likelihood, the species were dispersed from East to West and to the South of South America, and the specimens of Ecuador are more derived than those of Saint Vincent and the Grenadines.

Carollia brevicauda – Specimens from three different locations were analyzed (Peru, Panama and Venezuela). In maximum parsimony and maximum likelihood, the species were dispersed from South to North of America, and the specimens of Venezuela are more derived than those from Panama and these are more derived than those from Peru.

Carollia castanea – Four different locations were analyzed (Peru, Ecuador, Bolivia and Panama). In maximum parsimony the specimens located in Ecuador are more basal, followed by two derived groups, one consisting of specimens from Bolivia and Peru and another consisting of specimens from Panama. In contrast, the maximum likelihood showed different results, that specimens from Peru were more basal in the phylogenetic tree, followed by specimens from Bolivia, Ecuador and Panama (Figure 2).

Carollia perspicillata – Specimens from five different locations were analyzed (Brazilian Amazon, Minas Gerais, Brazil, Mexico, Ecuador and Suriname). In parsimony and maximum likelihood the specimens located in Brazil (Minas Gerais) are more basal, followed by two derived groups, one consisting of specimens of the Brazilian Amazon, Mexico and Suriname and another group consisting of specimens from Brazilian Amazon and Ecuador (Figure 2).

Ectophylla alba – It was analyzed specimens from two different localities (Panama and Costa Rica). In parsimony and maximum likelihood, the specimens located in Panama are basal, followed by specimens from Costa Rica. Showing dispersion towards the North to Central America.

Glossophaga comissarisi – It was analyzed specimens from two countries (Mexico and Panama). In maximum parsimony and likelihood, the specimens located in Panama are basal, followed by specimens from Mexico, showing dispersion towards the North to Central America.

Glossophaga soricina – Specimens from six different locations were analyzed (Panama, Paraguay, Venezuela, El Salvador, Mexico and Jamaica). In parsimony and maximum likelihood, the specimens located in Venezuela are basal, followed by specimens from Paraguay, Panama, El Salvador, Jamaica and Mexico, suggesting dispersion towards the north, from South America to North America (Figure 2).
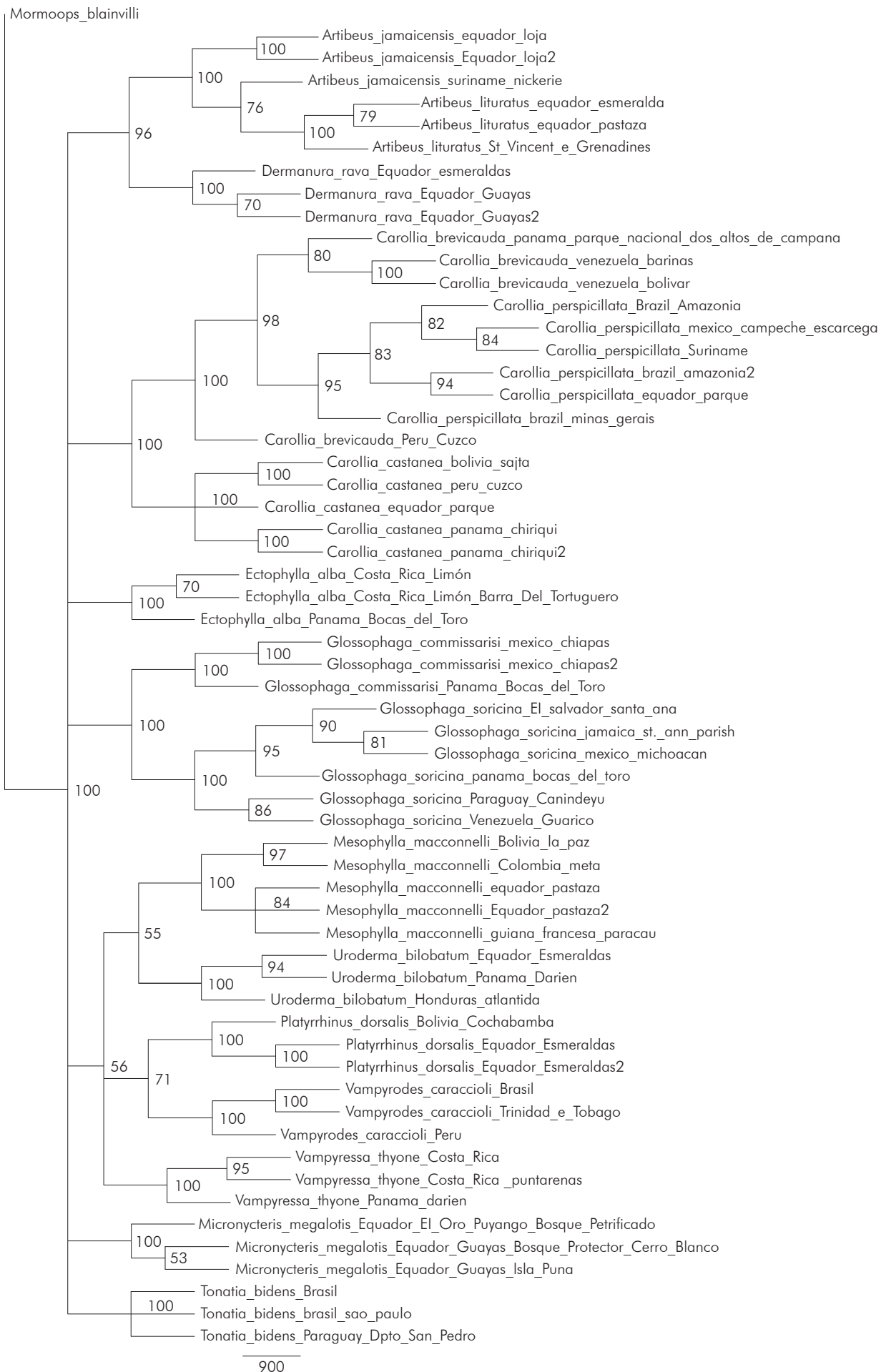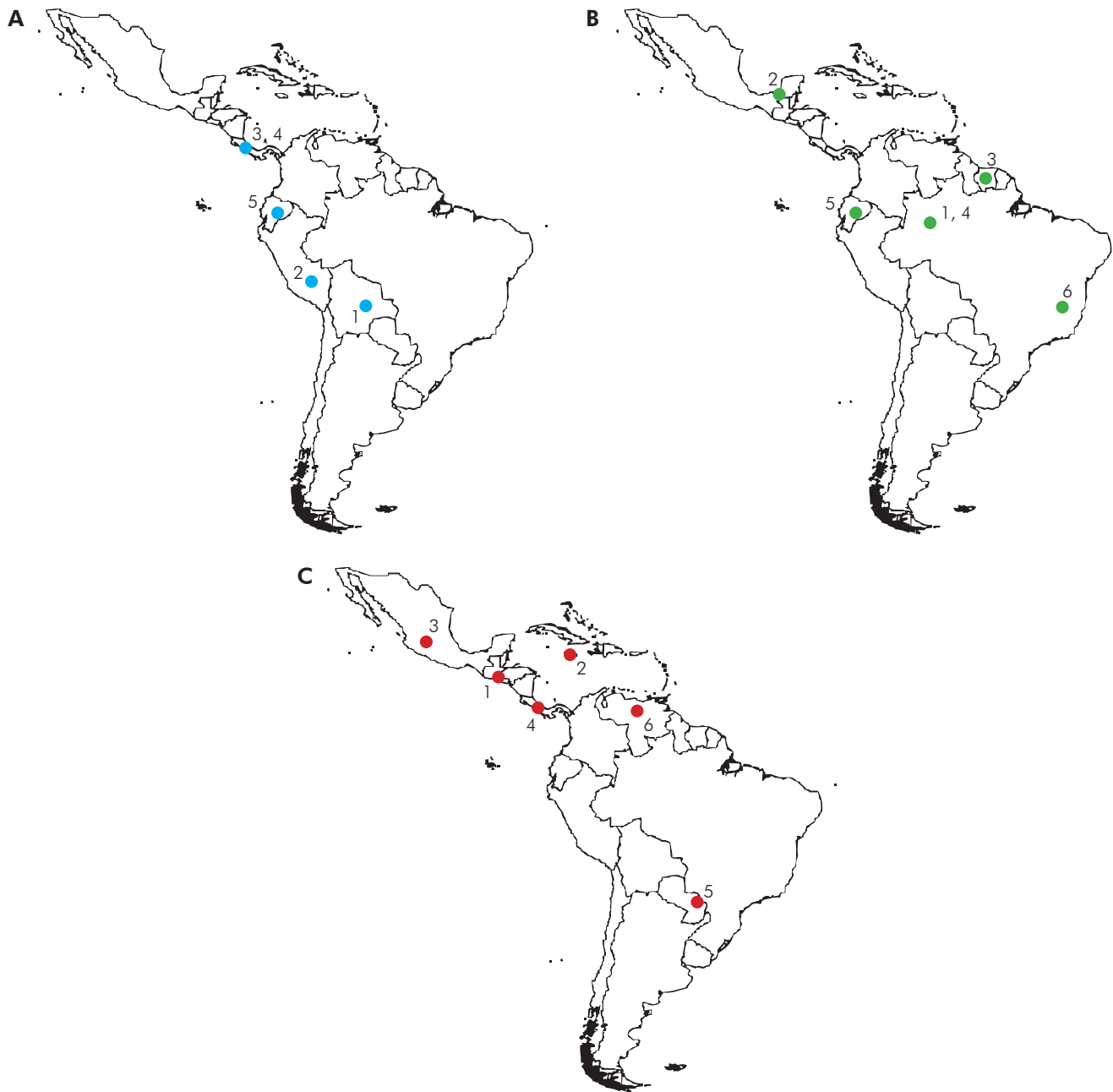
Figure 1 – Maximum Parsimony tree based on the *Cytochrome b* gene with 16 species of Phyllostomidae from various locations of the American Continent. It was based on the parameters described in Baker[21]

A: *Carollia castanea*; **B**: *Carollia perspicillata*; **C**: *Glossophaga soricina*.

Figure 2 – Geographical distribution for the three species of Phyllostomidae

Mesophylla macconelli – Specimens from four locations were analyzed (Ecuador, Bolivia, Colombia, French Guiana). In maximum parsimony, two sister groups assembled, one with specimens from Bolivia and Colombia with the same degree of phylogenetic relatedness and another group showing specimens from French Guiana and Ecuador, which are more derived. Regarding the analysis by maximum likelihood, the specimens from Ecuador are basal, followed by specimens from French Guiana, Bolivia and Colombia (most derived).

Platyrrhinus dorsalis – It was analyzed specimens from two different localities (Bolivia and Ecuador). In parsimony and maximum likelihood, the species have spread to Northern of South America, in which the specimens of Bolivia are more derived than the specimens from Ecuador.

Uroderma bilobatum – Specimens from three countries were analyzed (Honduras, Panama and Ecuador). In parsimony and maximum likelihood, the species have spread from Southern Central America to South America, where the specimens from Honduras are more basal, followed by specimens from Panama and Ecuador (both in the same degree of phylogenetic relatedness).

Vampyressa thyone – In maximum parsimony, the species showed dispersion to the North of Central America, from Panama to Costa Rica. However, analysis by maximum likelihood was different, North to South, from Costa Rica to Panama.

Vampyrodes caraccioli – Three specimens were analyzed in Peru, Trinidad and Tobago and Brazil. In parsimony and maximum likelihood, dispersion followed from Peru to Trinidad and Tobago and Brazil.

DISCUSSION

In the general analysis by maximum parsimony, it was noticed the most basal status of the specimen *Carollia brevicauda* from Peru (Cuzco) comparing specimens of *C. perspicillata* and *C. brevicauda* presented in Venezuela, proposing a possible origin of these specimens from the specimen of southern (Peru). A spread of these specimens could be possible to the north of the American Continent and eastward Brazil. It was found the same analysis result for genera *Glossophaga, Ectophylla, Vampyrodes, Vampyressa* and, thus, proposing a dispersion pattern to the north in several species of that family (Figure 1).

This dispersion pattern can also be seen in the individual analysis, that some species of South America have a possible dispersion pattern to the north, in Central America and North America, such as the species *Glossophaga soricina* and *Glossophaga comissarisi*, which may have dispersed from South America to the North searching for better habitat and food. About *Glossophaga soricina*, there are two distinct strains of the species, one to the east of the Andes and the other one in Central America, North America, Jamaica and West of the Andes, which can further be classified as different species[4] (Figures 2 and 3).
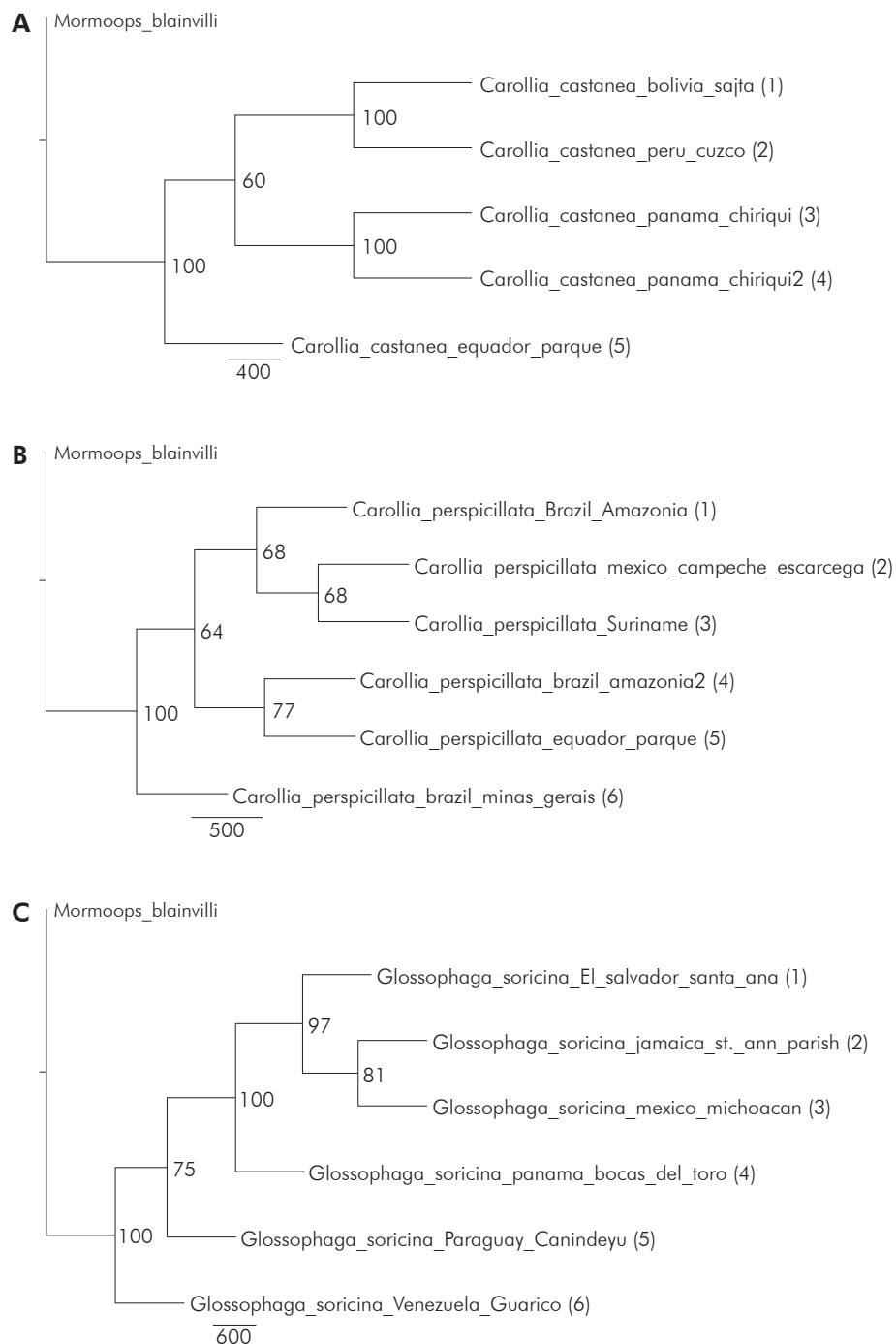
A: *Carollia castanea*; **B**: *Carollia perspicillata*; **C**: *Glossophaga soricina*.

Figure 3 – Most parsimonious trees showing geographic dispersion of individual species, they were based on the parameters described in Baker[21]

The Andes may also have influenced in species that have affinity for high altitudes. Kunz and Pena[43] described the presence of *Mesophylla macconeli* in regions with altitude up to 1,032 m, Baker and Clark[44] described *Uroderma bilobatum* to 1,800 m and Lewis and Wilson[45] described *Vampyressa pussila* in 1,500 ft, among other species that also have some affinity with high altitudes.

The possible location and dispersion of *Glossophaga* may have been influenced by their ecology. For example, *Glossophaga commissarisi* is in a variety of habitats, such as rainforests, subtropical savannas and others. Another example is *Glossophaga soricina* according to their habitat and time of year, they may have a variable eating behavior, such as those in Mexico, that their feeding habits is mainly of nectar and pollen from April to June, then they change their feeding behavior to insectivorous. Alvarez et al[46] has also described eating behavior of nectar and pollen during the dry season in Panama and eating fruits in the wet season.

Hoffmann and Baker[5] reported the emergence of the Isthmus of Panama as one of the factors of the dispersion to the North America, which was confirmed by studies with terrestrial mammals. The authors have also reported that the same situation may have happened with the bats, they might have taken advantage of the Isthmus "bridge" for dispersal between the continents. However, the same authors have mentioned that the phylogenetic variation in *Carollia* may have occurred by vicariance with the rise of the Andes mountains, preventing the spread of these bats and isolating individuals on the other side of the Andes. The same idea can be inferred for bats from other groups that may have this dispersion pattern to North. In this present study, *Carollia perspicillata* and *C. castanea* showed the same pattern of dispersal to the North of the American Continent, and *C. castanea* seemed to have a distribution along the Andes to Panama (Figures 2A, 3A, 2B and 3B), it can be possible due to an affinity to high altitudes, as previously mentioned for other species. However, it was also noticed similarities with the dispersion pattern to the North towards Panama and South, and another pattern towards Peru and Bolivia, as shown in figure 3, which differs from the idea of isolating of *Carollia* by the Andes.

The same pattern of vicariance may have occurred with *Uroderma bilobatum*, that has presented dispersion to Ecuador in the Andes Region, with the specimens from Panama as a sister group.

Other species such as *Artibeus jamaicensis* have dispersed to the West, probably because of better habitat with the emergence of forest refuges during the Pleistocene, causing several species disperse to new habitats in search of food, as occurred with the genus *Carollia*[5]. A good example of vicariance is the most basal status *Artibeus lituratus* present in St. Vincent and the Grenadines, which may have been a case of isolation, caused for the formation of islands.

As we obtained sequences of few specimens from close countries for *Vampyressa thyone* and *Ectophylla alba*, we cannot say that they have spread North to Central America, it needs better analyzes and specimens from other localities for a better theory of dispersion. However, both have a pattern in phylogenetic relatedness, where the species located in Panama are more basal than the ones found in Costa Rica, a possible spread towards the North.

Regarding the species *Platyrrhinus dorsalis*, Velazco and Patterson[8] describe that the ancestor of the genus *Platyrrhinus* may have arisen in the South of the Amazon River in Brazil and dispersed towards the Andes and the Amazon basin, originating several new species of the genus. According to these authors, the species were found in the Northern Andes, occupying the area of Ecuador, following the North to Venezuela. However, in our analysis we found evidence of a possible spread North to Venezuela.

The preference for specific types of habitat of various species may also influence the Phyllostomidae dispersion. Some species prefer humid and wet habitats, like the Amazon forest and other tropical forests, for exemple, *Artibeus jamaicensis*, *Mesophylla maconelli*, *Platyrrhinus dorsalis* and *Vampyrodes caraccioli*[47,48,49]. Others species, as example *Uroderma bilobatum*, prefer certain types of foods such as figs obtained in high trees of tropical forests[44].

CONCLUSION

It can be concluded that the Phyllostomidade family, in general, may have a dispersion pattern on the American Continent, it can be noticed that several species, in intraspecific analysiss, have a possible pattern, in the North America, as *Carollia brevicauda*, *C. castanea*, *C. perspicillata*, *Glossophaga comissarisi* and *G. soricina* or to the South, as *Uroderma bilobatum* and *Vampyrodes caraccioli*. Regarding the other species analyzed, it cannot be suggested a dispersion pattern, because the analisis presented a random dispersion or few specimens from different and distant localities.

Many other studies work at genus and species level, rarely at family level, due to lack of specimens from distant and different localities. Here it was performed an analysis of GenBank sequences for a possible dispersion theory to the North of the American Continent for Phyllostomidae family. The reduced number of retrieved sequences were low because of the lack of published sequences with its exact location of the specimen. However, the sequences obtained were really important due to the distinct and distant locations and features that can prove other dispersion theories, as the vicariance occurred by the emergence of the Andes Mountains. Thus, it concludes that the family may have a dispersion pattern (probably to the North), however other analysis must be performed in the future, as phylogenetic regression, molecular clock and the discovery of new sequences at other localities in the American Continent.

Dispersão geográfica da família Phyllostomidae (Chiroptera) baseado nas sequências do *citocromo b*

RESUMO

A ordem Chiroptera é uma das espécies de mamíferos mais bem sucedidas com uma grande distribuição geográfica. Essa ordem foi tradicionalmente dividida em duas subordens, Microchiroptera e Megachiroptera, e a família Phyllostomidae está incluída na primeira. No entanto, estudos com análise molecular mostram uma classificação diferente em duas subordens distintas: Yangochiroptera e Yinpterochiroptera. Os estudos com várias espécies descrevem uma grande dispersão desses animais da América Central para a América do Sul e espécimes de vários lugares, a criação de novos cariótipos e sequências de nucleotídeos diferentes, especialmente no gene *citocromo b* amplamente conhecido. Neste estudo, analisou-se uma dispersão filogeográfica da família Pyllostomidae usando o gene mitocondrial *citocromo b*, um possível padrão de dispersão para essa família e novas propostas evolutivas. Todas as sequências foram obtidas a partir da base de dados *on-line* (GenBank), a análise e a formação de árvores filogenéticas foram realizadas pelos métodos de máxima parcimônia e de máxima verossimilhança. Foram observados alguns padrões de dispersão de espécies do gênero *Carollia* e *Glossophaga* na análise individual e outro padrão de dispersão de espécies do sul ao oeste. Porém, na análise geral, um padrão de dispersão para o norte do Continente Americano foi evidenciado para a família, depois da América do Sul à América Central, apesar de muitos acidentes geográficos causarem especiação de alguns gêneros, tais como o isolamento das montanhas dos Andes. Uma análise mais aprofundada, com um maior número de amostras de diferentes locais, deve ser feita para confirmar esta teoria.

Palavras-chave: Filogeografia; Quirópteros; Genes; *Citocromos b*.

Dispersión geográfica de la familia Phyllostomidae (Chiroptera) basada en las secuencias del *citocromo b*

RESUMEN

El orden Chiroptera es una de las especies de mamíferos de mejores resultados y con una gran distribución geográfica. Ese orden ha sido tradicionalmente dividido en dos subórdenes, Microchiroptera y Megachiroptera, y la familia Phyllostomidae está incluida en la primera. Sin embargo, estudios con análisis molecular muestran una clasificación diferente en dos subórdenes distintas: Yangochiroptera e Yinpterochiroptera. Los estudios con varias especies describen una gran dispersión de esos animales de América Central para América del Sur y especímenes de varios lugares, la creación de nuevos cariotipos y secuencias de nucleótidos distintos, especialmente en el gen *citocromo b* ampliamente conocido. En este estudio se analiza una dispersión filogeográfica de la familia Pyllostomidae usando el genoma mitocondrial *citocromo b*, un posible estándar de dispersión para esa familia y nuevas propuestas evolutivas. Todas las secuencias se obtuvieron a partir de la base de datos *online* (GenBank), el análisis y la formación de los árboles filogenéticos se realizaron por los métodos de máxima parsimonia y máxima verosimilitud. Se observaron algunos estándares de dispersión de especies del género *Carollia* y *Glossophaga* en el análisis individual y otro estándar de dispersión de especies del sur al oeste. Sin embargo, se evidenció en el análisis general, un estándar de dispersión hacia el norte del Continente Americano para la familia, después de América del Sur a América Central, a pesar de que muchos accidentes geográficos causan la especiación de algunos géneros, como el aislamiento de las montañas de los Andes. Un análisis más profundo, con un número de muestras de diferentes locales más grande debe hacerse para confirmar esta teoría.

Palabras clave: Filogeografía; Quirópteros; Genes; *Citocromos b*.

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