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# Diversification patterns in the North Andean Block: a perspective from biogeographical hypotheses

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*To my parents, Beatriz Ortiz S. and Jose Ayus R., for their love and by its support throughout my life.*

*To my sister, Daniela Ayus O., the person who has helped me to be stronger.*

*To Edward Rueda D. by its support in difficult times.*

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### Abstract

**TITLE:** DIVERSIFICATION PATTERNS IN THE NORTH ANDEAN BLOCK: A PERSPECTIVE FROM BIOGEOGRAPHICAL HYPOTHESES\*

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**KEY WORDS:** DIVERSIFICATION, ANDES, BIOGEOGRAPHY, DISPERSAL-VICARIANCE ANALYSIS, HYPOTHESIS TESTS.

We used 637 species from six taxonomic classes to identify the pattern(s) of diversification, occurring in the North Andean Block estimating phylogenetic relationships, divergence times, dispersal-vicariance events, and ancestral distributions. We assessed four hypotheses that explain the diversification in the NAB. For each hypothesis we specified: three sets of unequal rates of dispersal between areas and a temporal stratification, containing four-time intervals for the Miocene. The North Andean taxa showed three ancestral distributions such as the Amazonian region, Central America, and Central Andes where we recovered the major dispersal events. The pattern from North Andean Cordilleras to lowlands fit better the diversification inside the NAB. However, according to the smaller log-likelihood deltas obtained between hypotheses, the taxa followed two patterns, from lowlands to highlands and *vice-versa*. We found seven out of 15 groups that diversified at the rhythm of the North Andean uplift showing different times to reach each Cordillera. The south-to-north pattern was supported by 80% of the groups. Furthermore, exchanges between South and Central America were identified occurring between 15 to 10 Ma. The two altitudinal patterns from lowlands to North Andean Cordilleras and *vice-versa* are plausible regardless the ancestral area estimated, and these patterns occurred multiple times in the same temporal frame (Miocene). However, the pattern from North Andean Cordilleras to lowlands fit better which might support a highlands origin inside or outside the NAB. Finally, the North Andean taxa followed the mountain building scenario, where the Central Cordillera raised first, later the Western Cordillera, and last the Eastern Cordillera.

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\*Bachelor Thesis

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## Resumen

**TÍTULO:** PATRONES DE DIVERSIFICACIÓN EN EL BLOQUE NORTE DE LOS ANDES: UNA PERSPECTIVA DESDE LAS HIPOTESIS BIOGEOGRÁFICAS\*

**AUTOR:** VIVIANA LIZETH AYUS ORTIZ\*\*

**PALABRAS CLAVES:** DIVERSIFICACIÓN, ANDES, BIOGEOGRAFÍA, ANÁLISIS DE DISPERSIÓN -VICARIANZA, TEST DE HIPÓTESIS.

Utilizamos 637 especies pertenecientes a seis clases taxonómicas para identificar el/los patrones de diversificación en el Bloque Norte de los Andes (BNA), estimando relaciones filogenéticas, tiempos de divergencia, eventos de dispersión y vicarianza y distribuciones ancestrales. Evaluamos cuatro hipótesis que explican la diversificación en el BNA, cada una con tres matrices de dispersión diferentes y una estratificación temporal para el Mioceno. Como distribución ancestral obtuvimos áreas adyacentes tales como Amazonas, Centroamérica y Andes Centrales en las cuales recuperamos la mayor proporción de eventos de dispersión. El patrón de Cordilleras hacia tierras bajas ajusta mejor a la diversificación dentro del BNA. Sin embargo, de acuerdo a los deltas de log-likelihood entre hipótesis, los *taxa* siguen ambos patrones, de tierras bajas a tierras altas y viceversa. Encontramos siete grupos que diversifican al ritmo del levantamiento Andino mostrando diferentes tiempos para alcanzar cada Cordillera. El 80% de los grupos soportan el patrón Sur-Norte. Además, identificamos pasos desde y hacia Sur y Centroamérica entre 15-10Ma. Los dos patrones, tierras bajas hacia Cordilleras del BNA y viceversa, son plausibles independientemente del área ancestral estimada, y pueden encontrarse varias veces en el mismo marco temporal (Mioceno). Sin embargo, el patrón de Cordilleras del BNA hacia tierras bajas ajusta mejor, lo que podría apoyar un origen en tierras altas dentro o fuera de la NAB. Por último, los *taxa* del BNA siguieron el escenario del levantamiento Andino, donde el orden de levantamiento es: Cordillera Central, Cordillera Occidental y finalmente la Cordillera Oriental.

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## Introduction

The North Andean Block (NAB) is located in the Neotropical region and is characterised for containing a high number of species (Myers *et al.*, 2000; Pennington *et al.*, 2004). Geologically, it is defined as a tectonic microplate (Kellogg *et al.*, 1995; Bird, 2003) located between the Nazca, the Caribbean, and South American plates (Bird, 2003). The northern and southern boundaries of the NAB are subduction zones (Collot *et al.*, 2002), to the east, it is a fault system (Freymueller *et al.*, 1993; Bird, 2003), and to the west, it extends to the union of the Caribbean and Panama plates (Bird, 2003). This block extends from Ecuador to Colombia– Venezuela, and generally is subdivided into three mountain systems: the Western, Central and Eastern Cordilleras including the Merida Andes (Bird, 2003, but see Audemard and Audemard 2002). The uplift of the three Cordilleras is divided into two periods with different geological history for each time frame (Gregory-Wodzicki, 2000). The initial period took place from the Oligocene to early Miocene (~23 Ma) and the second period from the late Miocene (~12 Ma) to early Pliocene (~4.5 Ma) (Hoorn *et al.*, 2010). The first range in raise up was the Central Cordillera with an intensified uplift during the Miocene. Meanwhile, the final uplift of the Eastern Cordillera was recorded for the Pliocene-Holocene.

The geological events that occurred inside this block caused geoclimatic changes at a South American level (Hartley, 2003; Ehlers and Poulsen, 2009). Thus, the diversification in the North Andean Block has been explained based on different paleoclimatic and geological events.

The refuge hypothesis was proposed, based on paleoclimatic data, to explain the diversification during the Pleistocene (~2.5 Ma Haffer, 1967, 1969; Patton and da Silva, 1998). Geological data, as the significant mountain building of the NAB (~20-5 Ma), has been used to explain the diversification in a temporal range greater than the Pleistocene. The Andean orogeny promoted diversification in the NAB, isolating populations in the Miocene (23.03-5.33 Ma) from south-to-north (Doan, 2003; Chaves *et al.*, 2011), from west-to-east (Chapman, 1917; Kattan *et al.*, 2004), and separating lowlands and highlands (García-Moreno and Fjeldså, 2000; Ribas *et al.*, 2007; Antonelli *et al.*, 2009).

The diversification in the NAB also is studied under a temporal stratification separating the Miocene-Pliocene (23.03-2.5 Ma) time frame from the early Pliocene-Pleistocene (2.59-0.01 Ma) (Velazco and Patterson, 2008; Schweizer *et al.*, 2011; Benham *et al.*, 2014).

Chazot *et al.* 2016 proposed a framework of biogeographic scenarios containing four main evolutionary mechanisms (speciation, extinction, older colonisation times, and migration) to investigate variation in diversity between Andean and non-Andean regions using the subtribe Godyridina. Each mechanism has been the support for the cradle (Fjeldså, 1994; Hutter *et al.*, 2013), museum (Stebbins, 1974; Smith *et al.*, 2007), time-for-speciation (Stephens and Wiens, 2002) and species-attractor (Beckman and Witt, 2015) hypotheses. However, there are still not studies with this framework assessing multiple taxonomic groups. Most diversification studies were focused on a specific taxonomic group and do not use, at the same time, multiple groups classified in different taxonomic categories.

We assessed four hypotheses to identify the pattern(s) of diversification occurring in the NAB. We took the three most common hypotheses used in the literature to explain the

diversification in this area and we formulated another hypothesis based on other affirmations in the literature.

**Origin: Amazonian region, Pattern: Lowlands to Highlands:** North Andean taxa originated in the Amazonian region. Taxa arrived at the valleys during the early-middle-Miocene (~15-10 Ma), and then followed the lowlands to highlands pattern in the NAB. The Amazonian region was connected to the Magdalena valley and also to the North-Caribbean zone; the Eastern Cordillera was not more than 40% of its current elevation (~15-11 Ma, Gregory-Wodzicki, 2000). Once established in the North Andean lowlands, the biota moved to highlands following the mountain-building for each Cordillera *ca.* (13-7 Ma) (~13-7 Ma) (Antonelli *et al.*, 2009; Brumfield and Edwards, 2007; Ribas *et al.*, 2007).

**Origin: Central America, Pattern: Lowlands to Highlands:** North Andean taxa originated in Central America. Taxa arrived first at valleys during the early-middle-Miocene (~15-10 Ma), and then followed the lowlands to highlands pattern in the NAB. The Amazonian region was connected to the Magdalena Valley and also to the North-Caribbean zone. Some taxa reached the Amazonian region early in time due to the final uplift of the Eastern Cordillera, which took place in the Plio-Pleistocene (~13-7 Ma, Hoorn *et al.*, 1995, 2010). Once established in North Andean lowlands, the biota arrived at the highlands following the mountain-building of each Cordillera *ca.* (13-7 Ma) (Daza *et al.*, 2010; Ornelas *et al.*, 2013).

**Origin: Central Andes, Pattern: Highlands to Lowlands:** North Andean taxa originated in the Central Andes. Taxa arrived first at the Cordilleras during the early-middle-Miocene (~15-10 Ma) and then followed the highlands to lowlands pattern in the NAB. The biota, following the south-to-north pattern, went to the Central Cordillera approximately 20-15 Ma (Initial uplift: 65

to 33 Ma; significant uplift: 23-10 Ma), then to the Western Cordillera by *ca.* 15 Ma (Significant uplift: middle Miocene (~13 Ma) to Holocene), and finally to the Eastern Cordillera (~10 Ma). From the North Andean highlands, the taxa followed the highlands to lowlands pattern towards the valleys and the Amazonian region ((Doan, 2003; Chaves *et al.*, 2011).

***Altitudinal and horizontal pattern:*** The North Andean biota followed two different patterns, one altitudinal (highlands and lowlands) and the other horizontal (between Cordilleras). The altitudinal pattern, lowlands to highlands, occurred from valleys following the mountain uplift (~15-7 Ma). Once the taxa were at the highlands a differentiation occurred among flanks of the Cordilleras (after ~7 Ma). Thus, each flank was associated with lowlands, subdividing the North Andean Block in three regions such as: Pacific region (Western Cordillera), inter-Andean region (Valleys, Central Cordillera, and Western flank of the Eastern Cordillera), and Eastern region (Eastern flank of the Eastern Cordillera and the Amazonian region) (Kattan *et al.*, 2004).

In the present study, we used multiple taxonomic groups and combining historical biogeography, we assessed the four hypotheses presented above to identify the pattern(s) of diversification occurring in the NAB and to assess two main questions: What is the hypothesis that best fits the diversification of the North Andean taxa? and what are the biogeographical and temporal scenarios of the Andean uplift?

## 2. Materials and Methods

### 2.1 Taxon and DNA sequence sampling

Following Sanmartín *et al.* (2001) and Sanmartín and Ronquist (2002), we established two compatible rules for choosing the study groups. The first rule was to use taxa that had at least three species distributed in the NAB, and the second rule was to select groups with sister clade(s) distributed in adjacent areas. We found 15 monophyletic groups belonging to six taxonomic classes (Magnoliopsida, Insecta, Amphibia, Reptilia, Aves, Mammalia) that agree with these rules. The total sample included 637 species representing 13 families and 65 genera (see Table 1. Appendix A). We downloaded the corresponding DNA sequences from GenBank (NCBI, Benson *et al.*, 2012). The number of available genes ranges from two (*Leptodeira* 1764 bp, Tanagers 2184 bp Sedano and Burns, 2010) to ten (Centroleninae 6160 bp).

### 2.2 Phylogenetic analyses and divergence time estimations

For each phylogeny, we aligned the DNA sequences under the multiple-sequence-alignment-algorithm implemented in MUSCLE (v.3.8.31, Edgar, 2004), and calculated the best evolutionary model using the Akaike Information Criterion (Akaike, 1974) as implemented in the R package Phangorn (v.2.1.1, Schliep, 2011). Phylogeny and divergence times were estimated for partitioned data set using Bayesian Inference approach. Preliminary analyses were

performed using MrBayes (v.3.2.2, Ronquist *et al.*, 2012), with 10 million generations, four Markov Monte Carlo chains, temperature set as 0.2, and sampling every 10000 generations; for each analysis, we used the Robinson and Foulds distance (RF) (Robinson and Foulds, 1981) to compare the reconstructed phylogeny with the trees reported in the literature. Phylogenetic and divergence times estimations were conducted in BEAST (v.1.8.2, Drummond and Rambaut, 2007; Drummond *et al.*, 2012) using an uncorrelated relaxed lognormal clock (Drummond *et al.*, 2006) with a Speciation Yule Process set as tree prior because we did not take into account extinction and we assessed different genera and species but not populations (Yule, 1924; Aldous, 2001). We performed two runs of 30 million generations, sampling every 1000 generations. We checked the convergence using Tracer (v.1.6, Rambaut *et al.*, 2014) considering an acceptable effective sample size (ESS) greater than 200 (Drummond *et al.*, 2009) and standard deviations below  $1 \times 10^{-3}$ . We conducted for each group a calibration prior exploration, assessing uniform and normal distributions, and selecting between them by Bayes factors (Kass and Raftery, 1995).

We used fossil information or secondary calibrations (estimated from previous studies) depending on the availability for each group (see Table 1. Appendix A). Thus, we estimated, for groups with secondary calibrations, relative divergence times and not absolute node ages due to the lack of fossil information for a specific group or its relative sister clades.

### **2.3 Historical biogeography**

We obtained the distributional data from the Global Biodiversity International Facility (GBIF) up to February, 2017 (Removing duplicates and points in the sea), as well as records in literature. We used a set of nine biogeographic areas based on two models of regionalisation (Cabrera and Willink, 1973; Morrone, 2014) (Areas out of the NAB; Central Andes, Central America, and the

Amazonian region; we considered the North Andean Cordilleras, as a whole, labeled as “highlands”, while the North Andean valleys and the North-Caribbean region were labeled as “lowlands” [0-800 m]). We modified graphically some of these areas with respect to the paleo maps of Hoorn *et al.* (1995, 2010) in order to adjust the areas according to the temporal scale of the hypotheses. We removed the area that corresponds to Chocó-Darién province (Morrone, 2014) and to represent the North Andean highlands we used the mixed area formed by Altoandean and Páramo provinces (Cabrera and Willink, 1973). We selected nine areas in order to avoid over-parameterisation and to limit the number of possible states in the analyses (Ree and Smith, 2008; Matzke, 2012) (e.g. with ten areas and a maximum range size of four, there are 382 possible states, while with nine areas there are 256 possible states).

**2.3.1 Ancestral area analyses.** To estimate historical patterns of dispersal and cladogenesis within each genus, we performed an ancestral area analysis. We estimated the ancestral distributions following two models, the dispersion-extinction-cladogenesis model (DEC, Ree and Smith, 2008) and the DIVALIKE model implemented in the R package BioGeoBEARS (v.0.2.1, Matzke, 2013a). We established a specific maximum range size for each group in order to constrain the number of states in the matrix and avoid the over-parameterisation (Matzke, 2012).

To test whether both methods, DEC and DIVALIKE, produce the same results we performed a Pearson correlation analysis between the likelihoods obtained. We compared the resulting areas by each method and quantified the percentage of composite or non-composite reconstructions, where composite estimations are a set of two or three possible areas (Castroviejo-Fisher *et al.*, 2014).

**2.3.2 Event analyses.** We conducted the event analysis as implemented in TreeFitter (v.1.3, Ronquist, 2001), using the default set of costs to maximize vicariance and duplication (Ronquist, 1997*b*). To assess the stability of the resulting cladogram we generated 300 pseudo-replicates re-sampling with no replacement using each time up to nine out of the 15 phylogenies as input data. We quantified the percentage of dispersal events towards lowlands (inter-Andean valleys and the North-Caribbean region) and/or highlands (North Andean Cordilleras).

## 2.4 Diversification Hypothesis Tests

As a result of the bibliometric analysis made from January, 1900 to December, 2016, we took into account the most common hypotheses used to explain the diversification of the North Andean taxa, as we described previously. Under a Maximum Likelihood approach we performed hypothesis tests for each taxonomic group using the dispersal-extinction-cladogenesis model (Ree and Smith, 2008) implemented in BioGeoBEARS (v.0.2.1, Matzke, 2013*a*). We specified for each hypothesis three sets of unequal rates of dispersal between areas ([1] 1 - 0.5 - 0, [2] 1 - 0.7 - 0.3 - 0, and [3] 1 - 0) and a temporal stratification containing four-time intervals ([1] 0 - 7, [2] 7 - 10, [3] 10 - 15, and [4] 15 - 20 Ma) (see Dispersal multipliers Appendix B). The stratification and the dispersal multipliers were designed to account for the major geological events such as the south-to-north uplift of the Andes, the uplift of each Cordillera in the NAB and the closure of the Western Andean Portal (Gregory-Wodzicki, 2000; Hungerbühler *et al.*, 2002; Hoorn *et al.*, 2010). According to the reconstructions obtained, we quantified the percentage of nodes that followed each pattern in different temporal intervals. We compared the

resulting maximum likelihood among dispersal multipliers and between hypotheses. We generated a lineage-through-time plot (Nee *et al.*, 1995) in the R package *ape* (v.4.1, Paradis *et al.*, 2004), as a graphical representation for the diversification over time for all groups.

We matched the changes along the curve with the geological events that could occur in each temporal stratification of the hypotheses. Simultaneously, we compared the reconstructions obtained after the hypothesis tests with the previous ancestral area estimations, in order to verify if after the hypothesis test the ancestral distribution(s) were different in the analyses and assess the influence of dispersal multipliers on the estimation of ancestral distribution. Besides, we compared the reconstructions of the hypothesis tests with the results of the events analysis. For this instance, we seek in the hypothesis test reconstructions, nodes that shown the same dispersal events and/or vicariance obtained under the events analyses. Finally, we dated each event found according to the date in the phylogenies.

We conducted all R analyses using the version 3.4.1 (R Core Team, 2017).

### **3. Results**

#### **3.1 Phylogenetic analyses and divergence times**

The resulting Robinson and Foulds distance (RF) between the reconstructed phylogeny and the trees reported in the literature was less than or equal to 0.5 in 90% of the comparisons (min=0.04, max=0.55, median=0.35, see RF Appendix C).

Our results indicated that for eight out of 15 phylogenies the basal node corresponded to the Miocene (23.03-5.3 Ma), three out of 15 phylogenies corresponded to the Oligocene (~33.9-23.03 Ma), and four out of 15 groups corresponded to the Eocene (~56-33.9 Ma). The groups classified in the Magnoliopsida class started to diversify in the late Eocene-Oligocene, between 35 to 25 Ma. We found that insecta taxa started to diversify in the Miocene between 15 to 10 Ma. In terms of specific groups, *Platyrrhinus* was the youngest group assessed (5.4 Ma, CI(95%)= 4.1-9.6 Ma), while *Pristimantis* was the oldest group assessed (42.3 Ma, CI(95%)= 34.5-50.4 Ma).

### 3.2 Ancestral distribution

The estimated ancestral distributions were similar between models. We obtained the same distributions in 53% of the basal nodes (see Table 3. Appendix D) but in 47% of the analyses the models reconstructed different but congruent set of areas. Meanwhile in 43% of the cases under the DEC model we obtained single areas while for the same node DIVALIKE recovered two areas (hereafter considered as composite reconstruction) (see Table 3. Appendix D). When the estimation differs among models, we found that the smallest set of areas is contained inside the largest set of areas (eight out of 15 groups, see Table 3. Appendix D).

We recovered, under DEC and DIVALIKE, equal reconstructions in the internal nodes that varied from 67% to 100% and we obtained a high correlation value of DEC and DIVALIKE log-likelihoods ( $R= 0.998$ ; CI(95%)= 0.996-0.999), even when the set of areas were not exactly the same (see Table 3. Appendix D).

We recovered single areas in 43.3% of the reconstructions, varied from 62% for the Amazonian region (I) to 15% for Central Andes (A) (Fig. 1). Nevertheless, we obtained

composite reconstructions along the groups showing a set of two areas as ancestral distribution (23.3%, e.g. *Centroleninae*: CI, *Napeogenes*: AI) or three areas as ancestral distribution (33.3%, e.g. *Pteronymia*: CHI (De-Silva *et al.*, 2017), *Pristimantis*: BCI). We found that in 29% of the composite reconstructions showing two areas, the Central Cordillera appeared together with the Amazonian region (C and I) (Fig. 1, see Table 4. Appendix D). The composite reconstruction obtained between the Eastern and Central Cordillera, the Central Andes and the Amazonian region (BCI and CI) represented 71% of the reconstructions showing two and three areas. Central America appeared in 23.5% of the composite reconstructions (e.g. HI *Amazilia*, CHI *Pristimantis*, and CHI *Pteronymia*).

### 3.3 Relationship of areas in the North Andean Block

We obtained two area cladograms where the main difference between them was the number of dispersal events and the frequency of vicariance. The Robinson and Foulds distance between cladograms was 0.71 but the relations obtained are similar in terms of the resulting relationship of North Andean lowlands. Vicariance events were evidenced in all internal nodes but the highest frequencies were obtained in five of the seven nodes of each cladogram (Fig. 2). The areas involved in vicariance events are the Amazonian region, Central Andes, and Central America (AHI), the Central and Eastern Cordilleras (BC), the Western Cordillera and Cauca valley (DF).

The lowlands in the NAB did not appear related to the highlands (Fig. 2). The North-Caribbean area and the Magdalena valley were related in the same node in both cladograms, probably because the connection of these areas predated the mountain building. Besides, the high frequencies of vicariance obtained in the node formed by the Western Cordillera and the Cauca valley, we obtained two dispersal events towards Central America (Table 1). There were more

dispersal events towards highlands (Cordilleras in the NAB) (47%) than to lowlands (inter-Andean valleys) (22%) (Table 1). There were areas such as the Amazonian region, the Central Andes, and Central America that presented dispersal events towards both, North Andean lowlands and highlands. When comparing the percentage of dispersal events from areas that disperse to both, North Andean lowlands and North Andean highlands, we obtained a major dispersion towards highlands (62%; Table 1. See also Table 5. Appendix E). We also obtained more dispersal events (41%) between Cordilleras in the NAB (Eastern, Central and Western Cordilleras). Inside the NAB 24% of the dispersal events were from North Andean Cordilleras to North Andean lowlands (Table 1).

### 3.4 Diversification pattern

We found that the hypothesis with origin: Central Andes and pattern: Highlands to Lowlands fitted best to the diversification of 73.3% of the groups showing in different time frames a highlands-to-lowlands pattern (Fig. 3). Nonetheless, the hypothesis of origin in the Amazonian region with a pattern from Lowlands to Highlands and the hypothesis based on horizontal and altitudinal pattern, fitted the diversification of taxa such as the Annonaceae and *Pristimantis* groups, respectively.

The hypotheses with different origin, Amazonian region or Central America and pattern from Lowlands to Highlands presented the lowest log-likelihood differences in five out of 15 groups. We found log-likelihood differences, between dispersal matrices, that varied from 111 to 0.01 likelihood units (Median= 8). Distinctive dispersion matrices (with different dispersal rates) did not generate larger changes in relation to the resulting maximum likelihood. The largest differences were obtained between the dispersal multipliers of the hypothesis origin: Central

Andes, pattern: Highlands to Lowlands (see Table 6. Appendix F). The minimal differences (41%) were among the results obtained by the dispersal matrices of the hypothesis origin: Central America and pattern: Lowlands to Highlands (see Table 6. Appendix F).

We recovered a different ancestral distribution when comparing with the distributions inferred in the ancestral area analyses. Thus, following the hypothesis that fitted best, the Central Andes appeared as the ancestral distribution, either in composite reconstructions (53%) or as a single area (33%).

The lowlands to highlands or *vice-versa* pattern were observed in different temporal ranges between groups. Thus, the same pattern was evidenced multiple times during the time of diversification of a specific group (Fig. 3). Considering four temporal intervals, each one of 5 million years, the percentage of nodes showing the lowlands to highlands pattern in the 5 to 0 Ma interval was 31.58%. From 15 to 10 Ma and from 10 to 5 Ma the percentage was 21.05% (Table 2). The highlands to lowlands pattern was found with a percentage of 26.32% in the 10 to 5 Ma interval. We found that both patterns fitted the diversification of the groups, even when the pattern highlands to lowlands fitted best.

We obtained the maximum and minimum percentages of nodes involved in changes from one area to another in the time intervals from 10 to 5 Ma (41.4%) and from 20 to 15 Ma (10.3%) (Table 2). We observed an increment in the number of lineages (Fig. 3) from the late-Miocene which coincides with the time interval with more evidence of both patterns highlands to lowlands and *vice-versa* (~10 to 5 Ma). We found the south to north pattern in 80% of the groups and the principal areas involved were: Central Andes, Eastern and Central Cordilleras in the NAB.

## 4. Discussion

### 4.1 Ancestral area

The correlated maximum likelihood of both models, DEC and DIVALIKE, show high similarity in the numerical calculation even when the areas estimated were not completely equal. In terms of likelihood, similar values can be obtained when some areas in composite reconstructions do not contribute to the overall likelihood obtained. Although under the DEC model we obtained more single areas than in DIVALIKE, both estimations were influenced by the history of the group and their sister clades (Castroviejo-Fisher *et al.*, 2014; Antonelli *et al.*, 2009). The parameters and distributions play a key role in the differentiation of both models, thus vicariance only differs between them when a maximum range size is greater than or equal to four (Matzke, 2013b). Even when both models focused in different processes, we might have the same results under specific parameters. Additionally, the distribution of sister species influences the resulting probabilities adding or decreasing the number of possible events (Matzke, 2013b). With our data set, we can infer that the DEC model reduces the ambiguity at basal nodes and it recovers single ancestral distribution in reconstructions with clades that have widespread organisms.

Our results showed three possible ancestral distributions for North Andean taxa (Fig. 1) presenting the largest number of dispersal events according to the event analyses. These ancestral areas are congruent with the ones proposed previously in different hypotheses (e.g. Doan, 2003; Brumfield and Edwards, 2007; Ornelas *et al.*, 2013). This indicates that the resulting ancestral

distribution is maintained under different parameters and area scenarios used to address ancestral area analysis. The set of two areas (composite reconstruction), composed by the Central Cordillera in the NAB and the Amazonian region, is similar to the ancestral distribution obtained in previous studies (Castroviejo-Fisher *et al.*, 2014; Antonelli *et al.*, 2009). We may suggest that composite reconstructions are related to the history of the group because these types of reconstructions appear when the sister clade of the groups is Amazonian and most of the internal nodes are North Andean. Still, the presence of a strictly Amazonian node in the phylogeny influence the ancestral area estimation (Fig. 3) as seen in Centroleninae, *Pristimantis*, and *Stenocercus* (Teixeira *et al.*, 2016).

#### **4.2 Relationship of areas in the North Andean Block**

Andean uplift and the asynchronous Andean formation (Case *et al.*, 1990; Hoorn *et al.*, 1995; Gómez *et al.*, 2003) are the major events involved in taxa separation between lowlands and highlands, as seen in our area relationships, and between southern and northern latitudes (Elias *et al.*, 2009; Doan, 2003). Authors such as Chaves *et al.* (2011) and García-Moreno and Fjeldså (2000), suggest that the North Andean taxa are originated from adjacent areas that are older than the North Andean Block, such as Central Andes and the Amazonian region. The node conformed by adjacent areas as Central Andes, Central America, and the Amazonian region support the previous idea. These areas were the same obtained in single reconstructions in the ancestral area analyses and presented the largest number of dispersions towards the NAB. The resulting relationship between the highlands is supported by the observed dispersions from highland to highland (Table 1; see also Table 5. Appendix E) within the NAB, which could be related to the

idea of sister flanks and divergence between Cordilleras (Kattan *et al.*, 2004). Dispersal events towards and from Central America supported connection between Central and South America.

### 4.3 Geological scenario

The connection of the Amazonian region and the North-Caribbean area has been hypothesised due to the southern part of the Eastern Cordillera started to rise along with the Central Cordillera (Hoorn *et al.*, 1995, 2010), separating the Magdalena and Amazonas Basins, however, this was not perceived with our data set. According to Gregory-Wodzicki (2000), the Eastern Cordillera was at no more than 40% of its modern elevation by 4 Ma and an intensified uplift (circa 4-5 to 3 Ma) has been associated with the South American-Panama collision (Farris *et al.*, 2011). However, *Podocnemis* (Vargas-Ramirez *et al.*, 2008) showed a vicariant node involving two species separated around 15 Ma and the Annonaceae family presented a Caribbean node separated from the Amazonian node between 20 to 15 Ma. Therefore, we establish that the Eastern Cordillera played a role as a barrier for the studied taxa distributed in these areas.

An earlier start for the formation of the Panamanian Isthmus, taking into account the hypothesis tests, was supported by groups such as *Amazilia* 15-10 Ma, *Pristimantis* 15-10 Ma, *Ithomia* 10-5 Ma, and *Leptodeira* 5-0 Ma (Fig. 3). Our results are congruent with some findings of Bacon *et al.* (2015), who obtained in their analyses organisms that probably passed through the Panama isthmus circa 20 Ma. Recent models suggest an early start for the isthmus formation in the Oligocene (Montes *et al.*, 2012) or near to 25 to 23 Ma (Farris *et al.*, 2011). Studies based on biological evidence indicate a formation between 3.5 to 3 Ma, while bathimetric evidence supports a formation approximately between 14 and 12 Ma (Duque-Caro, 1990; Coates *et al.*, 1992, 2004).

The North Andean block presented an initial significant uplift by late Oligocene to early Miocene (*ca.* 23 Ma) and the most intense peaks of mountain building followed during the late Miocene (*ca.* 12 Ma) and early Pliocene (*ca.* 4.5 Ma) (Hoorn *et al.*, 2010). Alongside, the asynchronous mountain building is supported by our results. Central Andean taxa first colonised the Central Cordillera (Initial uplift: Late Cretaceous to Paleogene, Intensified uplift: Miocene. Cooper *et al.*, 1995; Gómez *et al.*, 2003; Hoorn *et al.*, 2010) within the 20 to 15 Ma time interval. Two groups with Central Andes as ancestral distribution colonised the Eastern Cordillera, probably the southern part of this range in the 20 to 15 Ma time interval. A major colonisation of the Eastern Cordillera occurred between 10 to 5 Ma because the initial mountain building was by 12 Ma and a high uplift rate was recorded during the Pliocene-Holocene (after *ca.* 5 Ma). When the ancestral distribution was the Amazonian region, the first range colonised was the Central Cordillera in the North Andean Block. The early colonisation of the Central Cordillera is congruent with the model of mountain building previously proposed.

#### **4.4 Diversification pattern**

Although the hypothesis with origin: Central Andes and pattern: Highlands to Lowlands did not fit all groups, it always presented lower likelihood differences in comparison with the hypothesis that fit better to each group (see Table 6. Appendix F) and implying that the major part of the groups could follow the highlands to lowlands pattern over time, however, based on the likelihood differences between hypotheses, we could state that the taxa followed multiple patterns as highlands to lowlands, lowlands to highlands and south to north in different time frames during their diversification.

The node reconstructions recovered after the hypothesis tests are not the same as the ones inferred in the ancestral area analyses because the dispersal matrix influenced the results. However, the hypothesis with an origin in the Amazonian region and lowlands to highlands pattern fitted better the diversification of the Annonaceae family showing the Amazonian region as the ancestral distribution in all tests and reconstructions. Annonaceae was not the only group that shared the ancestral area in both analyses (ancestral area and hypotheses tests). We found that even when the hypothesis that fit better was origin: Central Andes and pattern: Highlands to Lowlands, the area obtained in the ancestral area analyses was recovered by the hypotheses tests in *Amazilia* and *Leptodeira*.

The idea proposed by Pirie *et al.* (2006), dispersal events during the North Andean orogeny, to explain the diversification of the Annonaceae family could fit also other Amazonian groups and supports the lowlands to highlands pattern. Apart from the affirmation above, mountain-building could influence the diversification of different groups acting as a barrier or as a dispersal corridor (Ribas *et al.*, 2007; Elias *et al.*, 2009) and it might generate a single or multiple patterns over time (Fig. 3).

The movement from the Central Andes to the Cordilleras in the NAB represented the major percentage of changes from one area to another over time (Fig. 3; Table 3). This idea supports the south-to-north diversification pattern (Doan, 2003; Goicoechea *et al.*, 2012; Chaves *et al.*, 2011) that fit groups such as *Stenocercus* (Torres-Carvajal, 2007), *Pristimantis* (Pinto-Sánchez *et al.*, 2012), and *Tournefortia* (Luebert *et al.*, 2011), as has been seen in *Adelomya* or *Proctoporus* (Doan, 2003; Chaves *et al.*, 2011). Diversification at the rhythm of the Andean uplift as it is proposed in the south-to-north speciation hypothesis (Doan, 2003; Goicoechea *et*

*al.*, 2012; Chaves *et al.*, 2011) may explain the fit of the hypothesis with origin: Central Andes and pattern: Highlands to Lowlands. However, regardless the origin, the North Andean taxa might follow a South to North pattern of diversification inside the NAB at different periods of time (Fig. 3). *Amazilia* reinforces the previous statement because its ancestral area was Central America and it presented nodes that followed the south-to-north pattern. For this genus, the major divergence in Central America was during the formation of mountain systems in the area (Ferrari 1999). Our results showed two patterns in two major clades, from Mesoamerica to North Andean highlands and other from Mesoamerica to lowlands in South America. We suggest that these two patterns fit the diversification in two separate clades simultaneously (Fig. 3).

Given the hypothesis fit, groups such as Centroleninae, *Pristimantis*, and *Stenocercus* support a south-to-north pattern between 15 to 10 Ma (Fig. 3; Table 2) and the principal areas involved in this pattern are the Central Andes and the Eastern and Central Cordilleras, following Doan (2003), who states that the Andean taxa followed the Andean orogeny. However, Castroviejo-Fisher *et al.* (2014) did not find a south-to-north pattern of diversification in Centrolenidae. Based on their results, they found few dispersals from the Central Andes to the NAB. The age when this south-to-north pattern fit coincides with a period of intensified uplift (circa 20-10 Ma) and let us suggest that colonisation of the North Andean highlands started nearly 10 Ma (Hoorn *et al.*, 2010). According to our results, the 10 to 5 Ma interval presented most of the evidence for both patterns, highlands to lowlands and lowlands to highlands and also is the temporal range that showed an increment in the number of lineage through time (Fig.3). For this reason, we propose that it does not exist a unique pattern within the NAB. These patterns

did not begin at the same time (Fig. 3) and in many cases these patterns overlapped, comprising different nodes in the same taxon.

Bearing in mind the fit of each pattern, it is more plausible the highlands to lowlands pattern (Fig. 3; Table 3). This pattern could be associated with the major dispersal events obtained towards highlands before the 10 to 5 Ma interval. This result also explains that these patterns could be independent and a result of multiple colonisations of the Andes (Chazot *et al.*, 2016) and, as in *Mionectes* (Miller *et al.*, 2008), did not exhibit the lowlands to highlands pattern or *vice-versa* over time.

Correspondingly, we can suggest, based on our results, the evidence of “attraction” towards the Andes from adjacent areas likely followed the species-attractor hypothesis (Beckman2015). The species from the Amazonian region could have dispersed to the Andes multiple times following the assumption of multiple colonisations (Chazot *et al.*, 2016). Thus, it is possible to infer, based on the proportion of North Andean lineages *versus* Amazonian or Central American lineages, that taxa such as Annonaceae, *Leptodeira* and the *Tournefortia* clade support this idea.

We can deduce that highland taxa from the Central Andes had more time to diversify than those from adjacent lowlands, this way, those taxa from the Central Andes probably colonised North Andean lowlands first. Here we found clades (e.g *Ithomia*, *Napeogenes*, *Stenocercus*) with Central Andes as ancestral distribution that probably fit the time-for-speciation hypothesis (Stephens and Wiens, 2002). The highlands to lowlands pattern could be explained by the mechanism of older colonisation times involved in this hypothesis. García-Moreno and Fjeldså (2000) state that the highland biota diversified from the lowlands because they are older than the

highlands, while opposite to this Chazot *et al.* (2016) state that highland biota came from older highlands.

Chazot *et al.* (2016) proposed a high speciation rate in the Andes as the main mechanism of diversification. Even when the speciation rate was not evaluated, we observed groups such as Centroleninae, Cinchoneae, *Ithomia*, *Napeogenes*, *Pristimantis*, and *Stenocercus* containing nodes where the Andean Cordilleras acted as a barrier for the diversification (Fig. 3). The number of lineages in adjacent Andean highlands was larger than the number of lineages in adjacent lowlands (Fig. 3, Centroleninae and *Pristimantis*). We suggest that these groups could fit the cradle hypothesis (Fjeldså, 1994; Hutter *et al.*, 2013). As proposed by Graham *et al.* (2004) and Hughes and Eastwood (2006), the geographical heterogeneity favoured the geographic diversification where the Cordilleras acted as a barrier, although, the asynchronous North Andean uplift (Case *et al.*, 1990; Cooper *et al.*, 1995; Hoorn *et al.*, 1995) also generated the opportunity for diversification at different times.

## 5. Conclusions

In terms of likelihood differences and the fit of each hypothesis, the two altitudinal patterns are plausible no matter the ancestral area estimated, and we could evidence these patterns overlapping and occurring multiple times in the same temporal frame (Miocene). However, the highlands to lowlands pattern fit better for the North Andean taxa which might support a highlands origin inside or outside the NAB.

Our analyses showed that the closing of the Panamanian Isthmus is not as recent as has been hypothesized. This supports an earlier start of the Isthmus formation. We found that diversification of North Andean taxa followed the Andean uplift and match to the times previously proposed. The taxa followed the orogeny scenario, where the Central Cordillera starts its uplift first, later the Western Cordillera, and then the Eastern Cordillera.

Finally, we proposed that two evolutionary mechanisms, the speciation rates and older colonisation times, could be involved in the diversification of North Andean taxa. This needs to be assessed in future studies using multiple taxa taxonomically differentiated and following or varying the scenario proposed recently by Chazot *et al.* (2016) and thus, compare whether under this scenario is recovered as a single pattern.

## References

- Akaike, H. (1974). A new look at the statistical model identification. *IEEE transactions on automatic control*, 19(6), 716–723.
- Aldous, D.J. (2001). Stochastic models and descriptive statistics for phylogenetic trees, from Yule to today. *Statistical Science*, 23–34.
- Antonelli, A., Nylander, J.A.A., Persson, C., & Sanmartín, I. (2009). Tracing the impact of the Andean uplift on Neotropical plant evolution. *Proceedings of the National Academy of Sciences*, 106(24), 9749–9754.
- Audemard, F.E. & Audemard, F.A. (2002). Structure of the Mérida Andes, Venezuela: relations with the South America-Caribbean geodynamic interaction. *Tectonophysics*, 345(1), 1-26.
- Bacon, C.D., Silvestro, D., Jaramillo, C., Smith, B.T., Chakrabarty, P., & Antonelli, A. (2015). Biological evidence supports an early and complex emergence of the Isthmus of Panama. *Proceedings of the National Academy of Sciences*, 112(19), 6110–6115.
- Beckman, E.J. & Witt, C.C. (2015). Phylogeny and biogeography of the New World siskins and goldfinches: Rapid, recent diversification in the Central Andes. *Molecular phylogenetics and evolution*, 87, 28–45.

- Benham, P.M., Cuervo, A.M., Mcguire, J.A., & Witt, C.C. (2014). Biogeography of the Andean metaltail hummingbirds: Contrasting evolutionary histories of tree line and habitat-generalist clades. *Journal of Biogeography*, 42(4), 763–777.
- Benson, D.A., Cavanaugh, M., Clark, K., Karsch-Mizrachi, I., Lipman, D.J., Ostell, J., & Sayers, E.W. (2012). GenBank. *Nucleic acids research*, 41(D1), D36–D42.
- Bird, P. (2003). An updated digital model of plate boundaries. *Geochemistry, Geophysics, Geosystems*, 4(3).
- Brumfield, R.T. & Edwards, S.V. (2007). Evolution into and out of the Andes: A Bayesian analysis of historical diversification in *Thamnophilus antshrikes*. *Evolution*, 61(2), 346–367.
- Cabrera, A. & Willink, A. (1973). Biogeografía de América Latina. *Secretaría General de la organización de los Estados Americanos. Serie de Biología*, 13.
- Case, J.E., Shagam, R., & Giegengack, R.F. (1990). Geology of the Northern Andes; An overview. *GSA Bulletin*, 76, 567–589.
- Castroviejo-Fisher, S., Guayasamin, J.M., Gonzalez-Voyer, A., & Vilà, C. (2014). Neotropical diversification seen through glassfrogs. *Journal of Biogeography*, 41(1), 66–80.
- Chapman, F.M. (1917). The distribution of bird-life in Colombia: a contribution to a biological survey of South America. *Bulletin of the AMNH*, 36.
- Chaves, J.A., Weir, J.T., & Smith, T.B. (2011) Diversification in *Adelomyia* hummingbirds follows Andean uplift. *Molecular Ecology*, 20(21), 4564–4576.

- Chazot, N., Willmott, K.R., Condamine, F.L., De-Silva, D.L., Freitas, A.V.L., Lamas, G., ... & Mallet, J. (2016). Into the Andes: multiple independent colonizations drive montane diversity in the Neotropical clearwing butterflies Godyridina. *Molecular Ecology*, 25(22), 5765–5784.
- Coates, A.G., Collins, L.S., Aubry, M.P., & Berggren, W.A. (2004). The geology of the Darien, Panama, and the late Miocene-Pliocene collision of the Panama arc with northwestern South America. *Geological Society of America Bulletin*, 116(11-12), 1327–1344.
- Coates, A.G., Jackson, J.B.C., Collins, L.S., Cronin, T.M., Dowsett, H.J., Bybell, L.M., Jung, P., & Obando, J.A. (1992). Closure of the Isthmus of Panama : The near-shore marine record of Costa Rica and western Panama closure of the Isthmus of Panama. *Geological Society of America Bulletin*, 104(7), 814–828.
- Collot, J.Y., Charvis, P., Gutscher, M.A., & Operto, S. (2002). Exploring the Ecuador-Colombia active margin and interplate seismogenic zone. *EOS, Transactions American Geophysical Union*, 83(17), 185–190.
- Cooper, M.A., Addison, F.T., Alvarez, R., Coral, M., Graham, R., Hayward, A.B., ... & Pulham, A.J. (1995). Basin development and tectonic history of the Llanos Basin, Eastern Cordillera, and middle Magdalena Valley, Colombia. *AAPG bulletin*, 79(10), 1421–1442.
- Daza, J.M., Castoe, T.A., & Parkinson, C.L. (2010). Using regional comparative phylogeographic data from snake lineages to infer historical processes in Middle America. *Ecography*, 33(2), 343–354.

- De-Silva, D.L., Mota, L.L., Chazot, N., Mallarino, R., Silva-Brandão, K.L., Piñerez, L.M.G., ... & Giraldo, C. E. (2017). North Andean origin and diversification of the largest ithomiine butterfly genus. *Scientific Reports*, 7, 45966.
- Doan, T.M. (2003). A south-to-north biogeographic hypothesis for Andean speciation: evidence from the lizard genus *Proctoporus* (Reptilia, Gymnophthalmidae). *Journal of Biogeography*, 30(3), 361–374.
- Drummond, A.J., Ho, S.Y.W., Phillips, M.J., & Rambaut, A. (2006) Relaxed phylogenetics and dating with confidence. *PLoS Biology*, 4(5), 699–710.
- Drummond, A.J., Ho, S.Y.W., Rawlence, N., & Rambaut, A. (2009). A rough guide to BEAST 1.4. 2007. *Edinburgh: University of Edinburgh*.
- Drummond, A.J. & Rambaut, A. (2007). BEAST: Bayesian evolutionary analysis by sampling trees. *BMC evolutionary biology*, 7(1), 214.
- Drummond, A.J., Suchard, M.A., Xie, D., & Rambaut, A. (2012). Bayesian phylogenetics with BEAUti and the BEAST 1.7. *Molecular biology and evolution*, 29(8), 1969–1973.
- Duque-Caro, H. (1990). The choco block in the northwestern corner of South America: Structural, tectonostratigraphic, and paleogeographic implications. *Journal of South American Earth Sciences*, 3(1), 71–84.
- Edgar, R. (2004). MUSCLE: Multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research*, 32(5), 1792–1797.

- Ehlers, T.A. & Poulsen, C.J. (2009). Influence of Andean uplift on climate and paleoaltimetry estimates. *Earth and Planetary Science Letters*, 281(3), 238–248.
- Elias, M., Joron, M., Willmott, K., Silva-Brandao, K.L., Kaiser, V., Arias, C.F., ... & Jiggins, C.D. (2009). Out of the Andes: patterns of diversification in clearwing butterflies. *Molecular Ecology*, 18(8), 1716–1729.
- Farris, D.W., Jaramillo, C., Bayona, G., Restrepo-Moreno, S.A., Montes, C., Cardona, A., Mora, A., Speakman, R.J., Glascock, M.D., & Valencia, V. (2011). Fracturing of the Panamanian Isthmus during initial collision with South America. *Geology*, 39(11), 1007–1010.
- Fjeldsa, J. (1994). Geographical patterns for relict and young species of birds in Africa and South America and implications for conservation priorities. *Biodiversity & Conservation*, 3(3), 207–226.
- Freymueller, J.T., Kellogg, J.N., & Vega, V. (1993). Plate motions in the North Andean region. *Journal of Geophysical Research: Solid Earth*, 98(B12), 21853–21863.
- García-Moreno, J. & Fjeldså, J. (2000). Chronology and mode of speciation in the Andean avifauna. *Bonn. Zool. Monogr*, 46, 25–46.
- Goicoechea, N., Padial, J.M., Chaparro, J.C., Castroviejo-Fisher, S., & De la Riva, I. (2012). Molecular phylogenetics, species diversity, and biogeography of the Andean lizards of the genus *Proctoporus* (Squamata: Gymnophthalmidae). *Molecular Phylogenetics and Evolution*, 65(3), 953–964.

- Gómez, E., Jordan, T.E., Allmendinger, R.W., Hegarty, K., Kelley, S., & Heizler, M. (2003). Controls on architecture of the late Cretaceous to Cenozoic southern middle Magdalena Valley basin, Colombia. *Geological Society of America Bulletin*, 115(2), 131–147.
- Graham, C.H., Ron, S.R., Santos, J.C., Schneider, C.J., & Moritz, C. (2004). Integrating Phylogenetics and Environmental Niche Models To Explore Speciation Mechanisms in Dendrobatid Frogs. *Evolution*, 58(8), 1781–1793.
- Gregory-Wodzicki, K.M. (2000). Uplift history of the Central and Northern Andes: A review Uplift history of the Central and Northern Andes. *Geological Society of America Bulletin*, 112(7), 1091–1105.
- Haffer, J. (1967). Speciation in Colombian forest birds west of Andes. *Novitates Zoologicae*, 2294, 1–57.
- Haffer, J. (1969). Speciation in Amazonian forest birds. *Science*, 165(3889), 131–137.
- Hartley, A. (2003). Andean uplift and climate change. *Journal of the Geological Society*, 160(1), 7–10.
- Hoorn, C., Guerrero, J., Sarmiento, G.A., & Lorente, M.A. (1995). Andean tectonics as a cause for changing drainage patterns in Miocene northern South America. *Geology*, 23(3), 237–240.
- Hoorn, C., Wesselingh, F.P., Ter Steege, H., Bermudez, M.A., Mora, A., Sevink, J., ... & Jaramillo, C. (2010). Amazonia through time: Andean uplift, climate change, landscape evolution, and biodiversity. *Science*, 330(6006), 927–931.

- Hughes, C. & Eastwood, R. (2006). Island radiation on a continental scale: exceptional rates of plant diversification after uplift of the Andes. *Proceedings of the National Academy of Sciences*, 103(27), 10334–10339.
- Hungerbühler, D., Steinmann, M., Winkler, W., Seward, D., Egüez, A., Peterson, D.E., Helg, U., & Hammer, C. (2002). Neogene stratigraphy and Andean geodynamics of southern Ecuador. *Earth-Science Reviews*, 57(1), 75–124.
- Hutter, C.R., Guayasamin, J.M., & Wiens, J.J. (2013). Explaining Andean megadiversity: the evolutionary and ecological causes of glassfrog elevational richness patterns. *Ecology Letters*, 16(9), 1135–1144.
- Kass, R.E. & Raftery, A.E. (1995). Bayes factors. *Journal of the American Statistical Association*, 90(430), 773–795.
- Kattan, G.H., Franco, P., Rojas, V., & Morales, G. (2004). Biological diversification in a complex region: a spatial analysis of faunistic diversity and biogeography of the Andes of Colombia. *Journal of Biogeography*, 31(11), 1829–1839.
- Kellogg, J.N., Vega, V., Stailings, T.C., & Aiken, C.L. V (1995). Tectonic development of Panama, Costa Rica, and the Colombian Andes: constraints from global positioning system geodetic studies and gravity. *Geological Society of America Special Papers*, 295, 75–90.
- Luebert, F., Hilger, H.H., & Weigend, M. (2011). Diversification in the Andes: Age and origins of South American *Heliotropium* lineages (Heliotropiaceae, Boraginales). *Molecular Phylogenetics and Evolution*, 61(1), 90–102.

- Matzke, N.J. (2012). Founder-event speciation in BioGeoBEARS package dramatically improves likelihoods and alters parameter inference in Dispersal-Extinction-Cladogenesis (DEC) analyses. *Front. Biogeogr*, 4, 210.
- Matzke, N.J. (2013a). BioGeoBEARS: BioGeography with Bayesian (and likelihood) evolutionary analysis in R Scripts. *R package, version 0.2*, 1, 2013.
- Matzke, N.J. (2013b). *Probabilistic historical biogeography: new models for founder-event speciation, imperfect detection, and fossils allow improved accuracy and model-testing*.
- Miller, M.J., Bermingham, E., Klicka, J., Escalante, P., do Amaral, F.S.R., Weir, J.T., & Winker, K. (2008). Out of Amazonia again and again: episodic crossing of the Andes promotes diversification in a lowland forest flycatcher. *Proceedings. Biological sciences / The Royal Society*, 275(1639), 1133–1142.
- Montes, C., Cardona, A., McFadden, R., Morón, S.E., Silva, C.A., Restrepo-Moreno, S., ... & Bayona, G. A. (2012). Evidence for middle Eocene and younger land emergence in central Panama: implications for Isthmus closure. *Geological Society of America Bulletin*, 124(5-6), 780–799.
- Morrone, J.J. (2014). Biogeographical regionalisation of the Neotropical region. *Zootaxa*, 3782(1), 1–110.
- Myers, N., Mittermeier, R.A., Mittermeier, C.G., Da Fonseca, G.A.B., & Kent, J. (2000). Biodiversity hotspots for conservation priorities. *Nature*, 403(6772), 853–858.

- Nee, S., Holmes, E.C., Rambaut, A., & Harvey, P.H. (1995). Inferring population history from molecular phylogenies. *Philosophical Transactions of the Royal Society of London B: Biological Sciences*, 349(1327), 25–31.
- Ornelas, J.F., González, C., de los Monteros, A.E., Rodríguez-Gómez, F., & García-Feria, L.M. (2013). In and out of Mesoamerica: Temporal divergence of *Amazilia* hummingbirds pre-dates the orthodox account of the completion of the Isthmus of Panama. *Journal of Biogeography*, 41(1), 168–181.
- Paradis, E., Claude, J., & Strimmer, K. (2004). APE: analyses of phylogenetics and evolution in R language. *Bioinformatics*, 20(2), 289–290.
- Patton, J.L. & da Silva, M.N.F. (1998). Rivers, refuges, and ridges. The Geography of Speciation of Amazonian Mammals. *Endless Forms. Species and Speciation*, 202–213.
- Pennington, R.T., Lavin, M., Prado, D.E., Pendry, C.A., Pell, S.K., & Butterworth, C.A. (2004). Historical climate change and speciation: neotropical seasonally dry forest plants show patterns of both Tertiary and Quaternary diversification. *Philosophical Transactions of the Royal Society of London B: Biological Sciences*, 359(1443), 515–538.
- Pinto-Sánchez, N.R., Ibáñez, R., Madriñán, S., Sanjur, O.I., Bermingham, E., & Crawford, A.J. (2012). The great American biotic interchange in frogs: multiple and early colonization of Central America by the South American genus *Pristimantis* (Anura: Craugastoridae). *Molecular Phylogenetics and Evolution*, 62(3), 954–972.
- Pirie, M.D., Chatrou, L.W., Mols, J.B., Erkens, R.H.J., & Oosterhof, J. (2006). ‘Andean-centred’ genera in the short-branch clade of Annonaceae: testing biogeographical hypotheses

- using phylogeny reconstruction and molecular dating. *Journal of Biogeography*, 33(1), 31–46.
- Rambaut, A., Suchard, M., Xie, D., & Drummond, A. (2014). Tracer v1.6 <http://beast.bio.ed.ac.uk>. *Tracer (Online 2015, May 29)*.
- R Core Team (2017). R: A Language and Environment for Statistical Computing. Vienna, Austria.
- Ree, R.H., Moore, B.R., Webb, C.O., & Donoghue, M.J. (2005). A Likelihood framework for inferring the evolution of geographic range on phylogenetic trees. *Evolution*, 59(11), 2299–2311.
- Ree, R.H. & Smith, S.A. (2008). Maximum likelihood inference of geographic range evolution by dispersal, local extinction, and cladogenesis. *Systematic Biology*, 57(1), 4–14.
- Ribas, C.C., Moyle, R.G., Miyaki, C.Y., & Cracraft, J. (2007). The assembly of montane biotas: linking Andean tectonics and climatic oscillations to independent regimes of diversification in *Pionus* parrots. *Proceedings of the Royal Society of London B: Biological Sciences*, 274(1624), 2399–2408.
- Robinson, D. & Foulds, L.R. (1981). Comparison of phylogenetic trees. *Mathematical Biosciences*, 53(1), 131–147.
- Ronquist, F. (1997a). Dispersal-Vicariance analysis: a new approach to the quantification of historical biogeography. *Systematic Biology*, 46(1), 195–203.

- Ronquist, F. (1997b). Phylogenetic approaches in coevolution and biogeography. *Zoologica scripta*, 26(4), 313–322.
- Ronquist, F. (2001). TreeFitter 1.0. Computer program distributed by author.
- Ronquist, F., Teslenko, M., Van Der Mark, P., Ayres, D.L., Darling, A., Höhna, S., Larget, B., Liu, L., Suchard, M.A., & Huelsenbeck, J.P. (2012). MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic biology*, 61(3), 539–542.
- Sanmartín, I., Enghoff, H., & Ronquist, F. (2001). Patterns of animal dispersal, vicariance and diversification in the Holarctic. *Biological Journal of the Linnean Society*, 73(4), 345–390.
- Sanmartín, I. & Ronquist, F. (2002). New solutions to old problems: widespread taxa, redundant distributions and missing areas in event-based biogeography. *Animal Biodiversity and Conservation*, 25(2), 75–93.
- Schliep, K.P. (2011). phangorn: Phylogenetic analysis in R. *Bioinformatics*, 27(4), 592–593.
- Schweizer, M., Seehausen, O., & Hertwig, S.T. (2011). Macroevolutionary patterns in the diversification of parrots: Effects of climate change, geological events and key innovations. *Journal of Biogeography*, 38(11), 2176–2194.
- Sedano, R.E. & Burns, K.J. (2010). Are the Northern Andes a species pump for Neotropical birds? Phylogenetics and biogeography of a clade of Neotropical tanagers (Aves: Thraupini). *Journal of Biogeography*, 37(2), 325–343.

- Smith, S. A., De Oca, A.N.M., Reeder, T.W., & Wiens, J.J. (2007). A phylogenetic perspective on elevational species richness patterns in middle American treefrogs: Why so few species in lowland tropical rainforests? *Evolution*, 61(5), 1188–1207.
- Stebbins, G.L. (1974). Flowering plants: evolution above the species level. *London: Arnold xviii, 399p.. Illustrations. General (KR, 197500089).*
- Stephens, P.R. & Wiens, J.J. (2002). Explaining Species Richness from Continents to Communities : The Time-for-Speciation Effect in Emydid Turtles. *The American Naturalist*, 161(1), 112–128.
- Teixeira, M., Prates, I., Nisa, C., Silva-Martins, N.S.C., Strüssmann, C., & Rodrigues, M.T. (2016). Molecular data reveal spatial and temporal patterns of diversification and a cryptic new species of lowland *Stenocercus* Dumeril and Bibron, 1837 (Squamata: Tropiduridae). *Molecular Phylogenetics and Evolution*, 94(1), 410–423.
- Torres-Carvajal, O. (2007). Phylogeny and biogeography of a large radiation of Andean lizards (Iguania, *Stenocercus*). *Zoologica Scripta*, 36(4), 311–326.
- Tschanz, C.M., Marvin, R.F., Cruz B., J., Mehnert, H.H., & Cebula, G.T. (1974). Geological evolution of the Sierra Nevada de Santa Marta, Northeastern Colombia. *Geological Society of America Bulletin*, 85(2), 273–284.
- Vargas-Ramirez, M., Castanomora, O., & Fritz, U. (2008). Molecular phylogeny and divergence times of ancient South American and Malagasy river turtles (Testudines: Pleurodira: Podocnemididae). *Organisms Diversity & Evolution*, 8(5), 388–398.

Velazco, P.M. & Patterson, B.D. (2008). Phylogenetics and biogeography of the broad-nosed bats, genus *Platyrrhinus* (Chiroptera: Phyllostomidae). *Molecular Phylogenetics and Evolution*, 49(3), 749–759.

Yule, G.U. (1924). A mathematical theory of evolution, based on the conclusions of Dr. JC Willis, FRS. *Philosophical transactions of the Royal Society of London. Series B, containing papers of a biological character*, 213, 21–87.

**Tables**

**Table 1.**

*Dispersal events obtained in the events analyses.*

Area	Switch to	Lowlands	Highlands	From ancestral areas to Highlands & Lowlands		Area	Switch to	Lowlands	Highlands	From Highlands		
				To Lowlands	To Highlands					To Lowlands	To Highlands	
<b>I 18.37%</b>	H					<b>D* 6.12%</b>	H					
	C		1				C		1			
	D		1				A			<b>0.33</b>		
	B		1			<b>C* 12.24%</b>	I					
	A						D		1			
	E	1					B		1			
	G	1					A					
	FD	1	1				FD	1	1			
EG	1				AI				<b>24%</b>	<b>41%</b>		
		<b>0.44</b>	<b>0.44</b>				<b>0.17</b>	<b>0.33</b>				
<b>H 14.29%</b>	I					<b>B* 16.33%</b>	I					
	C		1				C		1			
	B		1				D		1			
	D		1				F	1				
	G	1					A					
	BC		1		<b>38%</b>		<b>62%</b>	E	1			
EG	1					FD	1	1				
		<b>0.28</b>	<b>0.57</b>			AI			<b>0.375</b>	<b>0.375</b>		
<b>A 8.16%</b>	C		1			<b>FD 4.08%</b>	H					
	D		1				C		1			
	F	1								<b>0.5</b>		
E	1					<b>F 4.08%</b>	H					
		<b>0.5</b>	<b>0.5</b>				A					
<b>AI 10.20%</b>	H					<b>BC 2.04%</b>	H					
	C		1									
	D		1									
	E	1										
BC		1										
		<b>0.17</b>	<b>0.6</b>									
<b>AIH 4.08%</b>	D		1									
	BC		1									
			<b>1</b>									
								<b>Total of dispersions to highlands or lowlands</b>	<b>22%</b>	<b>47%</b>		
											* Highlands	

Note: Percentage of dispersal events from ancestral areas towards highlands and/or lowlands. The percentage of dispersion from highlands to lowlands and between highlands is shown on the right part of the table. Highlands are marked with an asterisk (\*). A: Central Andes, B: Eastern Cordillera, C: Central Cordillera, D: Western Cordillera, E: Magdalena valley, F: Cauca Valley, G: North-Caribbean, H: Central America, and I: Amazonian region.

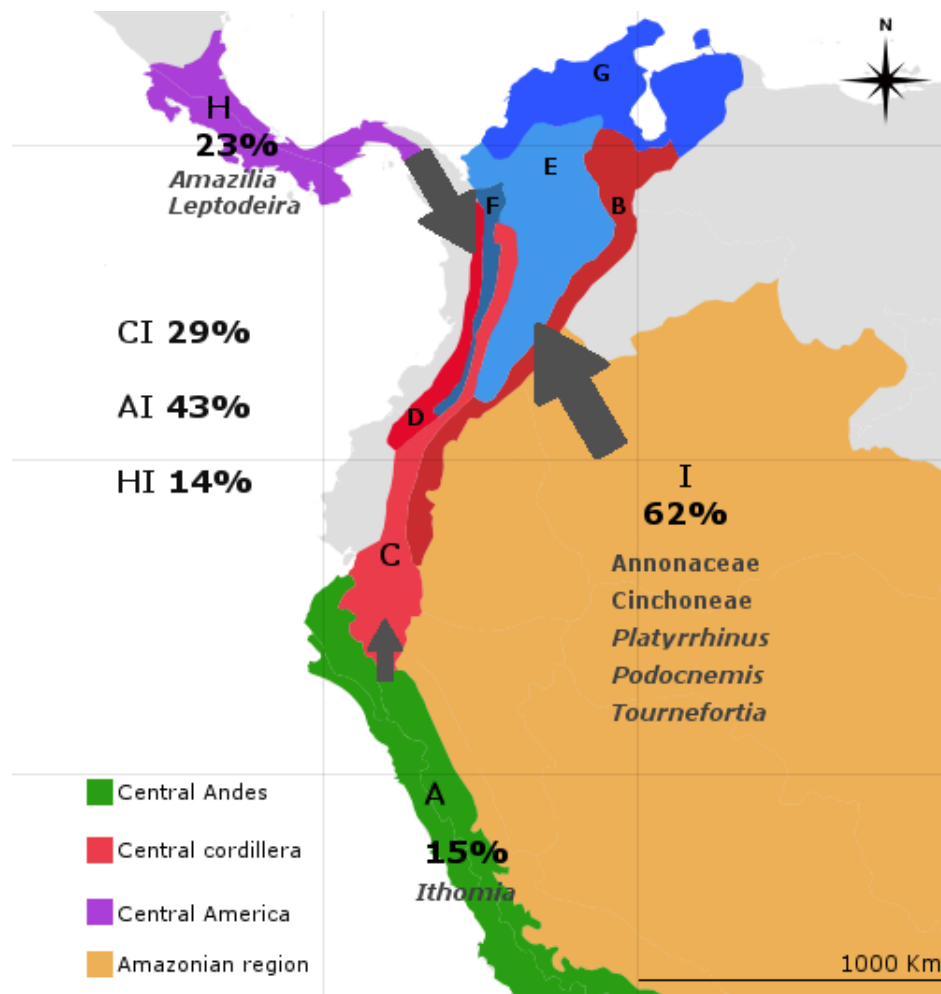
**Table 2.**

*Patterns observed over time.*

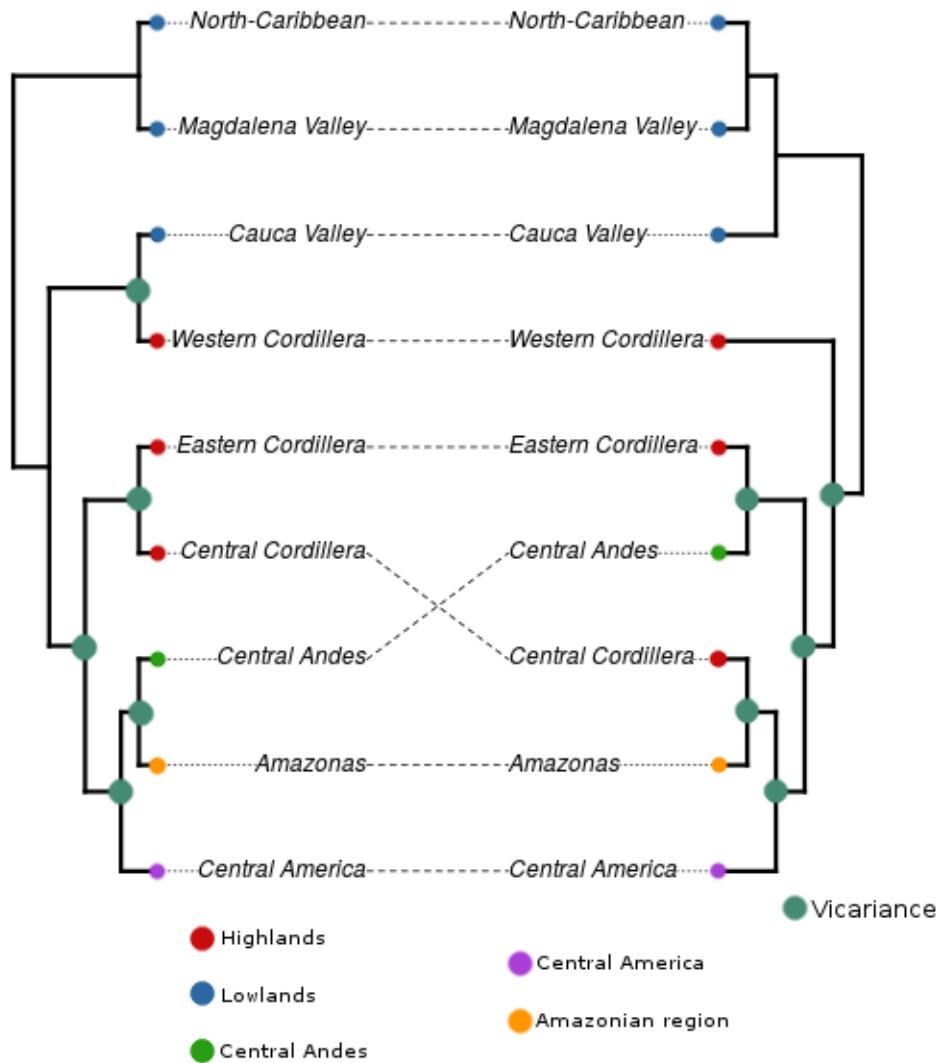
<b>Changes in nodes over time</b>		<b>Temporal intervals in Ma</b>			
<b>From node →</b>	<b>→To node</b>	<b>20-15</b>	<b>15-10</b>	<b>10-5</b>	<b>5-0</b>
Lowlands	Lowlands	–	–	–	4
Highlands	Highlands	–	4	–	6
Lowlands	Highlands	–	4	4	6
Highlands	Lowlands	–	–	5	–
Highlands & Lowlands	Highlands	–	–	4	–
Amazonian region	Lowlands	–	5	7	–
Central America	Lowlands	–	–	4	4
Central Andes	Lowlands	–	–	–	–
Amazonian region	Highlands	–	4	–	–
Central America	Highlands	–	–	–	4
Central Andes	Highlands	6	9	11	4
Central Andes	Highlands & Lowlands	–	–	6	–
Highlands	Amazonian region	–	4	5	4
Lowlands	Central America	–	–	4	–
Highlands	Central America	–	4	4	6
Amazonian region & Central Andes	Central America	–	–	–	4
Central Andes	Amazonian region	4	–	–	–
<b>TOTAL</b>		<b>10</b>	<b>34</b>	<b>54</b>	<b>42</b>
<b>Percentage by time bin</b>		7.14%	24.29%	38.57%	30.00%
<b>Percentage of the Lowlands to Highlands pattern</b>			21.05%	21.05%	31.58%
<b>Percentage of the Highlands to Lowlands pattern</b>				26.32%	
<b>Percentage of each area proposed as ancestral area in the hypotheses</b>	<b>Amazonian region</b>		15.52%		
	<b>Central America</b>			18.97%	13.79%
	<b>Central Andes</b>	10.34%	15.52%	18.97%	6.90%

Note: Four intervals analysed. Changes in nodes over time observed after the hypotheses fit.

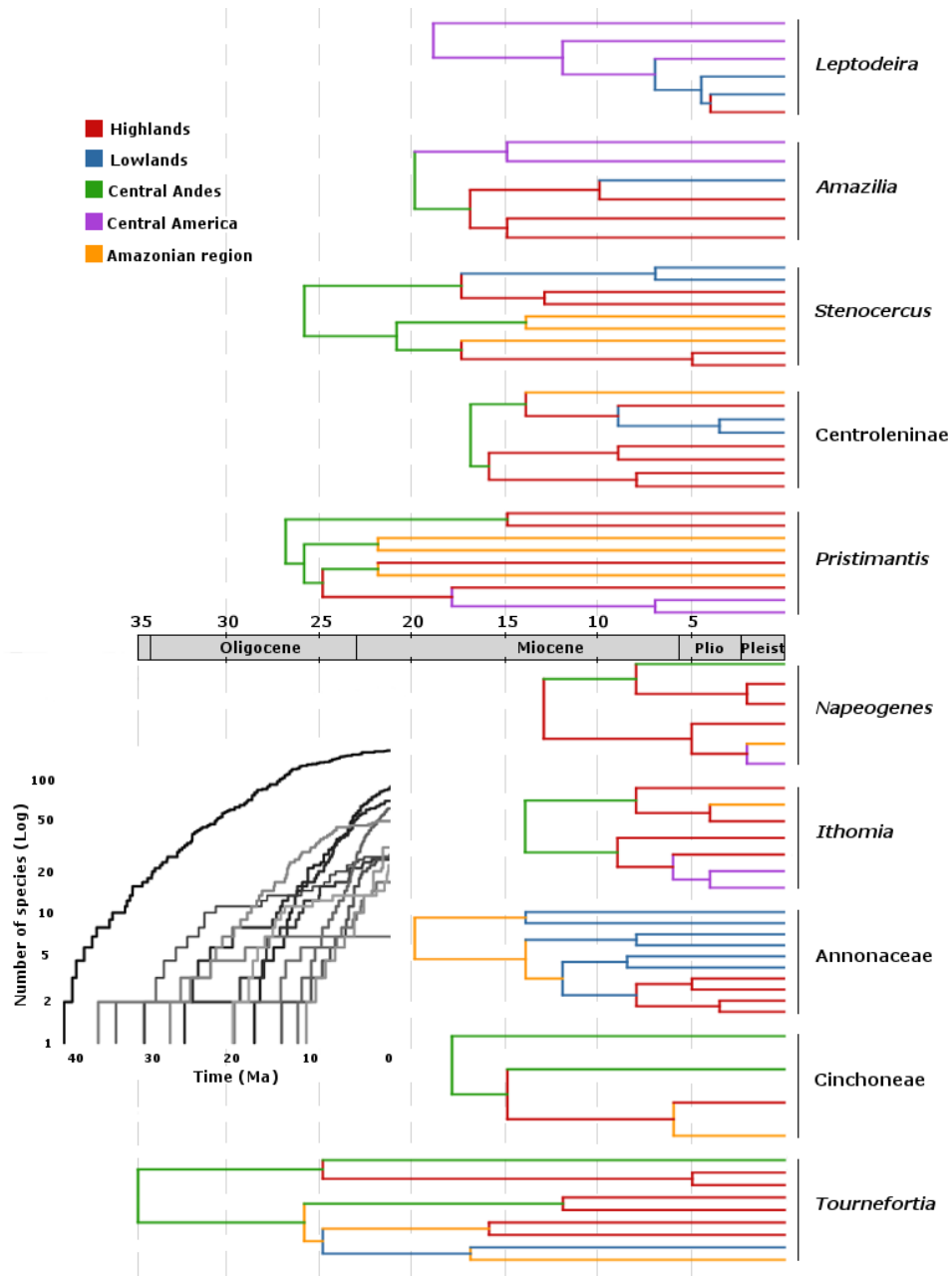
## Figures



**Figure 1. Summary of the ancestral area and events analyses.** Map of the North Andean Block (NAB) and adjacent areas. We show the percentage of different areas in composite (two areas 23.33%) and, non-composite (single areas 43.33%) reconstructions. The Amazonian region represents the 62% of the single areas obtained while Central America and Central Andes represented the 23% and 15%, respectively. AI and CI presented the major percentage within composite areas. Central Andes, Central America and the Amazonian region formed the node with highest dispersal events (41%). The arrows size is proportional to the number of dispersal events of each area. A: Central Andes, North Andean highlands (red) labeled as, B: Eastern Cordillera, C: Central Cordillera and, D: Western Cordillera. North Andean lowlands (blue) labeled as, E: Magdalena Valley, F: Cauca Valley, G: North-Caribbean. H: Central America and I: Amazonian region.



**Figure 2. Cladograms of areas obtained after the stability test in the event analyses.** Vicariant nodes showed as circles. Lowlands in the NAB appeared related in a single node, blue tip label. The Robinson and Foulds distance for both cladograms was 0.71.



**Figure 3. Summary of ages and diversification patterns by related taxonomic groups.** In the phylogenies, the lowlands lineages are indicated in blue, and highlands in red based on our hypotheses test. Lineages from adjacent areas are indicated in green: Central Andes, orange: Amazonian region and purple: Central America. A Lineage through time plot for all groups is showed on the left. To see *Platyrrhinus*, *Podocnemis*, *Pteronymia*, and *Thamnophilus* results see Fig. 1 Appendix F.

## Appendix

### Appendix A. Number of genes and calibration points used in this analysis

**Table 1.**

*Number of genes and calibration points used in this analysis for each group.*

Group	Taxonomic level	Class	Order	Ingroup	Outgroup	N° of genes	Nuclear genes	Mitochondrial genes	Chloroplastic genes	N° of bp	Authors	Calibration points	Age	Authors
Annonaceae	Family	Magnoliopsida	Magnoliales	59	3	4	0	0	4	2700	Pirie <i>et al.</i> (2006)	Maastrichtian seeds of Nigeria	98 Ma	Richardson <i>et al.</i> (2004) Doyle <i>et al.</i> (2004)
Cinchoneae	Tribe	Magnoliopsida	Gentianales	22	4	4	0	0	4	1700	Antonelli <i>et al.</i> (2009)	Fossil fruits and seeds of <i>Cephalanthus</i> . Late Eocene Gentianales	33 Ma	Mai & Walther (1985)
<i>Tournefortia</i> clade		Magnoliopsida	Lamiales	23	4	3	0	0	3	2340	Luebert <i>et al.</i> (2011)	Fossil pollen of <i>Tournefortia</i> , Early Oligocene Puerto Rico	30 Ma	Graham & Jarzen (1969) Graham (1996, 2003b)
<i>Ithomia</i>	Genus	Insecta	Lepidoptera	24	1	4	3	1	0	3200	Elias <i>et al.</i> (2009)	Split of <i>Napeogenes</i> and <i>Ithomia</i> . Butterflies fossils for Nymphalidae	21 Ma	Wahlberg <i>et al.</i> (2008)
<i>Napeogenes</i>	Genus	Insecta	Lepidoptera	24	4	3	2	1	0	3160	Elias <i>et al.</i> (2009)	Split of <i>Napeogenes</i> and <i>Ithomia</i> . Butterflies fossils for Nymphalidae	21 Ma	Wahlberg <i>et al.</i> (2008)
<i>Pteronymia</i>	Genus	Insecta	Lepidoptera	52	5	5	2	3	0	4350	De Silva <i>et al.</i> (2017)	Time of shared nodes with the phylogeny of Nymphalidae	15 Ma	Wahlberg <i>et al.</i> (2008)
Centroleninae	Subfamily	Amphibia	Anura	75	5	10	7	3	0	6160	Castroviejo-Fisher <i>et al.</i> (2014)	Oldest fossil of <i>Hyla sp.</i> Early Miocene. 50 Ma based on previous divergence time estimates of Hylinae	50-15.97 Ma	Rage & Roček (2003) Wiens <i>et al.</i> (2006) Roelants <i>et al.</i> (2007)
<i>Pristimantis</i>	Genus	Amphibia	Anura	138	4	5	2	3	0	2270	Pinto-Sanchez <i>et al.</i> (2012)	Node representing the common ancestor of Terrarana and hyliid Frogs	60-50 Ma	Heinicke <i>et al.</i> (2007) Roelants <i>et al.</i> (2007) Wiens (2007, 2011) Wiens <i>et al.</i> (2011)
<i>Leptodeira</i>	Genus	Reptilia	Squamata	15	2	2	0	2	0	1760	Daza <i>et al.</i> (2010)	Based on the oldest colubrid fossil known as the root of the tree	40 Ma	Rage <i>et al.</i> (1992) Head <i>et al.</i> (2005)
<i>Podocnemis</i>	Genus	Reptilia	Testudines	6	2	5	3	2	0	3990	Vargas-Ramirez <i>et al.</i> (2008)	Paleocene record of an Erymnocheilus-like fossil	65 Ma	Gaffney & Forster (2003)
<i>Stenocercus</i>	Genus	Reptilia	Squamata	42	2	3	0	3	0	1740	Torres-Carvajal (2007) Teixeira <i>et al.</i> (2016)	The most recent common ancestor of <i>Stenocercus</i> , <i>Uranoscodon</i> and <i>Plica</i>	49 Ma	Prates <i>et al.</i> (2015)
<i>Amazilia</i>	Genus	Aves	Apodiformes	20	10	3	0	3	0	1180	Ornelas <i>et al.</i> (2013)	<i>Eurotrochilus inexpectatus</i> <i>E. noniewiczzi</i>	30.5 Ma	Mayr (2004, 2007) Bochenski & Bochenski (2008) Louchart <i>et al.</i> (2008)
Tanagers		Aves	Passeriformes	96	14	2	0	2	0	2200	Sedano & Burns (2010)	Origin of the Thraupidae family	12.6 Ma	Cracraft & Barker (2009)
<i>Thamnophilus</i>	Genus	Aves	Passeriformes	27	3	3	0	3	0	2460	Brunfield & Edwards (2007)	<i>Thamnophilus bernardi</i> Late Pleistocene	~15,000–18,000 yrs	Oswald & Steadman (2015)
<i>Platyrrhinus</i>	Genus	Mammalia	Chiroptera	14	3	4	1	1	0	3260	Velazco & Patterson (2008)	Pleistocene records of <i>P. incarum</i> and <i>P. lineatus</i> Eastern Brazil	0.126 Ma	Czaplewski & Cartelle (1998) Fracasso & Salles (2005)

Note: Classification of each group, number of the ingroup sequences, type of genes, number of base pairs, and reference authors.

**Appendix B. Dispersal multipliers**

Unequal rates of dispersal between areas for each hypothesis.

[1] Origin: Amazonian region, Pattern: Lowlands to Highlands: 1 – 0.5 – 0.

7-0 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0.5	0.5	0	1	0	0	0	0
0	0	0.5	0.5	0	1	0	0	0
0	0.5	0	0	0	0	1	0	0
0	0	0	0	0	0	0	1	0
0	0	0	0	0.5	0	0	0	1

10-7 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	1	1	0	1	0	0	0	0
0	0	1	1	0	1	0	0	0
0	0.5	0.5	0	0	0	1	0	0
0	0	0	0	0	0	0	1	0
0	0	0	0	1	0.5	0.5	0	1

15-10 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0	0	0	1	0	0	0	0
0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	1	0
0	0	0	0	1	0.5	0.5	0	1

20-15 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0	0	0	1	0	0	0	0
0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	0	1	0
0	0	0	0	1	0.5	0.5	0	1

[2] Origin: Amazonian region, Pattern: Lowlands to Highlands: 1 – 0.7 – 0.3 – 0.

7-0 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0



15-10 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0	0	0	1	0	0	0	0
0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	1	0	0
0	0	0	0	0	1	0.5	1	0
0	0	0	0	0	0	0	0	1

20-15 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0	0	0	1	0	0	0	0
0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	1	0	0
0	0	0	0	0	1	0.5	1	0
0	0	0	0	0	0	0	0	1

[4] Origin: Central America, Pattern: Lowlands to Highlands: 1 – 0.7 – 0.3 – 0.

7-0 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0.7	0.7	0	1	0	0	0	0
0	0	0.7	0.7	0	1	0	0	0
0	0.3	0.3	0	0	0	1	0	0
0	0	0	0	0	0.3	0	1	0
0	0	0	0	0	0	0	0	1

10-7 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	1	1	0	1	0	0	0	0
0	0	1	1	0	1	0	0	0
0	0.3	0.3	0	0	0	1	0	0
0	0	0	0	0.3	0.7	0.3	1	0
0	0	0	0	0	0	0	0	1

15-10 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0	0	0	1	0	0	0	0
0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	1	0	0
0	0	0	0	0	0	1	0	0
0	0	0	0	0.3	1	0.7	1	0
0	0	0	0	0	0	0	0	1

20-15 Ma

A	B	C	D	E	F	G	H	I
1	0	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0



0	0	0	0	0	0	0	0	1
10-7 Ma								
A	B	C	D	E	F	G	H	I
1	0.3	0.7	1	0	0	0	0	0
0	1	0	0	1	0	1	0	0.3
0	0	1	0	1	1	0	0.3	0
0	0	0	1	0	1	0	0.7	0
0	0	0	0	1	0	1	0	0.3
0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	1	0	0.3
0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	1

15-10 Ma								
A	B	C	D	E	F	G	H	I
1	0.3	1	0.3	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0	0	0	1	0	0	0	1
0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	1	0	1
0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	1

20-15 Ma								
A	B	C	D	E	F	G	H	I
1	0.3	1	0.3	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0	0	0	1	0	0	0	1
0	0	0	0	0	1	0	0	0
0	0	0	0	0	0	1	0	1
0	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	1

[7] Altitudinal and horizontal pattern: 1 – 0.5 – 0.

20-15 Ma								
A	B	C	D	E	F	G	H	I
1	0	1	0	1	1	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0	0	0	1	1	1	0	1
0	0	0	0	1	1	1	0	0.5
0	0	0	0	1	1	1	0	0.5
0	0	0	0	0	0.5	0	1	0
0	0	0	0	1	1	1	0	1

15-10 Ma								
A	B	C	D	E	F	G	H	I
1	0.5	1	0	1	1	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0.5	1	0	1	0.5	1	0	0.5
0	0	1	0.5	0.5	1	1	0.5	0
0	0	0	0	1	1	1	0	0.5
0	0	0	0	0	0	0	1	0
0	0	0	0	0.5	0	0.5	0	1

10-7 Ma								
A	B	C	D	E	F	G	H	I
1	0.5	1	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0

0	1	1	1	0	0	0	0	0
0	0	1	1	0	0	0	0	0
0	0.5	1	0	1	0	1	0	0.5
0	0	1	0.5	0	1	0.5	0.5	0
0	0	0	0	1	0.5	1	0	0
0	0	0	0.5	0	0.5	0	1	0
0	0	0	0	0	0	0	0	1

7-0 Ma

A	B	C	D	E	F	G	H	I
1	0	1	0	0	0	0	0	0
0	1	0	0	1	0	1	0	1
0	0.5	1	0.5	1	1	1	0	0
0	0	0.5	1	0	1	0	1	0
0	0	0	0	1	0	1	0	1
0	0	0	0	0	1	0	1	0
0	0	0	0	0	0	1	0	1
0	0	0	0.5	0	0.5	0	1	0
0	0	0	0	0	0	0	0	1

[8] Altitudinal and horizontal pattern: 1 – 0.7 – 0.3 – 0.

20-15 Ma

A	B	C	D	E	F	G	H	I
1	0	1	0	1	1	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0	0	0	1	1	0.7	0	1
0	0	0	0	1	1	1	0	0.3
0	0	0	0	1	1	1	0	0.3
0	0	0	0	0.7	1	0	1	0
0	0	0	0	1	0.7	0.3	0	1

15-10 Ma

A	B	C	D	E	F	G	H	I
1	0.3	1	0	1	1	0	0	0
0	1	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0
0	0.3	1	0	1	0.3	1	0	0.3
0	0	1	0.7	0.7	1	1	0.3	0
0	0	0	0	1	1	1	0	0.3
0	0	0	0	0	0	0	1	0
0	0	0	0	0.3	0	0.5	0	1

10-7 Ma

A	B	C	D	E	F	G	H	I
1	0	1	0	0	0	0	0	0
0	1	0	0	0	0	0	0	0
0	1	1	1	0	0	0	0	0
0	0	1	1	0	0	0	0	0
0	0.7	1	0	1	0	1	0	0.3
0	0	1	0.7	0	1	0.7	0.3	0
0	0	0	0	1	0.7	1	0	0
0	0	0	0.3	0	0.3	0	1	0
0	0	0	0	0	0	0	0	1

7-0 Ma

A	B	C	D	E	F	G	H	I
1	0	1	0	0	0	0	0	0
0	1	0	0	1	0	0.7	0	1
0	0.7	1	0.7	1	1	1	0.3	0
0	0	0.7	1	0	1	0	1	0
0	0	0	0	1	0	1	0	0.3
0	0	0	0	0	1	0	1	0
0	0	0	0	0	0	1	0	1
0	0	0	0.3	0	0.3	0	1	0
0	0	0	0	0	0	0.3	0	1

### Appendix C. Robinson and Foulds distance

Comparisons between the reconstructed phylogeny with the trees reported in the literature.

<b>Taxa</b>	<b>RF</b>
Cinchoneae	0.04
<i>Napeogenes</i>	0.05
<i>Ithomia</i>	0.06
<i>Platyrhinus</i>	0.1
<i>Amazilia</i>	0.11
<i>Pteronymia</i>	0.2
Centroleninae	0.22
<i>Thamnophilus</i>	0.35
<i>Tounefortia</i> clade	0.39
<i>Leptodeira</i>	0.4
Tanagers	0.46
Annonaceae	0.49
<i>Podocnemis</i>	0.5
<i>Stenocercus</i>	0.55
<i>Pristimantis</i>	0.55
<b>MEDIAN</b>	<b>0.35</b>

### Appendix D. Ancestral area analyses

**Table 3.**

*Log-likelihood values and area(s) estimated by DEC and DIVALIKE models for each taxonomic group.*

Group	Area estimated		Log-Likelihood	
	DEC	DIVALIKE	DEC	DIVALIKE
<i>Amazilia</i>	HI	H	-95.05	-114.48
Annonaceae	I	I	-186.51	-186.97
Centroleninae	CI	CI	-300.17	-306.56
Cinchoneae	I	I	-113.27	-116.99
<i>Ithomia</i>	A	A	-109.91	-115.1
<i>Leptodeira</i>	H	H	-73.94	-76.96
<i>Napeogenes</i>	AI	ACI	-108.24	-109.36
<i>Platyrrhinus</i>	I	BCI	-58.83	-59.01
<i>Podocnemis</i>	I	I	-11.6	-10.92
<i>Pristimantis</i>	BCI	CHI	-485.48	-499.15
<i>Pteronymia</i>	CHI	CHI	-274.45	-280.31
<i>Stenocercus</i>	ACI	AI	-88.4	-97.03
Tanagers	ACI	ACI	-250.89	-260.21
<i>Thamnophilus</i>	CGI	GI	-83.98	-79.75
<i>Tournefortia</i> clade	I	AI	-87.74	-98.11

Note: \*Composite reconstructions refers to a set of 2 or 3 areas. A: Central Andes, B: Eastern Cordillera, C: Central Cordillera, D: Western Cordillera, E: Magdalena valley, F: Cauca Valley, G: North-Caribbean, H: Central America, and I: Amazonian region.

**Table 4.**

*Number of single and composite reconstructions obtained by model.*

	DEC	DIVALIKE	TOTAL	Proportion of each set of areas			
				I	A	H	
<b>Single area</b>	7	6	13	8	2	3	
<b>% Single areas</b>	0.47	0.40	43.33%	0.62	0.15	0.23	
<b>Two areas</b>	3	4	7	HI	CI	AI	GI
				1	2	3	1
<b>% Two areas</b>	0.20	0.27	23.33%	0.14	0.29	0.43	0.14
<b>Three areas</b>	5	5	10	ACI	BCI	CHI	CGI
				4	2	3	1
<b>% Three areas</b>	0.33	0.33	33.33%	0.40	0.20	0.30	0.10

Note: \*Composite reconstructions refers to a set of 2 or 3 areas. The proportion of each set within the reconstructions is shown on the right. A: Central Andes, B: Eastern Cordillera, C: Central Cordillera, D: Western Cordillera, E: Magdalena valley, F: Cauca Valley, G: North-Caribbean, H: Central America, and I: Amazonian region.

### Appendix E. Event analyses

**Table 5.**

*Dispersal events obtained in the events analysis.*

Area	Switch to	Lowlands	Highlands	From ancestral areas to Highlands & Lowlands		Area	Switch to	Lowlands	Highlands	From Highlands	
				To Lowlands	To Highlands					To Lowlands	To Highlands
I 25%	H					D* 13%	H				
	C			1			A				
	D			1			BA			1	
	B			1		CI			1		
	A								0.5		
	E		1				H			0%	54%
	G		1			C* 9%	A				
BA			1		BA				1		
H 22%		0.25	0.5						0.33		
	C			1		B* 3%	CI		1		
	B			1					1		
	A				41%	59%	CI 6%	B		1	
	G		1			A				1	
	EG		1				CIH 3%	BA		1	
	BA			1						1	
FEG		0.43	0.43								
A 19%	I					Total of dispersions to highlands or lowlands		21%	46%		
	C			1							
	D			1							
	F		1								
	E		1								
	CI			1		* Highlands					
		0.33	0.5								

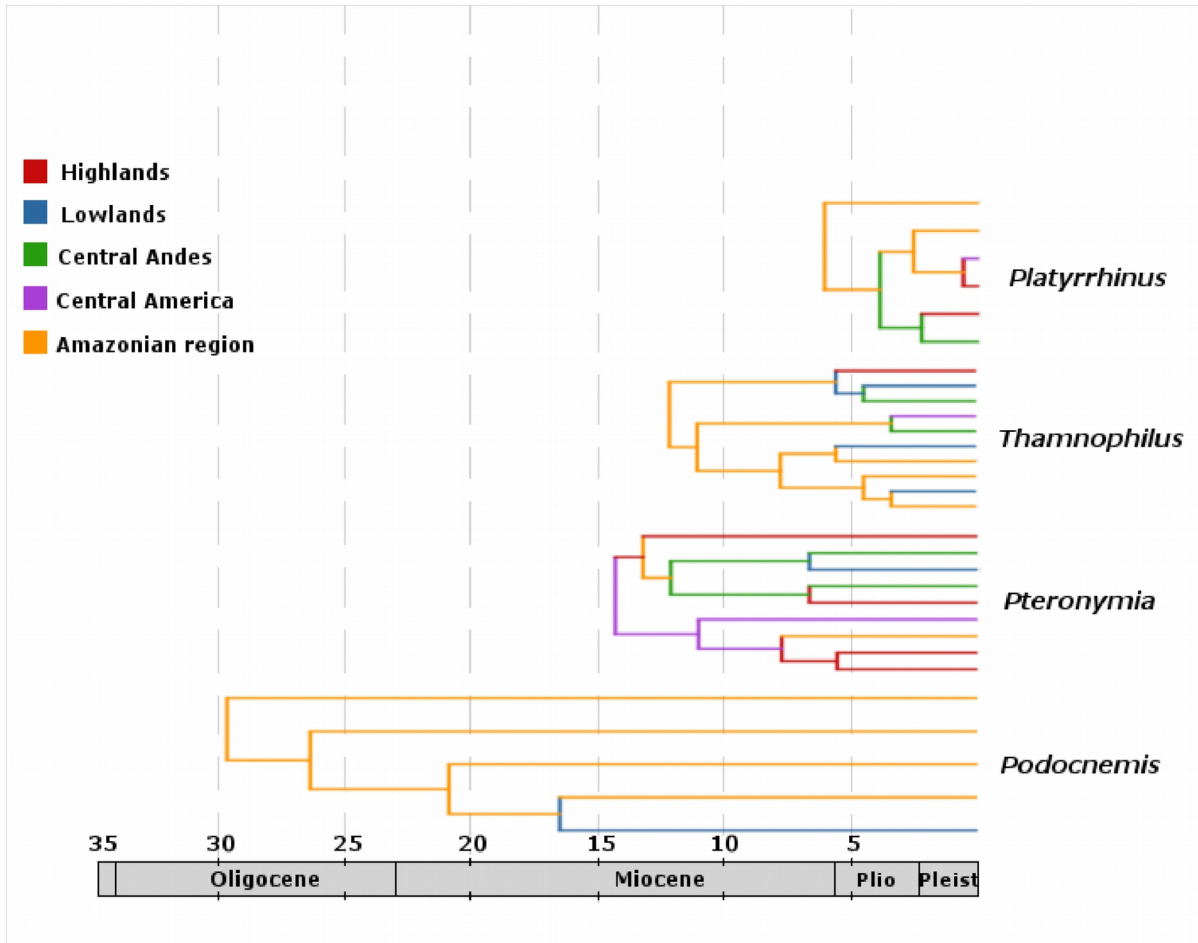
Note: Percentage of dispersal events from ancestral areas towards highlands and/or lowlands. The percentage of dispersion from highlands to lowlands and between highlands is shown on the right part of the table. Highlands are marked with an asterisk (\*). A: Central Andes, B: Eastern Cordillera, C: Central Cordillera, D: Western Cordillera, E: Magdalena valley, F: Cauca Valley, G: North-Caribbean, H: Central America, and I: Amazonian region.

### Appendix F. Hypothesis tests

**Table 6.**

*Log-likelihood of each hypothesis test and comparisons between hypotheses and dispersal matrices.*

Taxon	ALL equal scenario	Matrix	Hypotheses LogL			Altitudinal and horizontal pattern	Comparisons in terms of maximum likelihoods between hypotheses					
			Origin: Amazonian region, pattern: Lowlands to Highlands	Origin: Central America, pattern: Lowlands to Highlands	Origin: Central Andes, pattern: Highlands to Lowlands		△ 1&2	△ 1&3	△ 1&4	△ 2&3	△ 2&4	△ 3&4
<i>Amonaceae</i>	156.86	2_1	285.71	394.49	333.59	328.18	108.28	4.94	46.27	103.34	62.01	41.33
		3_1	281.91	390.93	334.36							
		4_1	282.67	390.19	286.85							
		Min △	0.76	0.74	46.74							
		Max △	3.80	4.30	47.51							
<i>Cinchoneae</i>	113.28	2_1	215.21	323.34	214.38	223.36	33.14	54.35	14.58	87.49	18.56	68.93
		3_1	208.78	353.63	214.72							
		4_1	238.54	241.92	154.43							
		Min △	6.43	81.42	59.95							
		Max △	29.76	111.71	60.29							
<i>Tournefortia clade</i>	87.74	2_1	189.54	213.18	150.41	154.04	26.44	61.70	30.47	88.14	56.91	31.23
		3_1	184.51	210.95	154.19							
		4_1	199.01	233.33	122.81							
		Min △	5.03	2.23	27.60							
		Max △	14.50	22.38	31.38							
<i>Ithomia</i>	117.35	2_1	219.69	219.34	153.74	253.58	4.57	85.49	47.01	90.06	42.44	132.50
		3_1	206.57	214.14	154.07							
		4_1	218.33	211.14	121.08							
		Min △	13.12	3.00	32.66							
		Max △	11.76	8.20	32.99							
<i>Napeogenes</i>	108.24	2_1	228.31	242.85	153.38	200.86	5.34	91.62	19.33	96.96	24.67	72.29
		3_1	220.19	225.53	155.40							
		4_1	238.57	228.18	128.57							
		Min △	8.12	2.65	24.81							
		Max △	18.38	17.32	26.83							
<i>Pteronymia</i>	276.45	2_1	300.71	374.49	343.19	288.90	79.45	3.72	1.77	83.17	81.22	1.95
		3_1	311.91	370.93	333.38							
		4_1	290.67	370.12	286.95							
		Min △	10.04	0.81	46.43							
		Max △	21.24	4.37	56.24							
<i>Centroleninae</i>	300.55	2_1	435.42	472.54	403.88	514.42	30.42	97.73	79.00	128.15	48.58	176.73
		3_1	445.27	466.73	399.95							
		4_1	463.92	465.84	337.69							
		Min △	9.85	0.89	62.26							
		Max △	28.50	6.70	66.19							
<i>Prisimantis</i>	485.58	2_1	761.93	813.94	676.28	611.49	29.96	78.73	131.04	108.69	161.00	52.31
		3_1	742.53	813.28	670.99							
		4_1	755.10	772.49	663.80							
		Min △	12.57	40.79	7.19							
		Max △	19.40	41.45	12.48							
<i>Leptodeira</i>	73.94	2_1	123.79	238.06	134.16	110.24	108.51	75.99	19.83	184.50	128.34	56.16
		3_1	132.58	232.62	120.08							
		4_1	155.55	232.30	47.80							
		Min △	8.79	0.32	72.28							
		Max △	31.76	5.76	86.36							
<i>Podocnemis</i>	11.6	2_1	20.80	16.28	7.78	10.30	3.98	12.51	2.73	8.53	7.31	1.38
		3_1	20.24	16.27	7.57							
		4_1	11.68	16.26	7.73							
		Min △	8.56	0.01	0.16							
		Max △	9.12	0.02	0.21							
<i>Stenocercus</i>	88.9	2_1	170.25	157.47	121.29	128.01	37.30	46.64	40.13	9.34	2.83	6.51
		3_1	167.34	130.04	120.70							
		4_1	168.55	138.64	121.11							
		Min △	1.21	8.60	0.41							
		Max △	2.91	27.43	0.59							
<i>Amazilia</i>	95.08	2_1	148.62	183.37	145.95	144.30	37.15	30.08	0.37	67.23	37.52	29.71
		3_1	142.14	187.17	145.60							
		4_1	167.19	179.29	112.06							
		Min △	6.48	4.08	33.54							
		Max △	25.05	7.88	33.89							
<i>Tangaras</i>	450.01	2_1	661.93	713.94	576.28	630.49	29.96	101.73	12.04	131.69	42.00	89.69
		3_1	642.53	713.28	570.99							
		4_1	655.10	672.49	540.80							
		Min △	12.57	40.79	29.48							
		Max △	19.40	41.45	30.19							
<i>Thamnophylus</i>	83.98	2_1	169.47	193.18	170.41	174.04	26.37	5.83	9.46	20.54	16.91	3.63
		3_1	164.58	190.95	174.29							
		4_1	170.01	193.33	171.81							
		Min △	4.89	2.23	1.40							
		Max △	5.43	2.38	3.88							
<i>Platyrhinus</i>	58.83	2_1	132.79	158.06	130.16	110.95	19.51	23.99	27.83	43.50	47.34	3.84
		3_1	133.58	152.62	110.08							
		4_1	166.55	152.30	108.80							
		Min △	0.79	0.32	2.00							
		Max △	33.76	5.76	22.08							



**Figure 1.** Summary of ages and diversification patterns of *Platyrrhinus*, *Podocnemis*, *Pteronymia*, and *Thamnophilus*.