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Review Article

Unveiling nearly half a century of *Platyrrhinus* research (Chiroptera: Phyllostomidae): a scientometric analysis and systematic review of neglected bats

Revelando quase meio século de pesquisa sobre *Platyrrhinus* (Chiroptera: Phyllostomidae): uma análise cienciométrica e revisão sistemática de morcegos negligenciados

A. C. S. Lima[a]*, I. Sampaio[a], E. C. Fraga[b] and M. C. Barros[b]

[a] Universidade Federal do Pará – UFPA, Departamento de Ciências Biológicas, Programa de Pós-graduação em Genética e Biologia Molecular – PPGBM, Belém, PA, Brasil

[b] Universidade Estadual do Maranhão – UEMA, Departamento de Química e Biologia, Laboratório de Genética e Biologia Molecular, Campus Caxias, Caxias, MA, Brasil

Abstract

Platyrrhinus is one of the most diverse genera of Neotropical fruit bats, yet scientific attention remains unevenly distributed among its taxa. In the present study, a comprehensive scientometric analysis combined with a systematic review (1977–2025) was performed to uncover the current state of scientific knowledge of the genus *Platyrrhinus* and diagnose the *Linnean, Wallacean, Raunkiaeran* and *Prestonian shortfalls* within the genus. For the scientometric analyses, only studies indexed in the Scopus database were considered, and for the systematic review, studies from Scopus and Web of Science were used. Scientometric analysis based on 106 articles from Scopus revealed significant growth in productivity over nearly half a century, peaking in 2024. Following Lotka's Law, we demonstrate that knowledge production is fragmented, with most authors publishing sporadically and lacking long-term research traditions. Geographically, research indicates that 16 countries, mainly Brazil and the USA, have produced knowledge about *Platyrrhinus*. A systematic review of 120 articles from Scopus and WOS identified a lack of information in different areas for at least 16 species of *Platyrrhinus* (e.g., *Platyrrhinus umbratus*, *Platyrrhinus angustirostris*, *Platyrrhinus albericoi* and *Platyrrhinus dorsalis*), where the few studies conducted for these species are mainly linked to morphological, molecular characterization and/or distribution records. Significant gaps persist in evolutionary biology, functional ecology, and life history for most species. These findings reveal a neglect of specific species; thus, a strategic framework for future inventories and biological studies aimed at mitigating these gaps and supporting the conservation of Neotropical bats is proposed here.

Keywords: neotropical biodiversity, knowledge gaps, scientometrics, scientific mapping, *Stenodermatinae*.

Resumo

Platyrrhinus é um dos gêneros mais diversos de morcegos frugívoros neotropicais, porém a atenção científica permanece distribuída de forma desigual entre seus táxons. No presente estudo foi realizado uma análise cienciométrica abrangente combinada com uma revisão sistemática (1977–2025), para desvendar o estado atual do conhecimento científico do gênero *Platyrrhinus* e diagnosticar os déficits de conhecimento do tipo Lineano, Wallaceano, Raunkiaeriano e Prestoniana no gênero. Para as análises cienciométricas, foi considerado exclusivamente estudos indexados na base de dados Scopus e para a revisão sistemática foi usado estudos do Scopus e Web of Science. A análise cienciométrica a partir de 106 artigos do Scopus revelou um crescimento expressivo na produtividade ao longo de quase meio século, com pico em 2024. Com base na Lei de Lotka, foi demonstrado que a produção de conhecimento é fragmentada, com a maioria dos autores publicando esporadicamente. Geograficamente, a pesquisa indica que 16 países, principalmente o Brasil e os EUA, produziram conhecimento sobre *Platyrrhinus*. Na revisão sistemática de 120 artigos do Scopus e WOS foi identificado uma falta de informação em diferentes áreas para pelo menos 16 espécies de *Platyrrhinus* (por exemplo, *Platyrrhinus umbratus*, *Platyrrhinus angustirostris*, *Platyrrhinus albericoi* e *Platyrrhinus dorsalis*), onde os poucos estudos realizados para essas espécies estão principalmente ligados à caracterização morfológica, molecular e/ou registros de distribuição. Lacunas significativas persistem em biologia evolutiva, ecologia funcional e história de vida para a maioria das espécies. Essas descobertas revelam uma negligência em relação a espécies específicas; portanto, aqui foi proposto uma estrutura estratégica para futuros inventários e estudos biológicos visando mitigar essas lacunas e subsidiar a conservação de morcegos neotropicais.

Palavras-chave: biodiversidade neotropical, lacunas de conhecimento, cienciometria, mapeamento científico, *Stenodermatinae*.

*e-mail: amanda01cristiny@outlook.com
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1. Introduction

The genus *Platyrrhinus* Saussure, 1860, also known as broad-nosed bats, is one of the most specious in the family Phyllostomidae and subfamily Stenodermatinae, with 19 species of bats endemic to the Neotropics (Simmons and Cirranello, 2025), distributed in two subgenera: *Platyrrhinus* and *Incanycteris* (Garbino et al., 2026). The geographic distribution of its species extends from southern Mexico to Paraguay and northern Argentina, with species richness concentrated in the Andean region (Velazco and Lim, 2014; Velazco et al., 2023).

The common morphological characteristics of *Platyrrhinus* species are: broad nasal leaf, absence of a tail, presence of facial and/or dorsal stripes, two accessory cusps on the second upper premolar, and a fringe of hairs on the margins of the uropatagium (Lim, 1993; Albuja, 1999; Velazco, 2005). Regarding subgenera, the species of the subgenus *Platyrrhinus* are characterized by small to medium-sized bats (forearm length 33–49 mm, weight 10–28 g), while *Incanycteris* constitutes medium to large-sized bats (forearm length 42–63 mm, weight 19–55 g) (Garbino et al., 2026). These bats feed mainly on fruits and, therefore, by dispersing seeds in different areas, they contribute to the reforestation and recovery of degraded areas (Willig et al., 1993; Gardner, 2008; Silvestre et al., 2016).

Notably, from the late 1970s to the 1990s, *Platyrrhinus* species were commonly classified as *Vampyrops* (e.g., Price, 1978; Ochoa and Ibañez, 1985). However, Gardner and Ferrell (1990) demonstrated the nomenclatural priority of *Platyrrhinus*, which was consolidated in the literature at the end of the 20th century. Integrated studies have been conducted for some *Platyrrhinus* species and have provided morphological, molecular, and biogeographical characterizations and aided in understanding the taxonomy and systematics of the genus, but this knowledge remains unevenly distributed (e.g., Velazco, 2005; Velazco and Patterson, 2008; Velazco et al., 2010; Velazco and Lim, 2014; Palacios-Mosquera et al., 2020; Ramírez-Fráncel et al., 2020; Garbino et al., 2024).

Platyrrhinus helleri exemplifies the taxonomic complexity of the genus. Historically, this species was considered a widely distributed species, being the most widespread and studied within *Platyrrhinus* (Simmons, 2005). After revisions with molecular analyses, it was revealed that the species was actually a complex and that the different lineages attributed to *P. helleri* corresponded to valid species, leading to the description of *P. angustirostris*, *P. fusciventris*, and *P. guianensis* (Velazco and Patterson, 2008; Velazco et al., 2010; Velazco and Lim, 2014), as well as the elevation of *P. incarum* to a full species (Velazco et al., 2010). Due to morphological similarities, errors in taxonomic identification are common in species of the *P. helleri* complex (sensu lato) (Velazco et al., 2010).

In addition to taxonomic studies, efforts to generate ecological data have also been undertaken for some species, such as: *P. lineatus*, *P. helleri*, and *P. recifinus* (e.g., Fenton et al., 2001; Tello and Velazco, 2003; Ortêncio Filho et al., 2010; Alho et al., 2011; Mello et al., 2014; Genelhú et al., 2023; Silveira et al., 2024). All these studies have provided important contributions to knowledge in different fields for *Platyrrhinus*. However, for many species, there is still a lack of basic ecological data, occurrence data, systematic information, abundance, diet, reproductive patterns, and other aspects, which underscores the importance of further research in these areas.

These shortcomings reflect broader conceptual and data gaps that hinder the true extent and understanding of biodiversity distribution, known as knowledge deficits (Hortal et al., 2015). Among these shortfalls, the *Linnaean shortfall* stands out, referring to the lack of knowledge about the actual number of described species, and the *Wallacean shortfalls*, associated with the lack of knowledge about the actual geographic distribution of taxa (Lomolino, 2004). Beyond taxonomy and distribution, the ecology and conservation of various groups face additional barriers, such as the *Prestonian shortfalls*, which reflects the scarcity of data on species abundance and population dynamics over time and space (Cardoso et al., 2011), and the *Raunkiaerian shortfalls*, which encompasses the lack of functional and adaptive information essential for understanding the ecological role of organisms (Hortal et al., 2015). Within the genus *Platyrrhinus*, these gaps manifest themselves heterogeneously.

To better understand which fields of knowledge remain undersampled, bibliometric information provides a useful overview, helping to identify trends in different contexts and highlight research gaps (Urbieta et al., 2022). While previous scientometric studies have addressed bats at broader scales (e.g., Jorge et al., 2017; Sivasekaran et al., 2021; Luciano et al., 2022; Urbieta et al., 2022), a review study focusing on species-rich but poorly studied taxa, such as the genus *Platyrrhinus*, remains unavailable, hindering the identification of current knowledge gaps and biodiversity shortfalls, such as Linnaean (taxonomic), Wallacean (distributional), and Raunkiaeran (functional/adaptive) and Prestonian (abundance) shortfalls (sensu Hortal et al., 2015; Lomolino, 2004).

Understanding the scientific production surrounding *Platyrrhinus* is essential to discovering which species remain poorly studied while others receive greater research attention. This study presents a comprehensive review of the state of the art of the genre through a scientometric analysis combined with a systematic review. The aim here is to identify temporal patterns, international collaboration networks, and thematic trends, ultimately highlighting the gaps and key knowledge shortfall that require further investigation to ensure effective conservation and biological understanding of *Platyrrhinus* bats.

2. Materials and Methods

2.1. Data collection and selection

The literature search focused on the Scopus (2025) and Web of Science-WoS (Clarivate, 2025) databases, which were selected because they are the most widely used sources worldwide for bibliographic research and scientometric analysis (Mongeon and Paul-Hus, 2016). The data were obtained in both platforms using the following descriptors: "(bats or Chiroptera or Stenodermatinae or Phyllostomidae) and (*Platyrrhinus* or *Vampyrops*)", in the topics: title, abstract or keywords.

The search covered the entire period of publication for each database, so from 1977 to October 2025 for WoS and from 1978 to October 2025 for Scopus. Records were selected by title, abstract, keywords, and, in some cases, full text. The selection was made by only one author and subsequently verified by the others.

2.2. Systematic review of studies on Platyrrhinus

The review of studies on *Platyrrhinus* was conducted considering all eligible articles in Scopus and WoS. Despite a search on other platforms, the articles did not differ from those found on the aforementioned platforms, and the systematic review was restricted to literature indexed in Scopus and WoS. The search retrieved a total of 243 articles (128 from Scopus and 115 from WoS). After evaluating the titles, abstracts, and full texts according to the eligibility criteria of this study, 204 articles were filtered (106 from Scopus and 98 from WoS) that met all the criteria. 86 duplicate records found in both databases were also removed, and two fundamental taxonomic works not indexed in Scopus or WoS (Owen, 1987; Velazco, 2005) were manually added through citation tracking due to their critical importance for the taxonomy of the genus and historical context. Thus, a final total of 120 works was analyzed in this systematic review.

To document the review process, a flowchart was created following the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) statement (Moher et al., 2009) (Supplementary Figure S1). The articles were classified into 16 thematic categories adapted from Luciano et al. (2022), and considering the breadth of the topics, some articles were assigned to more than one category, meaning that the sum of the counts in the categories exceeds the total number of studies analyzed. Furthermore, the number of studies published for each *Platyrrhinus* species was analyzed and categorized among the 16 analyzed categories (Supplementary Table S1) in order to identify which areas of knowledge are in need of further investigation. This categorization was also developed to quantify knowledge shortfalls, such as those of Linnaean Wallacean, Raunkiaeran and Prestonian shortfalls within the genus.

It is important to emphasize that the species *Platyrrhinus nigellus* and *Platyrrhinus chocoensis* were counted among the valid species of which they are junior synonyms (*P. umbratus* and *P. dorsalis*, respectively), according to the currently accepted taxonomy for the genus. Furthermore, it was formally confirmed that *P. helleri* does not occur in Brazil (Garbino et al., 2024), so a cross-check was performed on all records attributed to *P. helleri* in light of the current taxonomy and the correct species was assigned to each article; those for which it was not possible to correctly identify the species were counted as *Platyrrhinus* sp. (Table S1).

2.3. Scientometric analysis

Descriptive statistical analyses and scientific mapping were conducted using the Bibliometrix 2.2.1 package (Aria and Cuccurullo, 2017), implemented in R 4.4.3 (R Core Team, 2025) and in VOSviewer software version 1.6.20 (van Eck and Waltman, 2010). For the scientometric analyses, only studies indexed in the Scopus database were considered, which corresponded to 106 articles filtered out of a total of 128 articles. This decision was made: i) because practically the same studies were retrieved in both databases, which corresponded to 81.13% of the studies; ii) to avoid bias due to the heterogeneous attribution of the number of citations between the databases; iii) because the number of studies retrieved from Scopus was higher than in WoS and iv) to avoid bias due to heterogeneous assignment in the indexing years on both platforms.

Reviews, observations, letters, notes, conference papers, and editorial material, as well as articles that did not correspond to the scope of this study, were excluded (example: studies that used *Platyrrhinus* species as examples for other experiments) (Supplementary Figure S1). Bibliometric data analyses using the Bibliometrix 2.2.1 package (Aria and Cuccurullo, 2017) were performed following a workflow adapted from Nunes et al. (2020), encompassing general bibliometric indicators, where was obtained: the average number of citations per document (including median and minimum and maximum citation values), number of citations per author, number of citations per country, average number of publications per year, number of articles per author, the most productive authors with the number of publications and the production of the main authors over time. The authors' productivity percentage was based on the total number of authorship participations/occurrences in the database.

To assess the productivity of each author, was obtained the h-index (Hirsch, 2007) calculated locally for each author within the *Platyrrhinus* dataset. To investigate scientific productivity, the publication frequency of authors was analyzed descriptively using Lotka's Law (Lotka, 1926) through the Bibliometrix package. This law states that the scientific productivity of authors follows an inverse relationship, i.e., a small number of authors produce most of the scientific papers, while a large number of authors produce only a few articles (Lotka, 1926). Descriptive metrics were calculated using the complete dataset. For better visualization, the 10 most productive authors were highlighted in the results.

To analyze collaboration patterns and co-authorship networks in *Platyrrhinus* studies, was generated collaborative network analyses. The collaborative network of authors was generated using the Walktrap clustering algorithm in the Bibliometrix package (Aria and Cuccurullo, 2017), employing Jaccard's similarity coefficient to normalize the co-authorship links matrix. In this network, nodes represent individual researchers, and edges represent co-authorship connections between them. Edge weights were calculated based on the frequency of co-authored published articles, where one edge between authors was chosen to participate in the network. To ensure visual clarity while highlighting the most influential connectors, a limit of 50 authors with the highest scores for betweenness centrality was established. These metrics and network visualization procedures generated in Bibliometrix followed the methodology of Nunes et al. (2020).

Subsequently, using VOSviewer v1.6.20 software (van Eck and Waltman, 2010), interaction networks for collaborations between countries were constructed based on the institutional affiliations of all co-authors.

The cluster was calculated using the association strength method (van Eck and Waltman, 2010) and with a weighted edge. The size of each node is proportional to the number of publications, and the edges represent the frequency of international collaboration for the countries. It is also important to emphasize that the calculations of the proportion of articles per author and per country highlighted in the results were based on the institutional affiliations of all participating authors (*full counting*), so the country of each co-author was counted individually, causing the sum of participations per country to exceed the total number of documents analyzed.

3. Results

3.1. Scientometric analyses

For scientometric analyses, a total of 128 articles were retrieved from Scopus, of which 106 met the filtering and eligibility criteria, covering a period of 47 years (1978–2025; citation data extracted in October 2025). The studies were published in a total of 62 journals, with an average of 19.9 citations per document (median=11, range= 0-205). The number of co-authors contributed to the dataset, with an average of 4.9 co-authors per document out of a total of 417 authors. Most articles were published between 2010 and 2025, with peak productivity in 2024 (Figure 1A). The authors' productivity shows a pattern consistent with Lotka's Law, where 86% of the authors produced only one article (360 authors) and 14% produced between two and 11 articles (57 authors) of the retrieved scientometric dataset (Figure 1B).

The most productive authors based on the number of publications were Velazco PM (n = 11; 3.8%), Fischer E (n = 7; 1.6%), and Torres JM (n = 6; 0.7%) (Figure 2A). In terms of local h-index, these authors also stood out with the highest values within this dataset for Velazco PM (h-index = 8), Fischer E (h-index = 7), and Torres JM (h-index = 6), respectively (Figure 2B). Most of the 10 most productive authors published their work on *Platyrrhinus* in the last 22 years. Velazco is the researcher with the longest and most consistent publication record of articles on *Platyrrhinus*, with publications between 2003 and 2024 (Figure 2C). Among the 10 most productive authors, the work that received the highest number of citations (TC) was that of the authors Torres JM, Herrera HM, and Lourenço EC (TC: 8) in 2023 (Figure 2C).

In the collaboration network, co-authorship links between authors were grouped into ten clusters. Most clusters revealed connections among most or all participating authors, with five clusters showing one or more co-authorship links between different clusters, while five clusters showed no connection with other groups. Regarding network topology, the authors with the highest values of betweenness centrality included Torres JM (brown cluster), Velazco PM (red cluster), Fischer E (blue cluster), and Herrera HM (brown cluster) (Figure 3).

Among the countries with the highest number of citations related to knowledge about *Platyrrhinus*, Brazil stood out (1,012 citations), followed by the United States (563 citations) and Mexico (221 citations), respectively (Figure 4). The collaborative network between countries led to the formation of six clusters comprising 15 countries (Figure 5A). Only Trinidad and Tobago had publications restricted to authors from the same country; therefore, this isolated node was excluded from the collaborative network. The countries with the highest number of publications were Brazil (n = 68 studies), the USA (n = 22 studies), Colombia (n = 11 studies), and Peru (n = 9 studies). According to these data, production led by researchers based in Brazil accounted for nearly half of the global knowledge production on *Platyrrhinus* (49.6%).

In the organization of clusters, it was observed that Brazil formed a cluster with Italy, Sweden, and Russia (red cluster), showing co-authorship links with the other five clusters, totaling 11 connected countries. The USA formed a cluster with Venezuela and Mexico (dark blue cluster) and established co-authorship links with nine countries. Peru formed a group with Cuba and Ecuador (green cluster) and established co-authorship links with five countries. Colombia formed a group with Canada (yellow cluster) and established co-authorship links with four countries. The United Kingdom formed a group only with Norway (violet cluster) and also established four co-authorship links. Portugal formed a single-country cluster in the network (light blue cluster) and established co-authorship links with Brazil and the USA (Figure 5A).

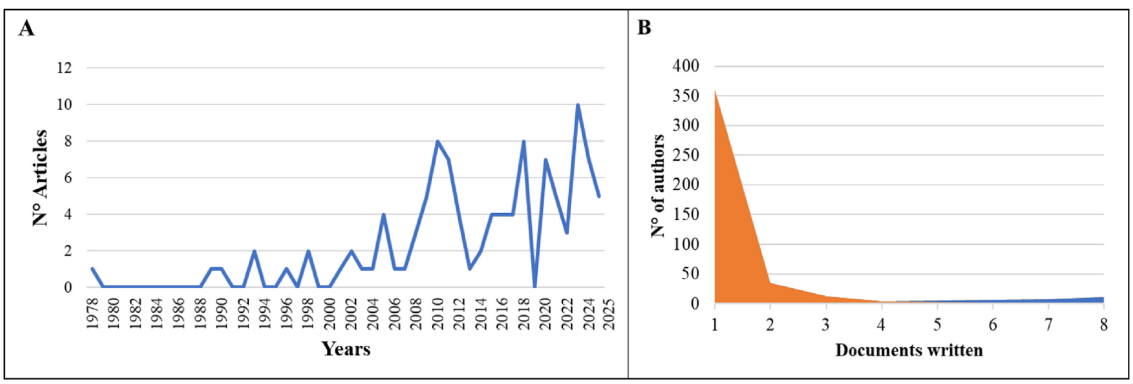


Figure 1. Annual scientific production on the genus *Platyrrhinus*. (A) Number of documents published per year; B- Author productivity according to Lotka's Law.

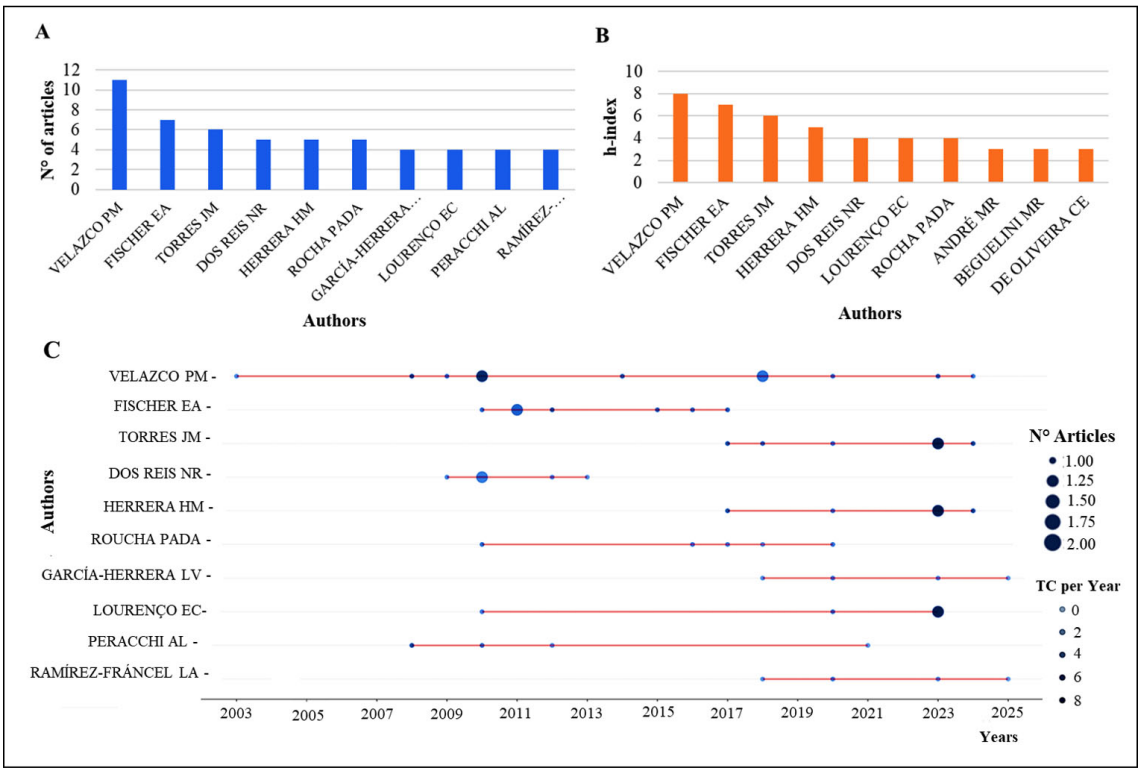


Figure 2. Authors' overview of the scientific knowledge of *Platyrrhinus* publications retrieved from the Scopus database. (A) Distribution of the proportion of articles considering the 10 most productive authors; (B) Scientific impact based on the h-index; (C) Productivity of the top 10 authors over time, between 2003 and 2025. TC represents the total number of citations per year, and the dot size represents the number of publications per year.

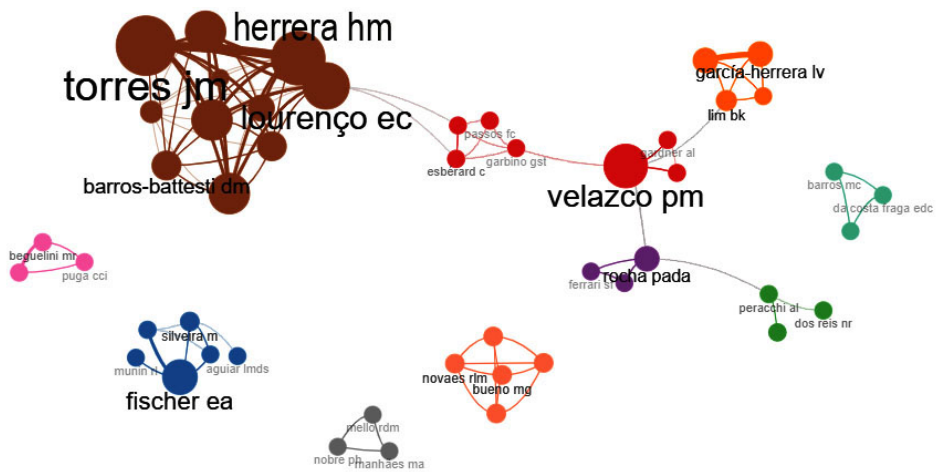


Figure 3. Collaboration network among authors who have published studies on species of the genus *Platyrrhinus*. The node size is proportional to the number of publications and with higher values of betweenness centrality; each color represents the clusters of authors wh o collaborate most with each other, and the edges demonstrate the direct co-authorship links between the researchers.

The average publication year of researchers based in the USA and Brazil occurred around 2010 and 2014, respectively, whereas the average publication year of researchers based in Peru and Colombia was more recent, around 2018 and 2020, respectively (Figure 5B)

3.2. Review of systematic studies

Thematic classification revealed a greater bias towards distributional and descriptive data, highlighting the persistence of the Wallacean shortfall within the genus, since knowledge about the distribution of species remains

incomplete, geographically biased, and unevenly distributed among regions and species. The research categories were distributed as follows: Composition, distribution, and/or biogeography (n=45); Genetics (n=27); Morphology and/or geometric morphometrics (n=20); Taxonomy, systematics, and/or phylogeny (n=17); Epidemiology (n=17); Diet (n=16); Parasites and/or associations (n=16); and Conservation (n=10). In contrast, critical biological and ecological fields remained underrepresented, such as reproductive biology (n=6), habitat use (n=6), shelter ecology (n=5), physiology (n=5), vertical structure (n=4), and activity patterns (n=3), while movement and methodological studies were scarce (n=1 each). The scarcity of studies addressing biological attributes and aspects of natural history indicates a significant knowledge gap regarding the functional ecology of *Platyrrhinus*, reinforcing the occurrence of a Raunkiaeran shortfall within the genus.

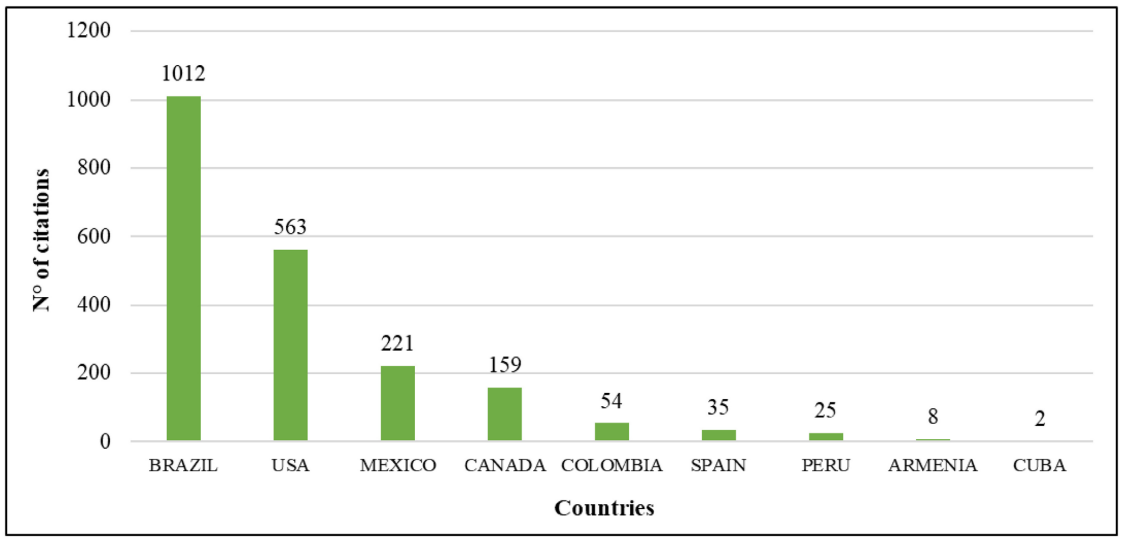


Figure 4. Productivity of the main countries producing scientific knowledge for the genus *Platyrrhinus* by number of citations.

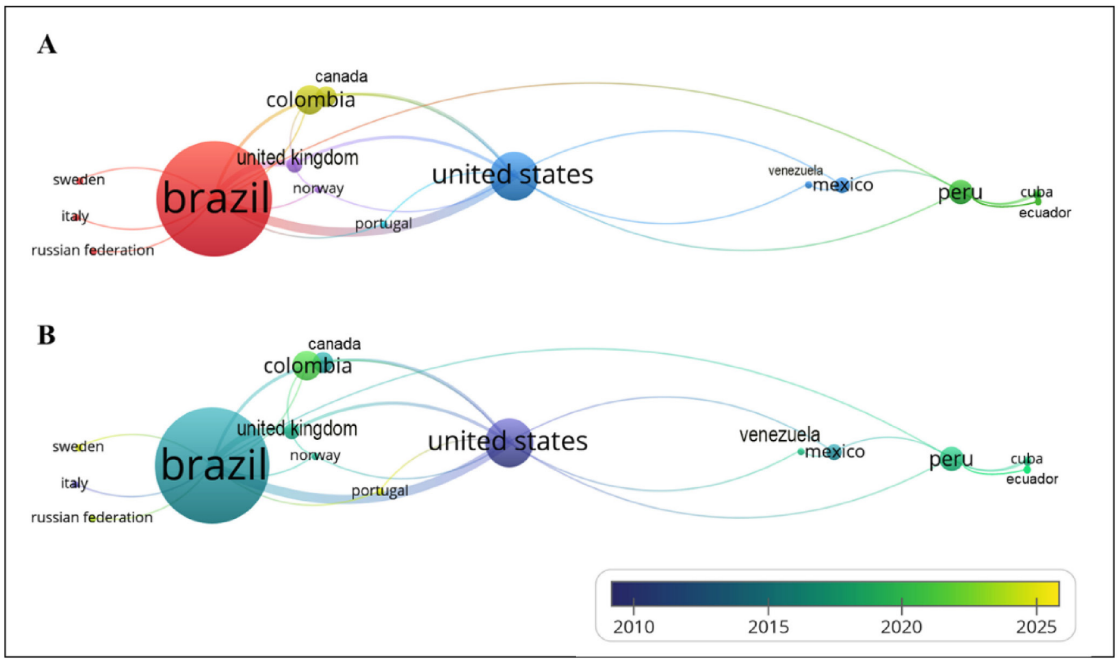


Figure 5. Collaborative networks for *Platyrrhinus* bat studies produced by researchers affiliated with institutions based in 15 countries. (A) Countries that collaborated the most in terms of number of publications; (B) Countries that collaborated the most over time. The color scale represents the average publication years, with cooler colors indicating older publications and warmer colors indicating more recent publications. The size of the nodes represents the number of publications per country and the lines indicate connections between countries.

Regarding species-specific effort, scientific production is highly skewed toward a few taxa. *Platyrrhinus lineatus* dominated the literature (n=64), followed by *P. helleri* (n=18) and *P. recifinus* (n=12). Conversely, low research representation characterizes other species of the genus: 14 species were the subject of only 3 to 9 papers over nearly half a century, while *P. aquilus* and *P. nitelinea* were recorded in only one study each. It was also observed that in some articles it was not possible to identify the species of *Platyrrhinus* under study (*Platyrrhinus* sp=7) (Figure 6, Table S1). This uneven distribution of effort suggests that most *Platyrrhinus* species remain effectively poorly studied, highlighting profound Linnaean (taxonomic), Raunkiaeran (functional/adaptive) and Prestonian (abundance) shortfalls.

The thematic category analysis confirmed a greater representation of *P. lineatus*, which was more represented in nine of the evaluated areas. with emphasis on Composition, Distribution, and/or Biogeography (n=17), Parasites and/or associations (n=15), Genetics (n=12), Diet (n=12), Epidemiology (n=11), reproductive biology (n=6) and Conservation (n=6). In contrast, *P. helleri* was more frequent in the Taxonomy/Systematics (n=7) and Physiology (n=3) categories. the Morphology and/or geometric morphometrics category, the species *P. recifius* (n=5) was the most representative, but it did not differ much from other species such as *P. helleri* (n=4) and *P. guianensis* (n=4), and others with similar values to these latter species. The categories of Activity Patterns and Sampling Methods exhibited the highest fragmentation,

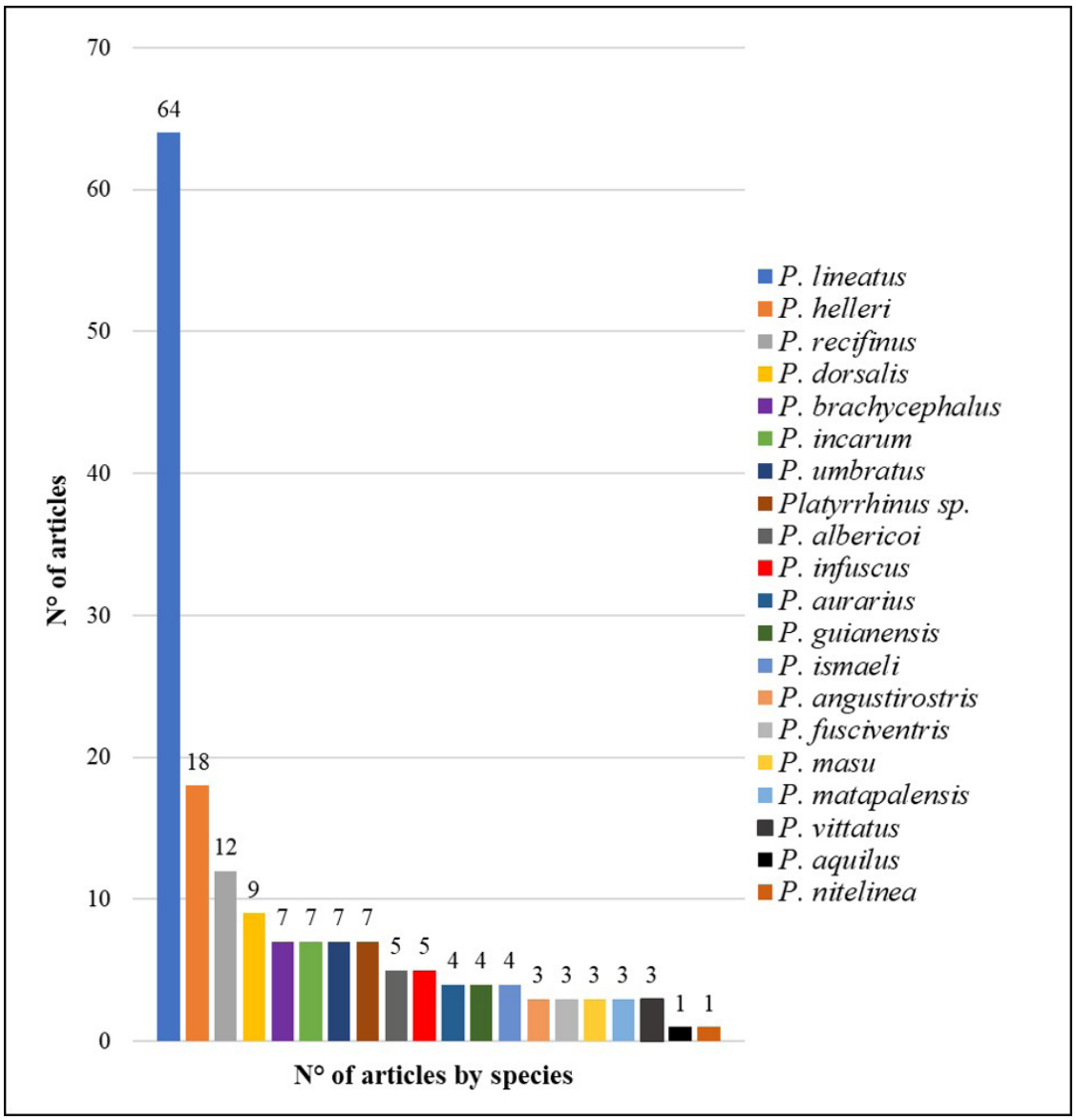


Figure 6. Distribution of the number of articles by species of bats of the genus *Platyrrhinus* available on the Scopus and WoOS platforms between 1977 and 2025.

with only a single study distributed among a few species, such as *P. ismaeli*, *P. lineatus*, and *P. umbratus* (Table S1).

4. Discussion

The scientific mapping and descriptive statistical analyses presented here have provided key indicators for understanding the trajectory of knowledge regarding the genus *Platyrrhinus*. These bats play vital ecosystem roles; by acting as seed dispersers, *Platyrrhinus* species contribute to plant recruitment and the regeneration of degraded areas in neotropical biomes. However, analysis based on Lotka's Law reveals that scientific output is generated by only a few researchers. These results indicate that most authors contribute occasionally, while only a small proportion demonstrate sustained, long-term publishing activity on the genre.

Within the analyzed dataset, publications on *Platyrrhinus* show a notable concentration among a small group of authors. Researchers such as Velazco PM, Torres JM, Fischer E, and Herrera HM present a consistent publication history and high impact according to the h-index, in addition to occupying central positions in the collaboration network (Figure 3) within the scope of this study. These authors function as key nodes connecting research clusters, reflecting how collaboration is structured within the examined corpus, and demonstrating how interdisciplinary partnerships are essential for the advancement of chiropterology.

Although the study identified the participation of researchers affiliated with institutions in 16 countries, Brazil and the United States accounted for the highest number of publications and citations (see Figure 4). Both countries maintain significant international collaborative networks, especially since 2003, followed by the recent and promising growth in output in Peru and Colombia. This geographic leadership reflects not only scientific output but also the presence of a well-established research infrastructure.

Furthermore, the configuration of collaboration networks (see Figure 5) indicates that countries with a high volume of publications are centrally positioned within the network, while others maintain limited and specific partnerships. Therefore, it is recommended that the expansion and consolidation of the field of study on *Platyrrhinus* be reinforced by strengthening these transnational connections. Collaboration among researchers from different countries is what gives greater visibility to research findings and leads to greater effectiveness in solving complex problems, including those related to conservation (Adams, 2013; McManus et al., 2020).

Most authors published articles on *Platyrrhinus* species within the last two decades (2010-2025). These studies have moved from a phase focused essentially on morphological studies, with species descriptions (Velazco, 2005; Velazco and Gardner, 2009) and surveys of geographic distribution (Fracasso and Salles, 2005), to integrative studies, with morphological, molecular, and ecological data analyses or geographic distribution (Palacios-Mosquera et al., 2020; Velazco and Lim, 2014; Garbino et al., 2024). This scientific advancement was probably driven by the increase in new research techniques, such as advances in molecular studies (multilocus molecular phylogeny; phylogeography and biogeographic inference) and the combined use of field collection techniques (collection with canopy nets, ultrathin mist nets, telemetry and tracking (radio-tracking / MOTUS), active collection with dip nets).

This technical evolution is directly reflected in the publication distribution across thematic categories, where the category "Composition, distribution, and/or biogeography" emerges as the most prominent, evidenced by the notable volume of descriptions and species records in South American countries, particularly Brazil (e.g., Fracasso and Salles, 2005; Ortêncio Filho and Reis, 2009; Velazco and Gardner, 2009; Reis et al., 2012; Palacios-Mosquera et al., 2020; Lopes et al., 2023; Garbino et al., 2024; Lima et al., 2025; García-Herrera et al., 2025). This trend may be associated with the growth of studies aimed at describing bat diversity patterns (Luciano et al., 2022). However, although publications on *Platyrrhinus* have increased considerably in this category in recent years, efforts are still needed to fill the gaps in the distribution and composition in different niches for the group, which remains partially unknown for many species of the genus.

The "Genetics" category represented the second largest in terms of studies, focusing on molecular identification and phylogeny (e.g., Santos et al., 2002; Velazco et al., 2010; Velazco and Lim, 2014; Lopes et al., 2023; Lima et al., 2025), particularly with studies on *P. lineatus* and *P. helleri* species complex. However, cytogenetic data (Souza and Araujo, 1990; Faria and Morielle-Versute, 2002; Beguelini et al., 2011) and molecular detection of pathogens (e.g., Perles et al., 2020; Mancilla-Agrono et al., 2022; Franco Filho et al., 2023; Dias et al., 2024; Gomez-Puerta et al., 2025) are still sporadic and have been published for only a few species, such as *P. lineatus*, *P. helleri*, and *P. infuscus*.

At the same time, in the category "Morphology and/ or Geometric Morphology", studies were identified that range from reports of anomalies (García-Restrepo et al., 2023) and visual systems (Baron, 1977) to craniometric descriptions integrated into taxonomy and phylogeny (e.g., Tavares and Velazco, 2010; Palacios-Mosquera et al., 2020; Ramírez-Fráncel et al., 2020, Lopes et al., 2023; Lima et al., 2025; García-Herrera et al., 2025). It is noteworthy that, among the studies analyzed, only one study had used geometric morphometrics to resolve synonymy in *P. dorsalis* and *P. umbratus* (Velazco et al., 2023), demonstrating that most morphological studies are still used to assist in the identification, taxonomy, and delimitation of species (e.g., Taddei and Vicente-Tranjan, 1998; Velazco and Lim, 2014; Garbino et al., 2024; Ferreira et al., 2025).

In the fields of taxonomy, systematics, and/or phylogeny, the works of Owen (1987) and Velazco (2005) substantially expanded the known diversity of the genus, while the works of Velazco and Patterson (2008) and Velazco et al. (2010) became references in separating species from the *P. helleri* complex. In general, the systematics of *Platyrrhinus* faces a pronounced Linnean shortfall, characterized primarily by a lack of comprehensive taxonomic revisions, unresolved species limits, and a scarcity of integrative taxonomic approaches. (e.g., Owen, 1987; Velazco, 2005; Velazco and Gardner, 2009; Velazco et al., 2010; Lima et al., 2025).

For the poorly studied species, we observe that in some cases the literature is basically restricted to their original descriptions, such as *P. aquilus* and *P. nitelinea* (Velazco and Gardner, 2009).

In the "Epidemiology" category, a growth in studies was observed, mainly from 2017 onwards. (e.g., Ferreira et al., 2017; Franco Filho et al., 2023; Torres et al., 2024; Gomez-Puerta et al., 2025). This may be related to economic and public health concerns regarding bats as potential reservoirs of pathogens (Luciano et al., 2022). However, for the genus *Platyrrhinus* specifically, direct evidence linking these species to disease transmission is still scarce, as most available records focus only on the detection of pathogens, rather than active transmission cycles. Consequently, although rabies is well documented in bats more broadly, caution is needed to avoid speculative assumptions about public health threats from bats in general (Moratelli and Calisher, 2015).

In contrast, key areas such as "Diet" (e.g., Mello et al., 2014; Silvestre et al., 2016; Pellon, 2022; Genelhú et al., 2023) and "Parasites" (e.g., Gettinger and Gribel, 1989; Dantas-Torres et al., 2009; André et al., 2023; Alcântara et al., 2023), reveal low representation in the reviewed corpus for most of the genus, with a focus almost exclusively on *P. lineatus.* This neglect also affects the Conservation category (e.g., Estrada and Coates-Estrada, 2002; Gorresen and Willig, 2004; Ortêncio Filho et al., 2010; Mendes and Marco, 2018; Otálora- Ardila et al., 2024); reproduction (e.g., Willig, 1985; Martins et al., 2015; Brito et al., 2020); habitat use and roosting ecology (e.g., Fenton et al., 2001; Tello and Velazco, 2003; Alho et al., 2011; Breviglieri, 2021; Silveira et al., 2024); and physiology, cytology, and/or biochemistry (e.g., Baron, 1977; Hermanson et al., 1998), which together account for 16% of scientific output.

The frequency of *P. lineatus* in various ecological areas can be attributed to its abundance throughout its wide geographic distribution (Velazco, 2005) and the significant number of studies conducted in Brazil, which concentrated much of their sampling efforts in that country. This bias masks the persistence of Linnaean shortfalls for rare species and Wallacean shortfalls for taxa with underestimated distributions (Lomolino, 2004). Due to the difficulty of identification in the field, rarity, and restricted distribution, as in the case of *P. aquilus* and *P. nitelinea*, such species remain poorly studied. Furthermore, these two species are classified as "Data Deficient (DI)" by the IUCN Red List (IUCN, 2025). The limited research in categories such as vertical structure and movement and activity patterns indicates a significant Raunkiaeran shortfall (Hortal et al., 2015), limiting our understanding of the functional traits and ecology of these species. Furthermore, the scarcity of population data for most of the group points to a Prestonian shortfall (Hortal et al., 2015).

It is worth noting that in seven articles, records of *Platyrrhinus* were reported only as "*Platyrrhinus* sp.". This reflects an expected problem for the genus, particularly for most species within the *P. helleri* complex, due to the substantial overlap in morphological characters among them, which makes field identification extremely difficult (Velazco et al., 2010, personal observation). It is therefore not uncommon, when reviewing this genus, to find records classified only as '*Platyrrhinus* sp.' across various collections. This reinforces that, for many of these species, the use of molecular data is essential for reliable identification, which well illustrates the Linnaean shortfall addressed in this article (personal observation).

Collectively, these shortcomings, combined with the taxonomic uncertainties that contribute to the Linnaean shortfall (Lomolino, 2004), demonstrate that current knowledge about *Platyrrhinus* remains highly biased and fragmented, hindering accurate conservation assessments for the genus and highlighting the need to prioritize historically neglected species. The patterns identified in the graph in Figure 6 and in Supplementary Table S1 provide a framework for prioritization future research, where the thematic gaps identified for species such as *P. aquilus* and *P. nitelinea*, among others, help to direct research efforts to areas beyond the basic systematic/taxonomic gap, which have not yet been fully resolved, especially for these species.

Improving the taxonomy, natural history, and conservation assessments of *Platyrrhinus* requires prioritizing research in understudied taxa and neglected thematic areas. This study highlights the need for local and international collaboration to fill persistent gaps in undersampled categories, such as the ecology, physiology, and reproductive biology of these bats. Furthermore, addressing these deficiencies depends on increased investment in museums and scientific collections, which remain essential for long-term biodiversity monitoring and taxonomic accuracy.

5. Conclusion

In the present study, scientometric analysis showed that although the genus *Platyrrhinus* has experienced a marked increase in publications since 2010, this progress is marked by profound asymmetries. Scientific output, led predominantly by authors affiliated with Brazilian institutions and collaborations between Brazil, the USA, Peru, and Colombia, remains concentrated among a small group of authors and in traditional thematic areas, such as biogeography and genetics. The frequency of *P. lineatus* in the literature, in contrast to the scarcity of data for most other species, may indicate a persistence of the Wallace (distribution) and Prestonian (abundance) shortfalls. At the same time, the lack of information on diet, reproduction, and physiology for taxa such as *P. umbratus*, *P. masu*, and *P. guianensis*, suggests a large Raunkiaeran shortfall (functional), which limits our ability to predict the ecological responses of these bats.

Finally, this study demonstrates that one way to aid in the conservation of *Platyrrhinus* is to expand studies into neglected areas, such as reproductive biology, ecological, epidemiological, cytogenetic, and evolutionary aspects, and we emphasize the importance of efforts focused on the least studied species. Addressing these taxonomic and functional imbalances is a fundamental step towards developing a more comprehensive understanding of evolutionary biology and supporting effective management strategies for Neotropical bats.

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Data Availability Statement

All data analyzed in this research were obtained from the Scopus (2025) and Web of Science-WoS (Clarivate, 2025) platforms, with the exception of the works by Owen (1987) and Velazco (2005). Data regarding the number of studies for each *Platyrrhinus* species are available in the Supplementary Information section of this article.

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Supplementary Material

Supplementary material accompanies this paper.

Supplementary Table S1. Species and number of studies by category and year of publication for the genus Platyrrhinus.

Supplementary Figure S1. Flowchart for identifying studies using the Scopus and Web of Science (WoS) databases for studies compiled for the genus Platyrrhinus.

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