



SOCIEDADE BRASILEIRA
DE ENTOMOLOGIA
FUNDADA EM 1937



Biology, Ecology and Diversity

Filling gaps in species distributions through the study of biological collections: 415 new distribution records for Neotropical Cryptinae (Hymenoptera, Ichneumonidae)



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ARTICLE INFO

Article history:

Received 30 June 2018

Accepted 1 September 2018

Available online 28 September 2018

Associate Editor: Rodrigo Gonçalves

Keywords:

Atlantic Forest

biodiversity

Cryptini

database

parasitoid wasp

ABSTRACT

Filling gaps in species distributions is instrumental to increase our understanding of natural environments and underpin efficient conservation policies. For many hyperdiverse groups, this knowledge is hampered by insufficient taxonomic information. Herein we provide 415 new distribution records for the parasitic wasp subfamily Cryptinae (Hymenoptera, Ichneumonidae) in the Neotropical region, based on examination of material from 20 biological collections worldwide. Records span across 227 sites in 24 countries and territories, and represent 175 species from 53 genera. Of these, 102 represent new country records for 74 species. A distinct "road pattern" was detected in the records, at least within Brazil, where 50.2% of the records fall within 10 km of federal roads, an area that occupies only 11.9% of the surface of the country. The results help to identify priority areas that remain poorly sampled and should be targeted for future collecting efforts, and highlight the importance of biological collections in yielding new information about species distributions that is orders of magnitude above what is provided in most individual studies.

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Introduction

A general comprehension of geographic distributions of major taxa is essential to understand natural environments, to recognize species diversity patterns and to plan conservation strategies (Gaston, 2000; Myers et al., 2000; Lamoreux et al., 2006). A proper understanding of species distributions is also paramount to underpin studies in evolutionary biology, phylogeography and taxonomy (Vamosi et al., 2007, 2009; Webb et al., 2002).

Because comprehensive revisionary works are less often produced for hyperdiverse groups, updates on distributional records of these species are comparatively rare and often published directly in catalogues, without unambiguous references to primary (specimen) records. Thus, it is hard to distinguish which records proceed from identifications confirmed by specialists, which affects the quality of any distributional study as a whole, and consequently any analysis based on such records. This problem is particularly evident when one compares the available data for vertebrates with the dearth of information for any speciose invertebrate group, in spite

of their significant role in ecosystem balance and relative amount of biomass they represent. Hence, filling gaps in our knowledge of species distributions is particularly important for hyperdiverse and historically neglected groups, especially in the context of a global biodiversity crisis (Myers et al., 2000; Soberón et al., 2000).

Cryptine wasps (Hymenoptera, Ichneumonidae, Cryptinae) are represented by 274 genera and over 2,800 described species (Santos, 2017). They are one of the dominant components of parasitic wasp diversity, particularly in tropical regions (Townes, 1970; see also Veijalainen et al., 2012). However, the group remains poorly understood from a taxonomic and evolutionary perspective. Recent advances have been made in higher-level systematics (Santos, 2017), but species-level taxonomy still lags behind an acceptable pace. Most cryptine species descriptions date from 1840 to 1920, and few revisionary works have been conducted since then. Hence, most species are still recorded only from their type locality, often stated vaguely or imprecisely in the original works. At the same time, the lack of taxonomic resources on this group results in poor curatorial state of most collections, hindering the collection of distribution data.

A series of taxonomic revisions of Neotropical groups started to change this situation in the past decade (e.g. Aguiar and Ramos, 2011; Aguiar and Santos, 2015; Santos and Aguiar, 2012, 2013,

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2015; Scherrer and Aguiar, 2012; Tedesco and Aguiar, 2013). The increased availability of reference work to accurately identify specimens to species level can foster a significant increase in the availability of distribution records. Herein, we use data generated from loaned specimens and visits by the first author to several collections worldwide to contribute toward that goal, presenting 415 new distribution records for Neotropical Cryptinae.

Material and methods

All data presented in this work proceed from specimens deposited in biological collections and directly observed by the authors; no literature data is included. Species were identified through comparison with determined species at the National Museum of Natural History (Washington, DC); by comparison with type species photographed at the respective collections; or by consulting the original descriptions and appropriate revisionary works (mostly Aguiar and Ramos, 2011; Santos and Aguiar, 2013). Species of Cryptini were not assigned to subtribes, given that previous research has demonstrated that such a classification is largely artificial (Laurenne et al., 2006; Santos, 2017). Rather than providing a comprehensive compilation of specimen-level data for Cryptinae, our goal was to provide the maximum amount of new geographical records driven by availability of previously or newly determined specimens in collections. Material from 20 institutions was examined, as follows (curators in parentheses). AMNH, American Museum of Natural History, New York, U.S.A. (J. Carpenter); APTA, Agência Paulista de Tecnologia dos Agronegócios, Ribeirão Preto, Brazil (N. Perioto); BMNH, The Natural History Museum, London, U.K. (G. Broad); CASC, California Academy of Sciences, San Francisco, U.S.A. (R. Zuparko); CMNH, Carnegie Museum of Natural History, Pittsburgh, U.S.A. (John Rawls); CNCI, Canadian National Collection of Insects, Arachnids and Nematodes, Ottawa, Canada (A. Bennett); DCBU, Departamento de Ecología e Biología Evolutiva, Universidade Federal de São Carlos, São Carlos, Brazil (A. Penteado-Dias); EMEC, Essig Museum of Entomology, University of California Berkeley, U.S.A. (P. Oboyski); FSCA, Florida State Collection of Arthropods, Gainesville, U.S.A. (K. Williams); IAVH, Instituto de Investigación de Recursos Biológicos Alexander von Humboldt, Bogotá, Colombia (C. Medina); MNHN, Muséum National d'Histoire Naturelle, Paris, France (C. Villemant); MUCR, Universidad de Costa Rica, Costa Rica (P. Hanson); MZUP, Museu de Zoologia da Universidade de São Paulo, São Paulo, Brazil (C.R.F. Brandão); UFES, Universidade Federal do Espírito Santo, Vitória, Brazil (M.T. Tavares); UNAM, Universidad Nacional Autónoma de México, Mexico City, Mexico (A. Zaldívar-Riverón); UNESP, Universidade Estadual Paulista Júlio de Mesquita Filho, São José do Rio Preto, Brazil (F. Noll); USMC, Universidad Nacional Mayor de San Marcos, Lima, Peru (G. Lamas); USNM, National Museum of Natural History, Washington, U.S.A. (R. Kula); USUC, Utah State University, Logan, U.S.A. (D. Wahl); ZSMC, Zoologische Staatssammlung München, Munich, Germany (S. Schmidt).

In early stages of this work, only geographic information was collected, though latter efforts compiled full label data for the specimens examined. The locality data collected were verified against all published records for each species in order to precisely identify new (i.e. unpublished) records. In order to avoid giving new record status to specimens collected very close to known localities, records were considered “new” when collected at least 60 km (37.3 miles) apart from the closest known records, or when they represented new records for an administrative state/province, regardless of distance. While this cutoff is somewhat arbitrary, it avoids artificial inflation of “new records” based on repeated sampling of the same natural area, for example different points within a same reserve or neighboring private lands. During the filtering process, records

that were found to be previously known, but never georeferenced, were included in a separate table in order to complement the new locality information.

Geographic coordinates, when not present in the specimen labels, were obtained from a variety of sources, including GoogleEarth version 7.3.1.4507 and the geoLoc tool at speciesLink (<http://splink.cria.org.br/geoloc>). A map in KML format was generated from the original table (see supplementary material) containing the following fields: taxon (species name), coordinates in decimals, location (country through locality), verbatim specimen label, museum repository, and specialists who conducted the identification (although all specimens were verified by the first author). Additional information (record novelty status, referencing and identification remarks, etc.) is included in the original table, but was not imported into the KML.

Tests for a “road-based” pattern focused on records within Brazil, where GIS files for federal roads are readily available, and the high number of individual records allows for statistical analyses. Following Soberón et al. (2000), the test was conducted by placing a 10 km buffer over existing inter-state federal roads and calculating the proportion of records that fell within the buffer area. The observed results were compared to an expected proportion assuming records were randomly distributed, given the area occupied by the buffer using a Pearson's chi-squared test (Patefield, 1981).

Results

A total of 415 new distribution records were compiled for 175 species from 53 genera. The compiled results are presented with full information in Appendix S1 (Appendix S2 with the same data in DarwinCore format). Records encompass 227 sites in 24 countries and territories, including all countries in continental South and Central America except Suriname (Fig. 1, Appendix S3). The new records include 102 new country records for 74 species. Brazil was the country with the largest number of records (175); not surprisingly, the vast majority of these records were concentrated along the coastal portion of the Atlantic Forest, an area more extensively sampled than any other region in the country. In fact, a distinct “road pattern” was detected in the records, at least within Brazil. A total of 103 out of 205 (50.2%) records and 38 out of 85 (44.7%) sites for the country (including new records and those newly georeferenced herein) fall within 10 km of federal roads, an area that occupies only 11.9% of the surface of the country ($\chi^2 = 51.138$, df = 1, $P < 0.00001$; Appendix S4). In the Neotropical region as a whole, areas that remain poorly sampled comprise the center of South America, including most of the Amazon basin, central Argentina and the arid region of northern Chile and southern Peru and Bolivia.

Discussion

Approximately half the species treated herein were previously known only from the type locality, as retrieved from literature records compiled in Yu et al. (2012) and thorough review of more recent literature. For several Neotropical species described in the 19th century (e.g. in the extensive works of Brullé, 1846; Taschenberg, 1876; Szépligeti, 1916), specific localities were not even presented in the description, which instead list broad geographic regions or countries (e.g. “from Brazil”). For these species, the new records provided herein represent the first georeferenced locality information.

Our results help to highlight priority areas for future sampling and open the venue for more comprehensive compilations. New geographic records for Ichneumonidae as a whole have been advanced more or less consistently in the past few years (e.g. Çoruh and Çalmasur, 2016; Di Giovanni et al., 2015; Di Giovanni and

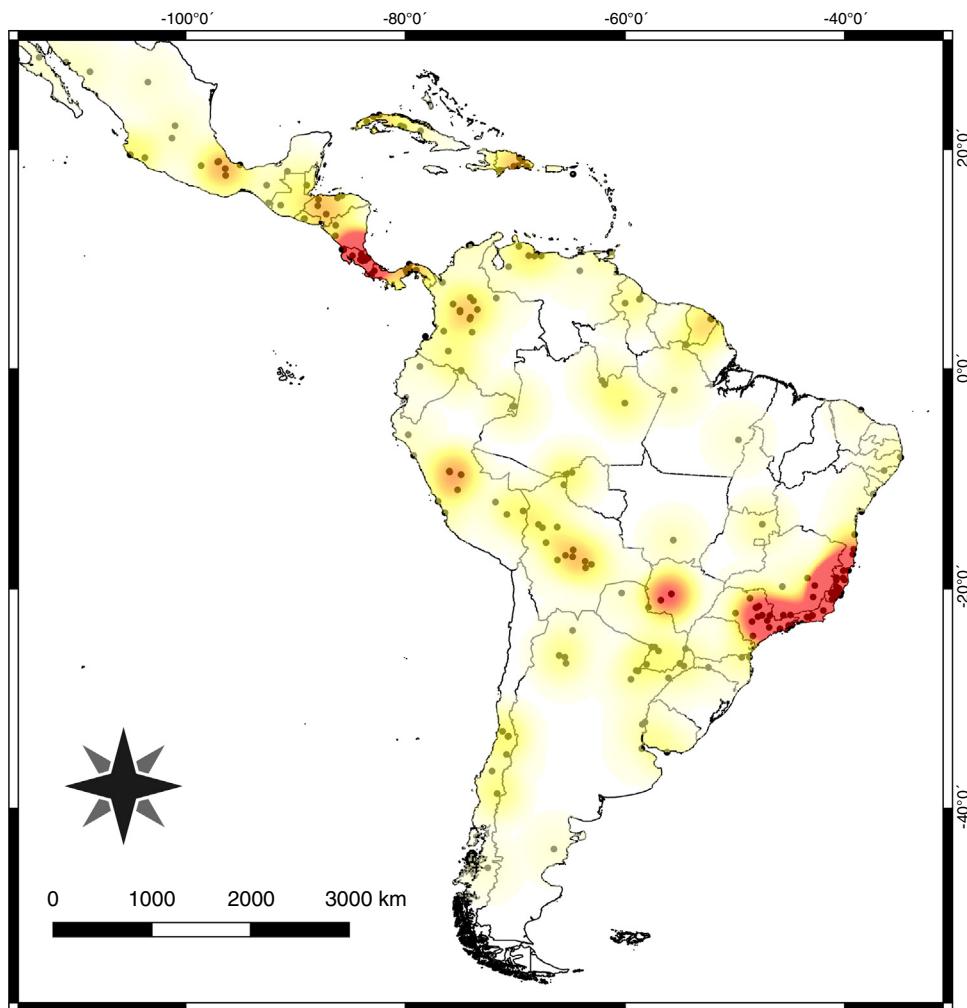


Fig. 1. Heatmap with new distribution records for Neotropical Cryptinae. Warmer colors (red) indicate higher density of records, while whiter areas indicate sparse records or lack thereof.

Riedel, 2017; González-Moreno and Bordera, 2011; Martínez and Torretta, 2015; Melo et al., 2015; Vas et al., 2015), but to our knowledge none in the scale or geographic scope presented herein. Albeit extensive, our dataset also helps to demonstrate the limitations of current sampling efforts, which seem to be for the most part limited to areas of easy access. For densely populated or highly threatened areas, such as the Brazilian Atlantic Forest, having records published as structured data (i.e. Darwin-core) is particularly valuable; as data accumulates, collection dates can be an important variable to test for past versus present distributions and species richness. At the same time, while the logistic reasons for sampling accessible areas are obvious, a deeper understanding of species distributions in the Neotropical region will clearly depend on active collecting programs in more remote areas. Additional work is needed in terms of compiling and geo-referencing literature records in order to allow for sound comparative studies.

Speeding up the increase of knowledge

While it is widely acknowledged that biological collections are foundational for understanding biodiversity, including the effects of biological invasions and climate change (Short et al., 2018; Suarez and Tsutsui, 2004), the vast majority of reports on new distribution records for insects comes from isolated surveys and field expeditions (e.g. Aranda, 2017; da Silva,

2017; Duarte et al., 2018; Niemiller et al., 2017). Collections, functioning as a repository from hundreds or thousands of individual collecting events, can yield new information about species distributions that is orders of magnitude above what is provided in most studies. The endeavor of making this massive stock of information available for researchers has been initiated through sizable projects of specimen digitization worldwide (e.g. Blagoderov and Smith, 2012; Soberón et al., 1996), and by special funding initiatives such as the National Science Foundation's "Advancing Digitization of Biodiversity Collections" program.

In spite of the tremendous advance represented by these initiatives, most projects still face a key limitation in that in almost all collections many taxa are still in poor curatorial state, particularly when it comes to the availability of specimens accurately determined to the species level – a crucial requirement for many biodiversity applications (Feeley and Silman, 2010; Goodwin et al., 2015). The results obtained in this study show that, in some cases, an efficient (or at least, cost effective) approach may be *in situ* curation followed by taxon-specific digitization. A trained taxonomist may often identify hundreds or thousands of specimens in days. Specimen-level data capture can then be conducted by non-specialists, either *in situ* or through quick imaging of specimen labels (even with a cell phone) followed by digitization and data parsing. The hundreds of new distribution records generated

herein serve as a proof of concept that it is possible to reduce the “taxonomic impediment” that has so far constrained the advance of knowledge on the distribution of poorly known groups.

Author contribution

Conceived and designed the study: BFS. Collected data: BFS and JPMH. Contributed specimens/materials/analysis tools: BFS and JPMH. Analyzed the data: JPMH. Wrote the paper: BFS and JPMH.

Conflicts of interest

The authors declare no conflicts of interest.

Acknowledgments

All curators mentioned in material and methods received the first author in their institutions and/or provided invaluable loan of Cryptinae specimens. Ana Dal Molin kindly prepared the KML file and reviewed an early version of the manuscript. Katja Seltmann (UCSB) kindly assisted the authors in formatting all records to Darwin Core standard. The first author is supported by a Peter Buck Postdoctoral Fellowship at the NMNH. The visits to biological collections were funded by a Doctoral Dissertation Improvement Grant from the National Science Foundation (award #1501802); a ‘mini-ARTS’ award from the Society of Systematic Biologists; an Annette Kade Graduate Student Fellowship and a Theodore Roosevelt Memorial Grant, both by the AMNH; a Jessup Award by the Academy of Natural Sciences of Drexel University; and an Essig Museum Visiting Taxonomist Award by UC Berkeley. The second author is supported by a CAPES scholarship funding.

Appendix A. Supplementary data

Supplementary data associated with this article can be found in the online version at doi:[10.1016/j.rbe.2018.09.001](https://doi.org/10.1016/j.rbe.2018.09.001).

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