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研究課題名（英文）Resolving a high-resolution global map of ant biodiversity for basic biology and applied conservation

研究代表者
ＥＣＯＮＯＭＯ　Ｅｖａｎ（Economo, Evan）

沖縄科学技術大学院大学・生物多様性・複雑性研究ユニット・准教授

研究者番号：３０６４８９７８

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研究成果の概要（和文）：主たるプロジェクト目標は、地球規模生物多様性について理解を深めるべく国レベルのチェックリストを超えるアリ高解像度地球規模多様性地図を作り他の分類群と比較する為に、我々の地球規模アリ生物多様性情報学(GABI)データベースを改良することである。第一の成果は、地理位置情報及び範囲マッピングのパイプラインを構築したことで、現在、60万件を超えるアリの分布記録をジオレファレンスし、位置情報認識済みのデータセットサイズを200万強にまで拡大した。第二の成果は、他の分類群と生物多様性パターン・ホットスポットを比較し大規模な多様性パターンを分析することで、すでに数多の論文が発表され、更に幾つか進行中である。

研究成果の学術的意義や社会的意義
This work has led to 12 academic publications and many more are still in progress. The data is also visible on antmaps.org and antwiki.org which gets over 25,000 visits per month, many from the general public.

研究成果の概要（英文）：The main project goal has been to improve our Global Ants Biodiversity Informatics (GABI) database to go beyond country level checklists and make a high-resolution global diversity map for ants and compare to other taxonomic groups to ask questions about global biodiversity. The first main success of our research has been to build a georeferencing and range mapping pipeline, and to date we have georeferenced over 600,000 species occurrence records increasing the size of the dataset to over 2 million georeferenced records. The second goal is to compare biodiversity patterns and biodiversity hotspots with other taxa and analyze large scale patterns, and a number of publications have already appeared with more in progress.

研究分野：Ecology, Evolution, and Behavior

キーワード：Biodiversity　Ants　Biogeography　Conservation　Ecoinformatics　Big data

様　式　Ｃ－１９、Ｆ－１９－１、Ｚ－１９、ＣＫ－１９（共通）

１．研究開始当初の背景

In the past several decades, the consolidation of large comprehensive datasets has resolved a global picture of biodiversity of some vertebrate groups and (to some extent) plants[1-7]. These data allow us to ask fundamental questions about the macroecology and macroevolution of biodiversity patterns, as well as provide an information base to guide global conservation efforts by allowing us to quantify hotspots of species richness, endemism[5-7]. However, despite this progress, there is a major hole in our knowledge: no comprehensive datasets exist for invertebrate animals, which make up the majority of Earth's biodiversity.

To address this need, in the last few years my lab has pursued the Global Ant Biodiversity Informatics (GABI) project[8,9], and have now successfully consolidated available geographic information on all 15,000 ant species distributions into one synthetic database. The project completed data entry of over 8500 publications- nearly the entire published literature on ants, and combined online and museum specimen databases. The GABI database constitutes 1.8 million geographic ant species occurrence records, which have been curated for quality and updated to reflect the most recent taxonomy, and is being used for biogeographic analyses (e.g. ref. 10).

This represents a "first draft" of global ant biodiversity, but further work is needed before it can be maximally useful for both biogeography and conservation. The vast majority of species occurrence records are not associated with lat.-long. coordinates, which have only been recorded by collectors in the last few decades, and often can only be assigned to a larger political level (e.g. prefecture or country). Thus, our data is currently organized around a system of 415 polygons around the globe (Figure 1), which represent a mixture of geologic and political regions, and are chosen for convenience to maximize data inclusion.

This polygon-based geographic system causes inherent biases and challenges in the analysis of biogeographic patterns, for example regions are not of equal area and shape, and many areas with heterogeneous climates are combined in a single large region. Second, the regions are still too large to be really useful for conservation, as most conservation planning occurs on a smaller scale within countries at which NGOs and governments decide to protect certain areas versus others.

２．研究の目的

The overall goals of the study are to address the above challenge and generate a next-generation high resolution version of the database and use it to map global ant diversity.　The steps to achieve this involve a) increasing the resolution of the global ant dataset by increasing the number of georeferenced points using an automated georeferencing pipeline, b) developing a computational pipeline to turn sets of points into species range maps using a combination of hull methods and species distribution modeling, c) use these species ranges for each species to produce global maps of biodiversity and compare them with other groups.

３．研究の方法

Georeferencing pipeline: Our starting point was approximately 2 million raw species occurrence records. Of these, around 70% were georeferenced (specifically, they had a latitude and longitude), but many had errors.　We aimed to use automated methods to both cross-check and fix existing points, and add predicted points to those records that didn't have them based on locality text (if available).　First, we constructed a set of functions to clean locality names before the main geocoding. We fixed locality strings by geocoding with mojibake to fix Unicode conversion errors, google to correct for incorrect fields, .　We then cleaned the country field by correcting spelling mistakes and corrected for localities with incorrect category assignment (for example, a city name in country field).　Once the data was as clean as possible, we ran it through both google geocoder and the program GeoLocate.　These return points and error bounds on the points.　We then perform a series of custom checks such as checking that the point is on land, etc., and finally run the points through Coordinate Cleaner to identify potential outliers.　Flagged errors were finally examined through manual review.

Species range mapping: We built a pipeline to turn a set of points associated with a species to a reasonable estimate of a species range using a flexible procedure that treats species differently with different numbers of records.　First, based on the number of valid occurrence points for a species, we calculated either an alpha hull (highest number of points), a convex hull (intermediate number), or a set of buffered points (lowest number).　The boundaries between these categories are flexible parameters in our pipeline, and we ran with different settings to estimate the effect on results.　Second, for species with a minimum number of points (another flexible parameter, but typically > 5-10), we performed environmental niche model within the range estimated by the hull methods using ENMEval and MaxEnt. Finally, the species ranges were stacked and mapped.

Diversity estimation and comparison: After we have created a species range map for all 15,000 species, we can estimate diversity patterns and compare them to other taxa. We retrieved data from biodiversitymapping.org which maintains high-resolution diversity data for Earth's species. The comparative analysis is still ongoing but we have detected considerable divergence between ant and vertebrate biodiversity patterns.

４．研究成果

Overall the georeferencing effort added 600,000 georeferenced points to the dataset, and corrected over 80,000 errors. This means that the total dataset is now approaching 2 million georeferenced records. In addition to increasing the number of points, importantly the spatial coverage increased considerably. This is because the spatial distribution of sampling effort has changed over time. And many areas that were heavily sampled in the era before GPS units became popular have not been sampled well in the past 30 years. The old records represent new data from undersampled areas with high biodiversity value, such as sub-Saharan Africa.

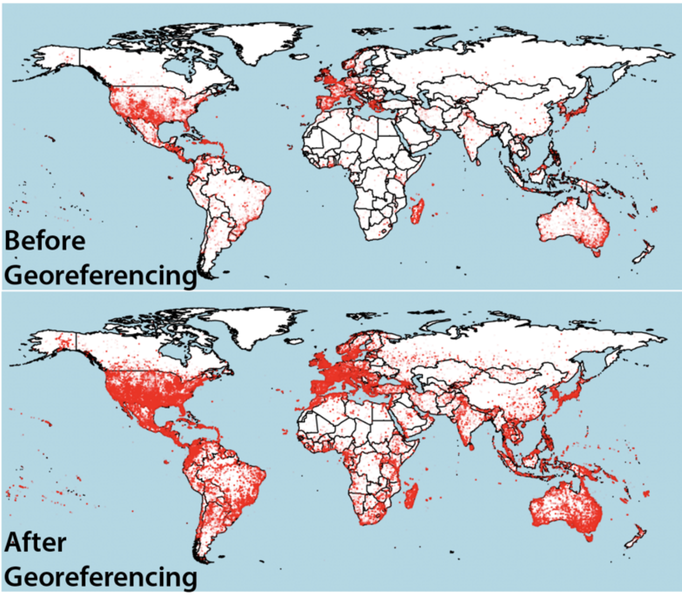

Figure 1: Results of the georeferencing effort. The project added over half a million georeferenced records to the dataset, and importantly increased the geographic coverage of the data considerably.

These data have made a scientific impact in a number of ways. First, we have recently performed global analyses of global diversity and distribution of all ants (Economo et al. 2018) and one hyperdiverse clade, *Pheidole*, in high resolution (Economo et al. 2019). Several more papers on global ant diversity are in progress. In addition, the GABI data has been used in a number of cross-taxon analysis focused on global patterns of introduced species (Dawson et al 2017, Nature Eco. Evo., Seebens et al. PNAS 2018, Moser et al 2018 PNAS). In addition, the public portal for accessing the data, antmaps.org and antwiki, are heavily trafficked with over 25,000 hits per month, thus they are making an impact on both the general public and the scientific community.

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〔図書〕（計０件）

〔産業財産権〕
○出願状況（計０件）

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権利者：
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番号：
出願年：
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○取得状況（計０件）

名称：
発明者：
権利者：
種類：
番号：
取得年：
国内外の別：

〔その他〕
ホームページ等
N/A

６．研究組織

(1)研究分担者
研究分担者氏名：

ローマ字氏名：

所属研究機関名：

部局名：

職名：
研究者番号（８桁）：

(2)研究協力者
研究協力者氏名：
ローマ字氏名：

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