

A dataset of European marine mites (Trombidiformes, Halacaridae)

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SUMMARY

We present a data set on marine mites (family Halacaridae) in European waters. The data set gathers all the published records of marine mites from the North European Seas, Lusitania, Mediterranean Sea and Black Sea marine provinces, all belonging to the temperate North Atlantic geographical realm. The database includes 3006 records collected from 260 original publications. For each record, the dataset provides complementary taxonomic, geographical, and ecological information, as well as remarks regarding the sampling methods used in each study. We use this dataset to briefly discuss potential knowledge gaps and biases across marine regions and habitats. We hope these data will provide a baseline for further studies in biogeography and ecology.

INTRODUCTION

We live in times of major concern about biodiversity, as unprecedented rates of biodiversity loss are altering key environmental processes and accelerating changes in ecosystem functions (Worm et al. 2006, Butchart et al. 2010, Ripple et al. 2017). Unfortunately, the data available for the distribution and biology of many groups of organisms are scarce or scattered in the literature, producing high levels of uncertainty that hamper our commitment to act against biodiversity crisis (Hooper et al. 2012). The accumulation of high-quality spatial distribution data of species in space and time is critical to ascertain not only the current extent of biodiversity losses but also its long-term effects (Magurran et al. 2010, Newbold et al. 2016, Oliver 2016), which are pivotal to ensure effective decision-making processes. Detailed information on species' distribution is not only important regarding the protection of a particular area or the assessment of spatial trade-offs between ecosystem services, but also to decide on conservation priorities and communicate about the implementation of policies (Martinez-Harms and Balvanera 2012, Townsend et al. 2014, Mammola et al. 2022).

Databases are efficient tools because they gather and organise selected information in a way that is easily accessible for both humans and machines. Databases have thus become an essential baseline in many biodiversity projects (Stein 2003, Bonamano et al. 2016, Hudson et al. 2016). There has been an increase number of published open access databases and data papers in the last years, focusing on different groups of animals (Madin et al. 2016, Froese and Pauli 2019, Garlaschè et al. 2019, Horton et al. 2020, García-Herrero et al. 2021, Pekár et al. 2021), and plants (The Plant List 2013, Farjon et al. 2014, USDA 2022, WFO 2022) or targeting specific habitats (Costello et al. 2013, Gerovasileiou et al. 2016, Martinez et al. 2018, Northeast Fisheries Science Center 2022). These databases have brought together information on the diversity and, ideally, abundance of target taxa, making it readily available for different

research communities that can address various biological and ecological questions.

Nonetheless, our ignorance around biodiversity is not equally distributed across the tree of life, and, in that regard, meiofaunal organisms have been often forgotten (Fonseca et al. 2018). Meiofauna encompass the diverse assemblage of creatures that are kept between a stack of meshes of 500 μm and 63 μm in size. Most meiofaunal organisms are microscopic animals but they might also include larger forms with elongated morphologies or contractile bodies (Schmidt-Rhaesa, 2020). Indeed, meiofauna is a useful model group to understand general eco-evolutionary processes, because meiofaunal organisms occur in large abundances and exhibit diverse phylogenetic affinities, allowing to test general hypotheses without the confounding factors of non-independence of the observations exerted by shared evolutionary history (Curini-Galletti et al. 2012). Meiofaunal species also show remarkably diverse responses to different environmental stressors, which may ultimately relate to the presence of certain traits (Kennedy and Jacoby 1999, Mascart et al. 2013, Broman et al. 2019).

We here provide a dataset including all available information on the distribution of marine mites (Halacaroidae: Halacaridae) in European waters. Halacaridae is a family of meiofaunal benthic organisms (Bartsch 2006), whose members are often found crawling on macroalgae and marine phanerogams, sandy deposits, gravels, or even animals belonging to various groups (Bartsch 2004). We know more than 1,200 species of halacarids, being the majority of these marine but also including representatives in brackish and fresh waters. The relatively low diversity of Halacaridae compared to other families of mites (Zhang 2011), more likely reflects the low attention historically paid to the group rather than its actual diversity (Appeltans et al. 2012). Indeed, the group has been overlooked in many recent biodiversity surveys (Willems et al. 2009, Curini-Galletti et al. 2012, Fonseca et al. 2014, Jörger et al. 2021), and there are no updated extensive reviews of the

species distribution despite our knowledge of marine mites has changed quite significantly in several aspects. This is unfortunate because halacarids have a worldwide representation (Bartsch 1989, 2004) and often form diverse and abundant communities (Paasivirta 1975, Pugh and King 1985, Little 1986, Di Sabatino and Cicolani 1999, Martínez, García-Gómez et al. 2021). Particularly in vegetated habitats, halacarids can reach densities of over 5000 individuals per m² (García-Gómez et al. 2022), and they can make up to 90% of the meiofaunal biomass in algae (Giere 2009). Because mites exhibit conserved morphologies that allow for an unequivocal identification of equivalent functional traits across species and genera, they also represent an ideal model for eco-evolutionary studies (Martínez, García-Gómez et al. 2021, García-Gómez et al. 2022).

Our aim here is to present an up-to-date open access database of halacarids in European marine waters, including all the records available in the literature along with the type of habitat in which they were found and remarks on different implemented sampling methods. To identify the knowledge gaps in Europe, we compared the species richness currently known in each European marine province with the estimated richness based on the sampling effort. We expect that this data will consolidate ongoing research lines using the family Halacaridae as an eco-evolutionary model, complementing future studies focusing on their life cycles, feeding biology, morphology, biogeography, macroecology, systematics, and phylogeny.

MATERIALS AND METHODS

Literature survey and compilation of species inventory

We compiled our dataset through standardised searches in Google Scholar, using the terms “Halacaridae”, “halacarid”, “marine mite*”, “Acari” followed by the geographical term “Europe”. For each search, we screened the title

and abstract of each retrieved publication, and we retained only those studies that reported Halacaridae records for Europe. All relevant articles were then downloaded and carefully read to extract all provided records. In order to maximise the completeness of our database, we cross-checked all the references cited in each downloaded paper for additional sources. Finally, we included the taxonomic validation and aphiaID of all European species and checked for both the original description and the references included in the World Register of Marine Species (Costello et al. 2013).

For each species’ record, we extracted the information on the location and its coordinates, as well as on the type of substrate, the depth and the methodology used to collect the samples. We inferred the missing coordinates using Google Maps at the maximum resolution allowed by the geographical information provided in each study. The different substrates were classified into four categories: (1) soft inorganic (i.e., sediments ranging from mud to gravel), (2) hard inorganic (i.e., rocks), (3) organic with vegetal origin (e.g., algae, marine phanerogams), (4) organic with animal origin (e.g., bryozoans, corals, sponges). Most of the variables follow Darwin Core Standards (DwC) (Wieczorek et al. 2012). The detailed description of each field is included in Table 1.

Geographical units

We assigned each record to two different spatial hierarchies. First, we defined geographical units following the maximum level of detail offered by the Biodiversity Information Standards (TDWG, formerly called Taxonomic Database Working Group), which corresponds to countries in Europe (www.tdwg.org). Then, the coast of each country was assigned to one or more marine provinces following the Marine Ecoregions of the World (MEOW) (Spalding et al. 2007, 2012). Specifically, the following marine provinces were analysed: (1) Northern European Seas, (2) Lusitania, (3) Mediterranean

Sea and (4) Black Sea, all of them included in the temperate North Atlantic realm.

Descriptive analyses

All analyses were performed with the statistical software R 2.10.0 (R Development Core Team 2009), using the *vegan* v. 1.15-4 package (Oksanen et al. 2013). We chose the package *ggplot2* v. 3.3.5 (Villanueva and Chen 2019) for graphical representation.

We calculated the species richness for each of the four marine provinces mentioned (Northern European Seas, Lusitania, Mediterranean Sea, and Black Sea) using occurrence data. We calculated the Chao2 estimator for the total species richness using the ‘specpool’ and ‘specaccum’ functions implemented in the R package *vegan* (Oksanen et al. 2013). This metric works satisfactorily as a point estimator when an undetected species in a sample has approximately the same probability of being detected as a singleton (Chao and Chiu 2016). We used sampling locality per marine province as the standard unit of sampling effort, following common practice in diversity analyses (Güler et al. 2016, Montes et al. 2021). Such an approach has been demonstrated to yield comparable results to the use of other measures of sampling effort, such as data on number of individuals recorded, or number of traps employed (Hortal et al. 2006). We considered that the number of records is related to survey effort, and that the probability of a species' occurring in a certain sampling locality relates to the number of records available for that locality.

Last, we represented the estimated total number of species in each marine province using species accumulation curves, i.e., the number of cumulative species recorded as a function of the number of sampling localities (Soberón and Llorente 1993, Gotelli and Colwell 2001). To avoid the influence of the distribution of species among the samples, the input of samples followed a random method and was subjected to 1000 permutations. Furthermore, we calculated the percentage of observed versus expected species using the Chao2 estimator based on

species' occurrences (Colwell, Mao and Chang, 2004).

RESULTS

Summary statistics

We gathered 3006 records of marine Halacaridae in European waters from 261 original publications. The dataset comprises 501 different localities from 22 countries (Fig. 1A). Overall, the information accounted for 230 species belonging to 9 subfamilies. The genera with more records were *Copidognathus* (21.42 % of all records) and *Rhombognathides* (15.50%); whereas the genera that accumulated more species were *Copidognathus* (53 species), *Rhombognathus* (17 species), *Halacarellus* (15 species), *Halacarus*, and *Agauopsis* (14 species each).

The North European Seas is the area where the greatest sampling effort (i.e., highest number of records and number of papers) has been performed with 119 species in 155 localities (Trouessart 1894, 1901, Viets 1927, 1928a, Bartsch 1975a, 1975b, 1976a, 1976b, 1977a, 1977b, 1979, 1980, Pugh and King 1985, Green and MacQuitty 1987), followed by the Mediterranean with 103 species in 68 localities (Angelier 1950, 1954, Monniot 1961, 1962a, 1962b, Morselli 1969, 1970, Mari and Morselli 1989, Martínez, García-Gómez et al. 2021). Conversely, we know 63 species in 42 localities within the Lusitanian province (Trouessart 1896a, b, André 1946, Bartsch 1976c, Giere 1979, Riesgo et al. 2010). The Black Sea has the lowest number of species listed: 52 species in 18 localities (Viets 1928b, 1935, Motas and Soarec 1940, Bartsch 2001).

The marine province with the highest estimated total richness (according to the Chao2 estimator) is the Mediterranean with 158 expected species (Fig. 1B), representing 65% of the known richness. In second place is the North European Seas with 143 expected species (Fig. 1E), representing 83% of the known richness. This is followed by the Lusitanian province with

120 expected species (Fig. 1D), which is 53% of the known species richness for this province. Finally, the Black Sea (Fig. 1C), for which 68

species are estimated, which is 77% of the known richness.

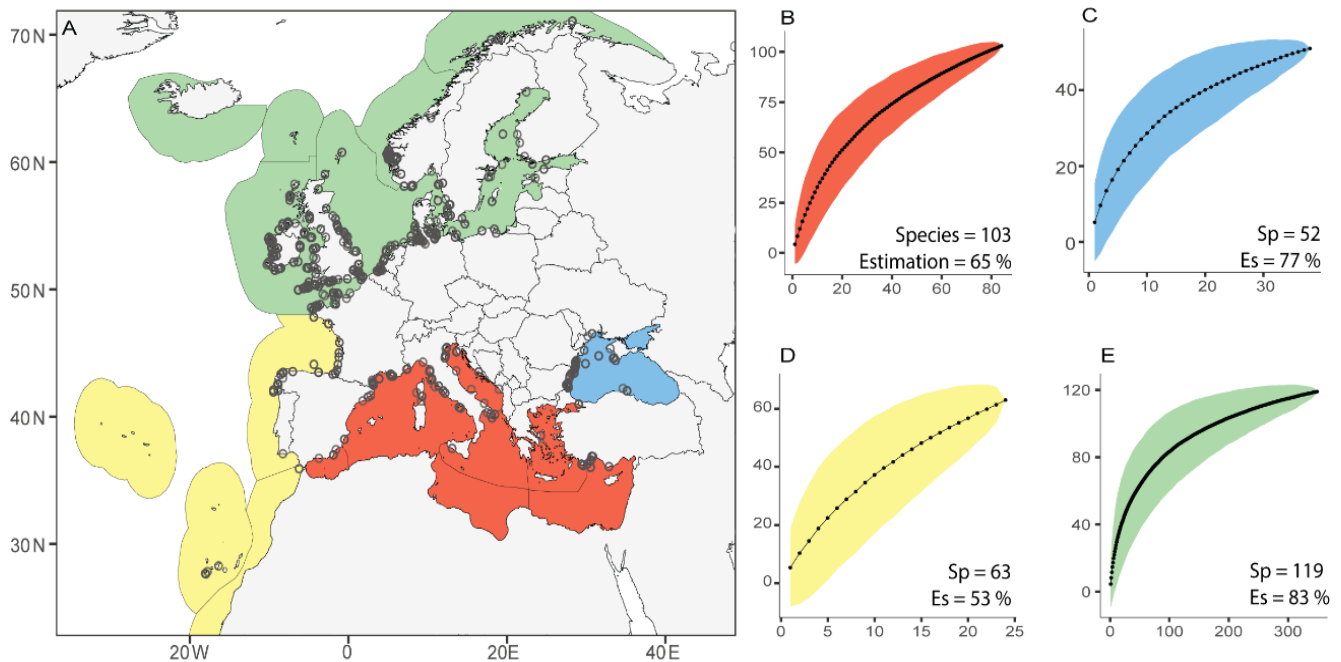


Figure 1. Number of species in our database, and estimated coverage based on Chao2 estimator. (A) Covered localities plotted on the corresponding marine province. Only the borders of the targeted countries are shown. Accumulation curves are presented for the (B) Mediterranean, (C) Black Sea, (D) Lusitania, and (E) Northern European Seas. Each plot shows the total number of species recorded in each province (Sp) and the estimated coverage (Es).

Dataset

This dataset consists of one unique table (as a .csv file, comma delimited), in which each row represents the single record of an halacarid species in one geographical point. Moreover, 28 additional variables are reported for each record (Table 1).

Dataset name: Marine Halacaridae from European waters.

Format name: xls/x/csv.

Character encoding: UTF_8.

Distribution: the data set is available as a supplementary material to this paper.

Date of publication: 15 July 2022.

Date of last review: 15 July 2022.

Update policy: none.

Language: English.

Resource citation: Rubio-López I., Pardos F., Martínez A., García-Gómez G., 2022. A dataset of European marine mites (Trombidiformes, Halacaridae). *Biogeographia*, 37, a018.

Management details

Database manager: Iñigo Rubio López.

Temporal coverage: from 1836 to 2022.

Record basis: Literature records.

Sampling methods: The data set was created collating different data sets and sampling records included in several published scientific papers.

Funding grants: None.

Geographic coverage

Study area: Europe, covering all coastal countries as well as the four marine provinces

within the Temperate Northern Atlantic realm defined by MEOW (Spalding et al. 2007): (1) Northern European Seas (NES), including South and West Iceland, Faroe Plateau, Southern Norway, Northern Norway and Finnmark, Baltic Sea, North Sea and Celtic Seas; (2) Lusitania (L), containing the South European Atlantic Shelf, Saharan Upwelling and Açores-Canary Islands-Madeira-Selvagens, (3) Mediterranean Sea (M), composed of the Adriatic Sea, Aegean Sea, Levantine Sea, Tunisian Plateau/Gulf of Sidra, Ionian Sea, Western Mediterranean and Alboran Sea and (4) Black Sea (BS).

Bounding box: 70°-20° N, 50°W - 50° E; WGS84 reference system.

Countries: Bulgaria, Croatia, Denmark, Estonia, Finland, France, Germany, Greece, Iceland, Ireland, Italy, Montenegro, the Netherlands, Norway, Poland, Portugal, Romania, Spain, Sweden, Turkey, Ukraine, United Kingdom.

Sampling design: The data set includes all the available publications on marine European Halacaridae, to the best of our knowledge, through standardised literature search using Google Scholar. We also added 47 new and unpublished records, mainly for the Iberian Peninsula and the Canary Islands.

Biogeographic region: Temperate Northern Atlantic realm.

Quality control for geographic data: Quality control was performed by displaying coordinates within the MEOW boundaries using the package *mapview* as implemented in R (v. 2.10.0, Appelhans et al. 2016). Anomalous records were individually revisited and amended.

Ecological data

Habitat type: Habitats were reported as they were found in the original literature. Some examples include gravel, coarse sand, mud, *Posidonia oceanica* meadows, *Zostera* spp. meadows, or algae. All those habitats were afterwards grouped into four categories: inorganic hard substrate, inorganic soft substrate, organic substrate with vegetal origin, and organic substrate with animal origin.

Depth: Depth range varies from intertidal to 4400 metres. Depth limits were categorised following the zonation by Templado et al. (2012). The boundary between shallow waters and deep sea was established at 200 metres.

Quality control for ecological data: Assignment of each record to any depth category and habitat was verified with the current knowledge regarding the ecology of each species, if available.

Literature search

Literature search method: We used Google Scholar to search all the available literature from 1836 to 2020. The queries included the words terms “Halacaridae”, “halacarid”, “marine mite*”, “Acari” followed by the geographical term “Europe”. From all the resulting literature, the records for the selected area were retained.

Literature list: A total of 260 original publications were carefully vetted to gather the data for marine halacarid mites.

Quality control for literature data: The completeness of the literature was confirmed by repeating the search twice, cross-checking with the literature lists reported in each paper, and against the reference lists available at the World Register of Marine Species (WoRMS) and Global Biodiversity Information Facility (GBIF).

Taxonomy

Taxonomic ranks: All extant Halacaridae taxa were considered in this database.

Species names: Only the current accepted name (according to WoRMS) has been compiled in the dataset. In a different column the synonyms for each species name can be checked. APHIA ID numbers have been included for each species, to facilitate the retrieval of the information.

Taxonomic methods: Field sampled Halacaridae were identified to the lowest possible taxonomic rank following the available literature and WoRMS resources.

Taxonomic specialist: Guillermo García-Gómez and Iñigo Rubio López.

Quality control for taxonomic data: All included taxonomic ranks have been verified by using WoRMS resources and checking Bartsch (2009). APHIA ID numbers for each species have been included to ensure quality control.

Taxonomic and ecological remarks: In the taxonomic remarks column of the dataset there is information on the synonyms. In the same column we also note the records allegedly flagged as dubious (e.g., misidentifications, *nomina dubia*, etc.). Species identification of European marine mites has been to date entirely morphological. Therefore, we also acknowledge there may be cryptic species' complexes within each of the reported species, warranting further research. The information on the biology, habitat, and/or ecology given in the original sources for each record can be found in the ecological remarks column of the dataset.

DISCUSSION

Despite the halacarid fauna in Europe is comparatively well studied (Bartsch 2004), our data relies on the available literature, whose heterogeneity regarding quality and degree of detail explains the gaps in our metadata and the biases in the distribution of the data.

The main bias in our dataset is related to the nature of the available publications, most of which had a taxonomic or faunistic scope and therefore lack estimations on species abundances. Because most of these papers reported single or very few records for a selected group of species (e.g., André 1939, 1940, 1941, 1942, Bartsch 1982, 1983a, 1983b, 1986, 1987, 1989b, 1992, 1998a) or a given geographic area (e.g., Bartsch 1975a, 1975b, 1976a, 1976b, 1979, 1980, 1985, 1991, 1996a) but do not address the whole halacarid communities, our dataset does not allow to unequivocally report species' absences nor precise species' abundances. We only recovered eight ecological studies that analysed halacarids at the

community level, providing a standardised sampling effort and a robust estimation for abundances allowing for reliable comparisons in the future (Bartsch 1978, 1979, Pugh and King 1985, Somerfield and Jeal 1995, 1996, Riesgo et al. 2010, Martínez, García-Gómez et al. 2021, García-Gómez et al. 2022).

Another source of heterogeneity in our dataset is geographically related, as there are areas that have been intensively studied (e.g. Roscoff, see Bartsch 1975a, 1976a, 1976b, 1977a, 1977b, 1979, 1980, 1984), but others have been historically entirely dismissed (e.g. Iberian Peninsula, see Riesgo et al. 2010, Martínez, García-Gómez et al. 2021, García-Gómez et al. 2022) (Fig. 1A). Indeed, the Northern European Seas region concentrates most of the sampling effort and its halacarid fauna might be considered as well known, whereas other regions such as the Lusitanian and Mediterranean provinces have been studied less intensively (Bartsch, 2004). The fact that we estimate 78% of the Black Sea halacarid fauna is known is not surprising, as this is the smallest province and has been comprehensively surveyed (Bartsch 1996, 2001, 2004, 2013, but see Durucan 2020 for a review). Geographical biases are also found beyond Europe. Halacarids have been extensively studied along the southern coast of South America (Pepato and Tiago 2004, 2005, Pepato and Da Silveira 2015, Pepato et al. 2019), Antarctica (Newell 1984, Bartsch and Pugh 1994, Pugh and Bartsch 1994, Bartsch 1995, 2008, 2016, Marshall et al. 1999, Marshall and Chown 2002) and Australia (Bartsch 1996b, 1998b, 2003a, 2003b, 2005, Otto 1999a, 1999b, 2000a, 2000b, 2001a, 2001b, Viets 1932). In contrast, little is known of the halacarid diversity in the Caribbean, Gulf of Mexico, and Africa (Bartsch, 2004).

Studies should, in theory, comprise statistically unbiased samples of biodiversity across space and time. Nonetheless, as most specimens were collected for qualitative taxonomic purposes, sampling designs were rarely evaluated. Moreover, most taxonomic studies usually favour sampling habitats where

halacarids are known to be abundant, producing an uneven sampling effort across depths and substrata. Most of the research has been performed in the intertidal zone, while surveys in deeper waters are infrequent. Likewise, the halacarid fauna present on algae (Bartsch 1978, 1979, 2004, Pugh and King 1985, Somerfield and Jeal 1995, 1996) has been comprehensively sampled, whereas the nature of the relationship between mites and other animal hosts (e.g. sponges, hydrozoans, bryozoans, barnacles, mussels, polychaetes, crustaceans) is unknown for most of these associations, as live observation of living material has not been executed (Chatterjee 2020, 2021a, 2021b, 2021c).

A final remark might be made regarding the current status of the systematics of Halacaridae, which might provide an additional source of uncertainty. Rigorous species delimitations are critical in evolutionary biology, ecology, conservation, and biogeography (Wiens and Penkrot 2002, Sites and Marshall 2003, Agapow et al. 2004, Rubinoff and Holland 2005, Wiens 2007, Schlick-Steiner et al. 2010). The complexity of species biology requires the study of species boundaries from many, complementary perspectives. There are a variety of methods for delimiting species currently available, and the need of rigour delineating species compels us to apply these methods comprehensively (Sneath and Sokal 1973, Dayrat 2005 but see Valdecasas et al. 2008, Will et al. 2005, Yates et al. 2011). In that regard, it is important to consider that most of the studies on marine mites have relied on morphology—therefore, further research including molecular markers might increase the number of species for any of these areas. Indeed, little is known about cryptic species in Halacaridae, but it has been suggested that certain species might encompass cryptic complexes (Newell 1951, 1984, Pepato et al. 2019, Abé 2021). One reason to expect cryptic species in Acari is the diversification that leads to genetic isolation in the absence of notable morphological differences (i. e. morphological stasis), which

has been reported in many taxa (e.g. Halt et al. 2009, Spencer et al. 2009, Jesse et al. 2010, Szudarek-Trepto et al. 2021). Furthermore, marine mites have relatively inconspicuous morphological traits, as it has been reported for other animals with minute size and minimalistic body structure (Skoracka et al. 2015). Future species' description would benefit for a more integrative approach, including not only DNA sequences but also light, scanning electron, and confocal laser scanning microscopical observations, as it has been demonstrated in other meiofaunal groups (Leasi and Todaro, 2009, Martínez et al. 2013, Bertolani et al. 2011, Worsaae et al. 2015). Considering that in systematics the most prominent and used attributes are morphological, this supports the occurrence of cryptic species in Acari (Skoracka et al. 2015).

It is clear that much remains to be done for halacarids (Fig. 1B-D). Future research might focus both on reporting species list, as well as on species descriptions from the many areas and biotopes that have been historically neglected by marine acarologists (Bartsch 2004). This is not surprising, since it pretty much resembles the reality of other meiofaunal organisms, for which our knowledge remains largely incomplete (Barbosa et al. 2010, Fontaneto et al. 2012). Let this database be a step forward in alleviating those biases.

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AUTHOR CONTRIBUTIONS

GGG and IRL designed this study. AM, GGG, and IRL discussed the structure of the database. IRL reviewed the literature and gathered the records. FP provided the samples, and lab space to perform this work. IRL wrote the first manuscript with significant input from AM and GGG. All authors read and approved the last version of the text.

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