SYMPOSIUM

Managing and Sharing the Escalating Number of Sponge "Unknowns": The SpongeMaps Project

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From the symposium "Assembling the Poriferan Tree of Life" presented at the annual meeting of the Society for Integrative and Comparative Biology, January 3–7, 2013 at San Francisco, California.

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Synopsis Contemporary collections of sponges in the Indo-west Pacific have escalated substantially due to pharmaceutical discovery, national bioregional planning, and compliance with international conventions on the seabed and its marine genetic resources beyond national jurisdictions. These partially processed operational taxonomic unit (OTU) collections now vastly outweigh the expertise available to make them better "known" via complete taxonomy, yet for many bioregions they represent the most significant body of currently available knowledge. Increasing numbers of cryptic species, previously undetected morphologically, are now being discovered by molecular and chemical analyses. The uncoordinated and fragmented nature of many previous collections, however, means that knowledge and expertise gained from a particular project are often lost to future projects without a biodiversity informatics legacy. Integrating these diverse data (GIS; OTUs; images; molecular, chemical, and other datasets) required a two-way iterative process so far unavailable for sponges with existing biodiversity informatics tools. SpongeMaps arose from the initial need for online collaboration to integrate morphometric data with molecular barcodes, including the Porifera Tree of Life (PorTol) project. It provides interrogation of existing data to better process new collections; capacity to create new OTUs; publication of online pages for individual species, so as to interpret GIS and other data for online biodiversity databases and services; and automatic links to external datasets for taxonomic hierarchy, specimen GIS and mapping, DNA sequence data, chemical structures, and images.

Introduction

Despite many decades of concerted effort exerted in searching for new bioactive marine natural products (secondary metabolites) (MNPs), it has been suggested that less than 10% of the world's marine biodiversity has been evaluated so far (Dias et al. 2012). If true, this continues to present huge opportunities for discovery of unique structural diversity, especially low-molecular-weight lead-compounds as potential new candidates for beneficial drugs (Dias et al. 2012). Does the evidence from biodiversity support these claims, and what proportion of species is currently "known" (described) versus "still unknown" (i.e., still awaiting discovery or collected but not yet identified)?

Among all marine animals, sponges (Phylum Porifera) continue to be the most productive sources of new bioactive compounds, accounting for approximately 50% of all MNPs discovered between 1990 and 2009 (Leal et al. 2012). Sponges are found in all the world's oceans and in many freshwater habitats, often dominant in the structural benthos. Approximately 8500 species are known (described and considered valid; World Porifera Database

Table 1 Number of "known" (described) and "unknown" (estimated) species of the most bioactive marine invertebrate phyla with their relative importance to the MNPs industry

Higher taxon	Phylum (class) bioactive taxa[a]	Described species[b]	Model: number estimated species (lower)[c]	Model: number estimated species (higher)[c]	Model: number estimated species (mean)	Model: % known species[c]	Number of new MNPs discovered since 1990[a]	% MNPs discovered since 1990[a]
Metazoa	Porifera	8553	25,853	26,553	26,203	32–33	4787	49
Eumetazoa	Cnidaria (Anthozoa)	6323	8847	9976	9412	62–79	2775	29
Eumetazoa: Bilateria: Lophotrochozoa	Ectoprocta (=Bryozoa)	5900	8700	11,100	9900	53–68	198	1
Eumetazoa: Bilateria: Lophotrochozoa	Mollusca	51,689	135,887	164,107	149,997	28–36	570	6
Eumetazoa: Bilateria: Deuterostomia	Echinodermata	7291	9617	13,251	11,434	55–76	805	8
Eumetazoa: Bilateria: Deuterostomia	Chordata (Tunicata)	3020	4600	5100	4850	59–66	677	7
	Total marine Eukarya species	230,187	704,977	972,128	838,553	27–28	9812	100

[a]Based on data from Leal et al. (2012); MNPs, marine natural products 1990–2009. [b]Based on data from the WoRMS (Appeltans et al. 2012a). [c]Based on the model of Appeltans et al. (2012b).

[WPD]; Van Soest et al. 2012b), yet it is postulated that this number represents only about one-third of the unknown (i.e., estimated) species (Appeltans et al. 2012b) (Table 1). Further, Leal et al. (2012) noted that while only 7.4% of all Porifera species have yielded new MNPs since 1990, this remains significantly higher than the proportion for Cnidaria (2.8%) and Echinodermata (2.1%) combined (Fig. 1). All three phyla have an approximately equivalent number of described species (Table 1), but for Porifera this represents only about 35% of the total estimated fauna. This makes sponges a useful economic model organism for investing efforts in their biodiversity informatics, whereas presently our estimates of their diversity and distributions are still largely matters of guesswork.

A recent synthesis of estimates of diversity for all marine eukaryotic species recovered an upper estimate of approximately 1 million species worldwide—based on (1) known (valid) published marine species (currently ∼220,000–230,000 species; World Register of Marine Species (WoRMS); Appeltans et al. 2012a), (2) statistical modeling of species' discovery, author productivity, and rates of synonymy, and (3) expert opinion of the content of unpublished marine collections, rates of cryptic morphospecies, rate of discovery of molecular cryptic species, and "average numbers of unknowns" encountered in marine field surveys (Appeltans et al.
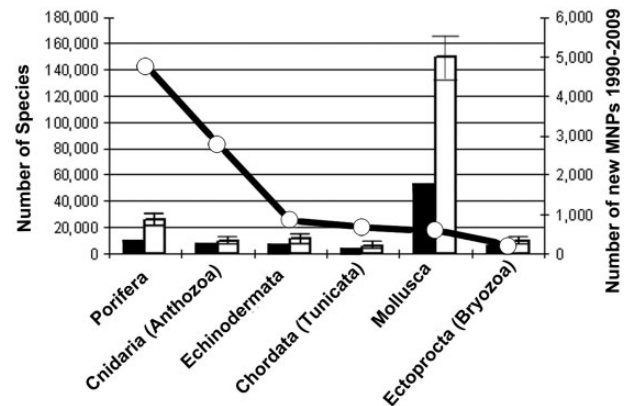

Fig. 1 Number of "known" (described) species (black columns) and "unknown" (estimated) species (white columns, with low- and high-confidence limits of these estimates indicated) of the most bioactive marine invertebrate phyla with the number of new MNPs discovered from them between 1990 and 2009 (black line). Data reanalyzed from Leal et al. (2012), Appeltans et al. (2012b), and WoRMS (Appeltans et al. 2012a).

2012b). This was a surprisingly more conservative estimate than previous models based on other methods of assessment: most recently 1.4–1.6 million eukaryotic marine species globally (extrapolated by Bouchet 2006), ∼2.2 million (±0.18 million) species (predicted by Mora et al. 2011), 1 million species of marine nematodes alone (Lambshead and Boucher 2003), and up to 10 million species possibly in the

deep sea alone as suggested by Grassle and Maciolek (1992). Over time our estimates of marine biodiversity asymptote toward the real counts; however, confidence levels for 2012 are still very uncertain—including those of sponges.

Notwithstanding that there are many species yet to be discovered in the oceans, for many or even most phyla, there are already existing vast *ex situ* collections hiding in museums and herbaria around the world. These collections range from partially sorted and identified to unsorted, and await timely taxonomic resolution to move from the realms of the "unknown" to the "known." This challenge was a basic tenet in the design of the recent Census of Marine Life 2000–2010 (CoML; www.coml.org), based on the economic financial uncertainty principle of "the known, unknown, and unknowable," with marine discovery focused on consolidating the "known," and what was within our current limits of understanding to discover the "unknown" that was not hindered by the pursuit of the largely technologically dependent "unknowable." These disclosures helped to chose which key environments to explore so as to maximize future knowledge that was at least achievable within available technologies, tools, and resources (Ausubel 2007). During the decade 2000–2010, the CoML acquired, among other things, millions of specimens collected from local to very remote oceanic habitats and 30 million digital observations; formed an affiliation with the WoRMS to compile an inventory of over 190,000 known marine species (Costello et al. 2013a); discovered potentially 6000 new species with ~1200 of them published by 2010 (Costello et al. 2010); facilitated over 80,000 species-pages published online by the Encyclopaedia of Life (EOL 2012); built a DNA library of over 37 000 marine eukaryote specimens and so far conducted genetic barcoding on 6200 species (Steinke 2012; Marine Barcoding of Life Initiative [MarBOL]); and found that many putative rare species were common and more widely distributed than previously known (Ausubel et al. 2010).

These new initiatives also included major acquisitions of sponges (see Van Soest et al. 2012a), primarily driven by the search for new pharmaceutical compounds, and from which clear evidence has emerged that bioactive compounds are not uniformly distributed across all orders of sponges (Fig. 2) or families (Fig. 3), and indicating the crucial role of more rapid and accurate taxonomic processes required to improve efficiencies in targeted collecting (dereplication) for MNPs. The legacy of these new collections (plus those already within the world's biodiversity collections prior to 2000) is that there
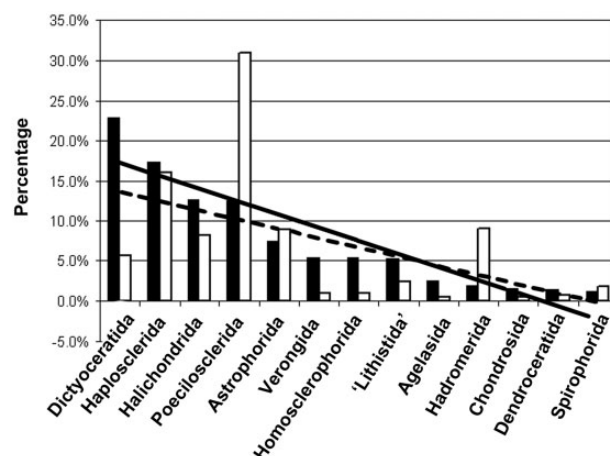
Fig. 2 Proportion of orders of Demospongiae with bioactive species (ranked from most bioactive to least bioactive), compared with known species diversity within each order. (Percentage of bioactive species, black columns, with solid linear trend line $R^2 = 0.8503$; percentage of known species diversity for each order, white columns, with dotted linear trend line $R^2 = 0.2679$). Raw data reanalyzed from Leal et al. (2012) and the WPD (Van Soest et al. 2012b; accessed on December 28, 2012). The "Order" Homosclerophorida is now recognized as a distinct fourth class of Phylum Porifera (Gazave et al. 2010). The first eight "Orders" account for 89.4% of all MNPs discovered from Porifera.
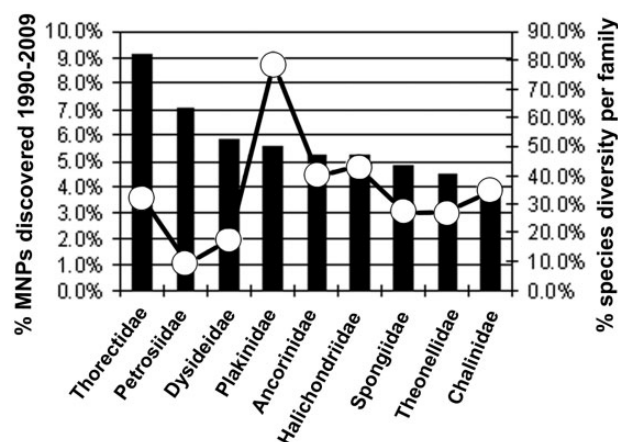
Fig. 3 Percentage of MNPs discovered between 1990 and 2009 for the nine most bioactive Demospongiae and homosclero-morph families (black columns) compared with the percentage of species diversity for each family relative to each order (white dots). Raw data reanalyzed from Leal et al. (2012) and the WPD (Van Soest et al. 2012b; accessed on December 28, 2012).

is now a very significant lag between collecting and documenting all the specimens, defining these within the Linnaean systematics, and making their unequivocal identities and distributions widely accessible—the differential being a gap between the "adequately

known," the "poorly known," and the "unknown" in the order of one or more magnitudes.

Contrary to some phyla (Costello et al. 2013b), expertise in sponge taxonomy continues to decline (i.e., the capability to process these growing collections of "unknown" sponge taxa based on their phenotypic characters) and threatens taxonomic productivity ("The Taxonomic Impediment"; Global Taxonomic Initiative [GTI] 2011). Conversely, biodiversity informatics and analytical tools (cybertaxonomy) and multiple datasets (particularly genetic barcoding) have become more widely accessible and sophisticated (Deans et al. 2012), promising a more rapid delivery of taxonomic end-products (Costello et al. 2013a), including those related to sponges (see brief review by Van Soest et al. 2012a).

For all these reasons, we have focused on the challenge of more rapidly documenting the world's sponge fauna that are already hiding in collections, and the development of an online, collaborative, integrative taxonomic infrastructure that fills the gap between collecting and curating collections at one end of the pipeline (e.g., aggregated museum databases such as the Online Zoological Collections of Australian Museums [OZCAM 2012]), and publishing formal taxa at the other end (e.g., as summarized by the WPD; Van Soest et al. 2012b). It is anticipated that this collaborative infrastructure, SpongeMaps (Hall 2013), will significantly progress the potentially hundreds of thousands of taxa through the taxonomic pipeline.

Results

Purpose

SpongeMaps grew from the frustration of a few sponge researchers working independently on many very large and often isolated collections worldwide. Its main purpose is to move multiple collections of sponges and multiple datasets, such as information hidden in notes, databases, image files, and other isolated datasets held by individual researchers, into a collaborative online workspace.

Unlike other "high-end" biodiversity taxonomic tools such as Scratchpads (Smith et al. 2012), LifeDesks (LifeDesks 2012), and IdentifyLife (http://www2.identifylife.org/index), SpongeMaps objectify the earlier processes of sponge taxonomy in providing a "universal" system of operational taxonomic units (OTUs or morphospecies concepts) in which collaborative inputs and selections of characters would more likely lead to similar taxonomic prognoses. By exposing individual raw datasets within a collaborative workspace, the likelihood of related species being assigned to different taxa would be reduced—minimizing duplication of effort and error, and especially improving efficiencies for those working independently on extensive marine surveys from similar, geographically adjacent faunas. SpongeMaps does not try to replicate the features of these other biodiversity informatics tools because its primary purpose is to promote collaboration on raw datasets behind password protection. Its data outputs, however, are delivered in formats useable by these other online tools. SpongeMaps also provides opportunities between collaborators to debate taxonomic identifications for particular taxa in real time and behind password protection, with the ability to collaboratively annotate descriptions of species. In this way, accelerating initial sorting of raw collections to OTU level, and detecting and correcting early misidentifications during the sorting process, can be achieved. Over time, with input by the international community of researchers on sponges, a large and more reliable dataset would become the first point of reference for those needing to sort and identify collections of sponges to an OTU-level taxon. For the present, however, SpongeMaps contains data that are pertinent mainly to the six major independent Australian sponge collections (there is no national museum of Australian natural history), but with ambitions to become international in its focus and content.

Initially, SpongeMaps' main developmental application (and funding for its development) was to provide biological context to specimen GIS datapoints on the various online biodiversity databases (such as the Ocean Biogeographic Information System [OBIS 2012] and Global Biodiversity Information Facility [GBIF 2012]) that feed into the biodiversity informatics data tools, such as the EOL (2012) and Atlas of Living Australia (ALA 2012). Another initial application was to develop an online support tool to integrate morphometric data with genetic barcodes for the MarBOL (Steinke et al. 2012) and Sponge Barcoding Projects (SBPs) (Wörheide et al. 2012). Presently, these morphological data and images supporting SBP sequence data are static and consequently are regularly out of date as information is revised and updated by the taxonomic community, and furthermore with manual uploading required by the SBP website. Automatic periodic harvesting of data from SpongeMaps provides a more iterative collaboration to maintain currency of the morphological data that supports the SBP. More recently, with the near completion of the recent Porifera Tree of Life (PorTol) project (Thacker et al. 2012), SpongeMaps offers a useful platform for incorporating all sequenced taxa

into a unified OTU system, exposing them to collaboration among the taxonomic community.

In its basic form, SpongeMaps is primarily a collaborative workspace that focuses on data from specimens, aggregating these into OTUs, providing infrastructure to compare images, descriptions, information about distribution, and other datasets in real time. The brief descriptions and accompanying datasets (such as GIS, images, and sequence data) posted on or linked to SpongeMaps are intended to provide key features that allow recognition both of similarities and differences among specimens. These traits form the basis of the next steps in the discovery and description of new taxa, and also more confident knowledge of the features and distributions of known taxa. Using multiple datasets from multiple collections—including the growing number of sponge DNA sequences—this latter aspect was seen as an important tool for more accurately analyzing species' distributions with less-complete reliance on the older published literature (e.g., Wörheide and Erpenbeck 2007). Although not designed to deliver fully formatted and comprehensively referenced taxonomic descriptions, SpongeMaps will certainly contribute to building online species-pages and eventually form the basis of peer-reviewed taxonomic descriptions, thus filling the gap within existing cybertaxonomic tools and aiming to facilitate the laborious formal taxonomic process.

SpongeMaps has private (password protected) and public portals. The former is a protected working space where individuals can collaborate for all taxa (irrespective of whether formally named in the Linnaean classification or only to an OTU level), with read-only (member), full editorial, and administrative levels of membership. Once individual editors (or consortia of collaborators) reach agreement and decide to release these taxa, SpongeMaps publishes species-pages directly to the online databases, and the latter similarly harvest image and other data reciprocally. Conversely, the public portal allows access to only those species that have been released online. These latter currently include only formally published taxa (∼20% of sponge OTUs in SpongeMaps), but eventually also some unnamed taxa (e.g., OTUs that underpin a chemical or molecular profile or dataset).

History

SpongeMaps.wiki (https://wiki.trin.org.au/Marine/Sponges/WebHome)

In its first iteration (Jolley-Rogers 2012), SpongeMaps was developed as a wiki based on the Foswiki project (Taxonomic Research and Information Network

[TRIN] 2012). This first iteration initially contained only data from the Queensland Museum Sessile Marine Invertebrate collection (numbering ∼31,000 specimens in ∼4500 OTUs), most identified only to OTU level and suspected of containing a large number of new taxa. Subsequently, other small datasets were incorporated from the Museum and Art Galleries of the Northern Territory, Western Australian Museum, and Australian Institute of Marine Science sponge collections from Australasia, and the University of Utah College of Pharmacy collection from Papua New Guinea, Solomon Islands, and Vanuatu. More data from other Australian sponge collections are soon to be added. Additional partners currently include the GeoBio-Center of the Ludwig-Maximilians-Universität Munich, Germany, producing molecular sequence data through the SBP (Wörheide et al. 2012), and with reciprocal morphological data from SpongeMaps to support the sequence data in the SBP; chemical data from the Eskitis Institute for Cell and Molecular Therapies, Griffith University, Brisbane; and anticipated to include the Porifera Tree of Life consortium (Thacker et al. 2012). Other international datasets will be sought once the SpongeMaps platform is fully operational and stable. Acceptance criteria include registered, georeferenced specimen data (preferably live), images, basic morphometric descriptions, and some level of taxonomic identification.

SpongeMaps.org (http://www.spongemaps.org/)

Building on the TRIN SpongeMaps.wiki structure (Jolley-Rogers 2012), a parallel portal was developed by the Queensland Museum (Hall 2013), using a different database platform (Caspio Bridge; Caspio 2012). Development of this parallel website focused more on managing, linking, and retrieving the various datasets than on manipulating the data—which can be done far more effectively by the purpose-developed online biodiversity informatics tools (such as the ALA and EOL). The emphasis on the SpongeMaps.org database is on fast-tracking collaborative data, assembling, and rapid export to biodiversity informatics portals. Although both versions operate on very different platforms, they have similar inputs and outputs.

Data inputs

Table 2 summarizes the data fields and their functionality in SpongeMaps. GIS data from sponge specimens in Australian collections currently are automatically streamed directly from institutional data-holders via the OZCAM data cache (OZCAM 2012) to the SpongeMaps portals, supported by the ALA (2012).

Table 2 List of data fields and their functionality currently included in SpongeMaps

Data type	Data fields and functionality
Taxonomy	Based on the nomenclature and taxonomic hierarchy of the WPD
Phylum	Name, authority
Class	Name, authority
Subclass	Name, authority
Order	Name, authority
Suborder	Name, authority
Family	Name, authority
Subfamily	Name, authority
Genus	Name, authority
Species	Name, authority, reference, WPD link (URL), institution
Morphology	Based on the standard data fields used by the Porifera research community, with flexibility to add new fields as needed
Description	Growth form, Colour, Oscules, Texture, Surface Ornamentation, Ectosomal Skeleton, Choanosomal Skeleton, Megascleres, Microscleres
Comments	Text field
Reference	Author, year, journal, title
Description Status	ALA and EOL ready (for public release)
Editorial Data	Text field
Specimens	These GIS data are exported directly from the Online Zoological Collections of Australian Museums (OZCAM 2012), based on DwC
Collection data	Museum registration number, locality, nation, longitude, latitude, depth, date, habitat, type status, identifier, reference numbers, comments
Images	Museum registration number, image name, file, photographer, medium, permissions, description
DNA data	GenBank record number, sponge barcoding record number, gene region, DNA sequence, museum registration number
Chemistry data	Chemical name, museum registration number
Chemistry	These data are currently held within SpongeMaps, but will be hosted elsewhere when the database grows significantly further
Chemical compound	CHEMBL link (URL), chemical name, systematic name, molecular formula, molecular weight, chemical family, SMILES code, structural features

The OZCAM schema is a subset of recommended and mandatory fields from the Darwin Core Schema (DwC) (http://www.ozcam.org.au/using-ozcam-data/), with data delivered to the GBIF directly via the ALA (see data standards at http://www.ala.org.au/about-the-atlas/atlas-data/). It is expected that ~50,000 georeferenced sponge specimens will be online by the end of June 2013, 60,000 images (consisting of photographs of *in situ,* on deck, and preserved specimens, light micrographs, SEMs, line drawings, and sketches). GIS data on international specimens of sponges that are not derived from the OZCAM cache (e.g., non-Australian data) can also be harvested from the OBIS (2012). Alternatively, a template for manual upload of data can also be used.

By comparison, data (aggregated morphological descriptions, images) on species of sponges need to be uploaded directly into SpongeMaps via the Member's login (either via individual data-point entry or in batch mode using spreadsheets, as noted above). Image data are currently hosted both by SpongeMaps.wiki and by SpongeMaps.org (Fig. 4), but in the longer term, it is anticipated that these will be hosted by Morphbank (2012).

The taxonomic lexicon that underpins SpongeMaps classification is provided by the WPD (Van Soest et al. 2012b), and the Australian Faunal Directory (Hooper 2012)—the latter with more details on type material, synonyms, and distributions for the Australian fauna than occurs in the WPD, but the former with species distributions beyond the Australian marine jurisdiction. The WPD also contains the primary taxonomic literature (at least those works not protected by copyright). SpongeMaps harvests GenBank (www.ncbi.

Fig. 4 Screen shot of a species-page from SpongeMaps.org, for the bioactive sponge *Pipestela candelabra* (also known as the "Bob Marley sponge" on account of its growth form), that was only described as new to science in 2008 despite being among the most widely distributed and moderately abundant species within the island arc across faunas of the Great Barrier Reef, Papua New Guinea, and Solomon Islands. It was discovered to have new tripeptide chemical compounds (the hemiasterlins, milnamide, and geodiamolide) that showed high bioactivity against certain animal cell lines and are now in preclinical trials for the treatment of cancer.

nlm.nih.gov) sequence data (at least those that are verified by registered museum specimens), and SBP database sequence data, with the latter reciprocally harvesting specimen GIS and morphological information contained within SpongeMaps (Wörheide et al. 2012). Chemical data via SMILES codes (and decoded within SpongeMaps to produce structural elucidation) are currently provided by Griffith University, but with opportunities for additional datasets and functionality.

Data outputs

SpongeMaps outputs are primarily individual "species-pages" published directly to the online portals (presently EOL and ALA) once released by the owners of the data. These datasets presently include morphometric descriptive data, images, geospatial specimen data (DCS), DNA sequences, and chemical structures contributed by members of the sponge taxonomic community. Once published these data are freely available to the public and provide biological context to the GIS data points online (OBIS, EOL, and ALA), and especially to those specimens identified only to the OTU-level, having not yet been formally named within Linnaean systematics.

Future developments

The present taxonomic pipeline targets the publishing of 500 sponge species-pages to the ALA and EOL by July 2013, including only formally named taxa. In the medium term, ~5000 OTU-level taxa currently known from the Australian faunal collections will be rationalized across the state and territory museum collections, aiming to provide a single unified OTU system. In the longer term, international datasets will be incorporated into the SpongeMaps OTU system, providing a better objective basis to test both the alleged widely ranging species' distributions and the plethora of geographically more restricted endemic species emerging from studies on sponges (e.g., Hooper et al. 2002). Although maintaining a policy of keeping the scope of the SpongeMaps platforms as simple as possible (to maintain its functionality and uptake by the community), it is anticipated that a mapping tool will be added to enable users to visualize their data—especially for those datasets that have not yet been harvested by the biodiversity informatics public portals such as the ALA and EOL.

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